

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:29:07 ; Search time 4527.51 Seconds
(without alignments)
18316.216 Million cell updates/sec

Title: US-09-325-095-32

Perfect score: 3412
Sequence: 1 ATGCTTCGAAGACCATCATC.....TAAACTAGTTCATTTCAAAA 3412

Scoring table:

IDENTITY NUC
Gapop 10*0, Gapexc 1*0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_estdb:*
3: em_estdb:*
4: em_estdb:*
5: em_estdb:*
6: em_estdb:*
7: em_estdb:*
8: em_estdb:*
9: gb_estc1:*
10: gb_estc1:*
11: gb_estc1:*
12: gb_estc1:*
13: gb_estc1:*
14: gb_estc1:*
15: em_estfun:*
16: em_estfun:*
17: em_estfun:*
18: em_estfun:*
19: em_estfun:*
20: em_estfun:*
21: em_estfun:*
22: em_estfun:*
23: em_estfun:*
24: em_estfun:*
25: em_estfun:*
26: em_estfun:*
27: em_estfun:*
28: gb_estc1:*
29: gb_estc1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2387.2	70.0	3866 11 AK051885	AK051885 Mus muscu
2	806	23.6	872 13 BQ228953	BQ228953 AGENCOURT
3	739.4	21.7	750 9 AL706270	AL706270 DKF2P6860
4	722	21.2	1063 12 BM470620	BM470620 AGENCOURT

Result No.	Score	Query Match Length	DB ID	Description
5	719.4	21.1	834 13 BX437220	BX437220 AGENCOURT
6	678.8	19.9	883 13 BU167122	BU167122 AGENCOURT
7	678.2	19.9	827 13 BX437219	BX437219 AGENCOURT
8	666	19.5	753 10 BG497751	BG497751 602543009
9	641.2	18.8	854 14 CB723732	CB723732 UI-M-PYO-
10	633	18.6	809 14 CB246283	CB246283 UI-M-ROO-
11	612	17.9	753 12 AU129890	AU129890 AGENCOURT
12	609.8	17.9	833 12 BM986382	BM986382 EST531169
13	607.8	17.8	759 14 CB520825	CB520825 UI-M-GHO-
14	607.2	17.8	789 13 BU852815	BU852815 AGENCOURT
15	603.6	17.7	785 14 CD349473	CD349473 UI-M-PYO-
16	602.8	17.7	706 9 AU134684	AU134684 AGENCOURT
17	594.2	17.4	844 10 BG31265	BG31265 602417308
18	566.2	16.6	1051 12 BG974639	BG974639 602844877
19	560.8	16.4	730 13 BU481912	BU481912 603470693
20	560.6	16.4	696 14 CD351100	CD351100 UI-M-PYO-
21	554.6	16.3	627 2 HSM084196	HSM084196 Homo sapi
22	551.6	16.2	864 10 BF242935	BF242935 601877985
23	544.2	15.9	759 12 BG867168	BG867168 602786782
24	540.6	15.8	798 10 BG436153	BG436153 602508555
25	540.2	15.8	836 10 BF691754	BF691754 602248287
26	538.4	15.8	548 9 AU280420	AU280420 AGENCOURT
27	534.8	15.7	767 14 CB964053	CB964053 AGENCOURT
28	532.4	15.0	601 10 BE379970	BE379970 601159472
29	506.4	14.8	784 14 CA511243	CA511243 UI-R-FUO-
30	501.8	14.7	505 2 HSM096925	HSM096925 Homo sapi
31	500	14.7	636 9 AV693521	AV693521 AGENCOURT
32	499.6	14.6	533 10 BE279196	BE279196 601156673
33	492.6	14.4	818 13 BU106943	BU106943 603739688
34	491.2	14.4	685 10 AW914263	AW914263 EST345567
35	489.8	14.4	614 13 BU478467	BU478467 603470610
36	486.2	14.2	663 10 BB657738	BB657738 BB657738
37	485	14.2	613 12 B1249391	B1249391 60295709
38	480.6	14.1	841 14 CA791375	CA791375 AGENCOURT
39	480.4	14.1	918 12 BF764374	BF764374 602110149
40	476.8	14.0	887 14 CA986999	CA986999 AGENCOURT
41	472	13.8	600 12 BG806901	BG806901 2042-70 M
42	466.6	13.7	531 9 AW209721	AW209721 u146d02.Y
43	466.2	13.7	978 13 BQ933837	BQ933837 AGENCOURT
44	461.8	13.5	563 13 BQ570031	BQ570031 g1143B05.
45	449.8	13.2	633 9 A1632172	A1632172 t885g07.x

ALIGNMENTS

RESULT 1
AK051885
LOCUS
DEFINITION
Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
enriched library, clone: D2J015E05 product: phosphatidylinositol
3-kinase, catalytic, alpha polypeptide, full insert sequence.
ACCESSION
AK051885
VERSION
AK051885.1 GI:26094824
HITS: CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M.,
Sunt,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
11076861
4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Kono,H., Adachi,D., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,K.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,T., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staudt,F., Suzuki,R., Tomita,M.,
Wagner,L., Mashio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hochmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzei,L.J., Mombereis,P., Nordone,P.,
Ring,B., Rimpold,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seta,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-Oka,K., Wang,K.H., Weitz,C., Whitaker,C., Williams,J.,
Wyshak-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,M., Kohlschki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3866)

REFERENCE
AUTHORS
JOURNAL
MEDLINE
PUBMED
11217851
6
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
Hoti,P., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shitaki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akihira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.go.jp,
URL:ftp://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:ftp://genome-gsc.riken.go.jp/
URL:ftp://fantom.gsc.riken.go.jp/
Location/Qualifiers

Source
1. 3866
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM:DB:230015E05"
/db_xref="taxon:10090"
/clone="D3J0015E05"
/issue_type="eyeball"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
misc_feature
1. 3866
/note="phosphatidylinositol 3-kinase, catalytic, alpha
polypeptide (MGDI:1206581, GI:NM_008639, evidence:
BLASTN, 99%, match=2855)"

BASE COUNT 1149 a 786 c 878 g 1053 t
ORIGIN
Query Match 70.0%; Score 2387.2; DB 11; Length 3866;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2663; Conservative 0; Mismatches 398; Indels 7; Gaps 3;
Oy 345 AGAATGTTGTTTCTGATCGCATCGCATGTCGGAATTTGATGTTGTTAAAGATCTGA 404
Db 33 ACATTTTCGTTTCTTTATTTGGCATGCCAGTGTGGAATTTGATGTTGTTAAAGATCTGA 92
Oy 405 AGTACAGACTTCGGAAGAAATATCTTAAATGTTTGAAGAACTGTGATCTTACGGA 464
Db 93 AGTCCAGACTTTCGGAAGAAATCTTGAATGTTTGAAGAACTGTGATCTTACGGA 152
Oy 465 TCTTAATTCATCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 524
Db 153 TCTTAATTCATCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 212
Oy 525 AGACTCCGAAGACAT 584
Db 213 AGAATCTCCGAAGACAT 272
Oy 585 GGTAAATGTTTCTTCAAAAT 644
Db 273 GGTAAATGTTTCTTCAAAAT 332
Oy 645 TGTGTCGAAGCAAT 704
Db 333 TGTGTCGAAGCAAT 392
Oy 705 ATGGAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 764
Db 393 CTGACGACGATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 452
Oy 765 TGAATGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 824
Db 453 TGAATGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 512
Oy 825 CTGATTAATGCTTGGAGAGATGCGCAATTTGAAGATGATGCTTAATTAATTAATTAAT 884
Db 513 CTGATTAATGCTTGGAGAGATGCGCAATTTGAAGATGATGCTTAATTAATTAATTAAT 572
Oy 885 TCAATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 944
Db 573 TCAATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
Oy 945 ACCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
Db 633 ACCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692
Oy 1005 AATTAATATCTTTGTCGAACCTTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1064
Db 693 AATTAATATCTTTGTCGAACCTTAAGATGATGATGATGATGATGATGATGATGATGATGAT 752
Oy 1065 TGTTCGAACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1124
Db 753 TGTTCGAACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 812

OY	1125	AGTACCTGTTCCATCCAGGTGGAAATGAAGGCTGAAATTAATGATATATACATCTCCGA	1183
Db	813	AGTACCTGTTCCAAATCCTAGGTGAAATGAAGGCTGAAATTAATGATATATACATCTCCGA	872
OY	1185	TCCTCTGTCGTGCTCGACCTTTGGCTTCCATTTGGCTCTGTGTAAAGGCCGAAGGGTGC	1244
Db	873	TCTTCTGTGTGCTGGCCCTTTGGCTTCCATTCGTCTGTGTAAAGGCCGAAGGGTGC	932
OY	1245	TAAAGAGAAACACTGTCCATTGGCATTGGGAAATATAAACTTTGTTGATTACACAGAC	1304
Db	933	TAAAGAGAGACACTGTCCGTGGCTCGGGGAAACATAAATCTGTTGATTATACAGAC	992
OY	1305	TCTACTATCTGGAAAAATGCGTTTGAATCTTTGGCCAGTACTCTCATGGAATTGAAGATT	1364
Db	993	CTTAGTGTCCGGGAAATGCGTTTGAATCTCTGGCCGTCTATCCGATGGGATTGAAGAACT	1052
OY	1365	GCTGAACCTTAATGSGTGTACTCGATCAAAATCCAAATAAAGAAATCCATGCTTAGAGTT	1424
Db	1053	GCTGAACCTTAATGSGTGTACTCGGATCAAAATCCAAATAAAGAAATCCATGCTTAGAGTT	1112
OY	1425	GGAGTTTGACTGTGTCAGCAGTGTGTAAAGTTCCAGATAATGCAAGTATGGAAGACA	1484
Db	1113	GGAGTTTGATTGTTCACAGAGTGTGTAAAGTTTCCAGATATGTCATGTCGAAGACAA	1172
OY	1485	TGCCAATTGTGTCTGATATCCCGAAGAACAGAGATTAGCTATTTCCACGAGACTGAGTAA	1544
Db	1173	TGCCAATTGTGTCCGTGCCGGAAGCTGGAATTCAGTTACTCCATACAGACTGAGTAA	1232
OY	1545	CAGACTAGCTAGAGCAATGAATTAAGGAAAAATGACAAAGACAAGCTCAAGCAATTTC	1604
Db	1233	CAGACTAGCTCAGAGCAATGAGTTTAAGAAAAATGACAAAGACAAGCTCCAGACAATTG	1292
OY	1605	TACACGAGATCCTCTCTGGAATCTCTGACAGAGAGAAAGATTTCTATGAGATCAG	1664
Db	1293	CACCCGGGACCCACTATCGAAATCAGTAACAAAGAAAGACTTCCATATGAGCCACAG	1352
OY	1665	ACACTATGTGTACTATATCCCGAAATTTCTAACCAATTTGTTCTGTGTTAAATGGA	1724
Db	1353	ACACTATGCGCTAATATATCTCGAATCTTCAACCAATTTGTTCTGTGTTCAAGTGGA	1412
OY	1725	TTCTGAGATGAAGTAGGCCGCAATGTATGTGTTGTTAAAGATTTGGCCTCCAAATCAAC	1784
Db	1413	TTCCAGAACGAAGTGGCCGAGATGTACTGCTTGTATAAAGATTTGGCCTCCAAATCAAC	1472
OY	1785	TGAACAGGCTATGGAATCTTCTGACTGTAAATTACCAGATCTATAGTTCGAGGTTTTGC	1844
Db	1473	AGAGCAACCATGGAATCTCTGACTGTAACTATTCAGATCTCTATAGTTCGAGATTTTGC	1532
OY	1845	TGTTCCGTGCTGGAAAAATATTTAACGATGACAACTTTCTCAGTATTTTAATCACT	1904
Db	1533	TGTTCCGTGCTTGAAGAAAAATATTTAACAGATGACAACTTTCTCAGTATCTCAACT	1592
OY	1905	AGTACAGGTCTTAAATATATGAAACAATATTTGATTACTGCTGTGAGATTTTATCGAA	1964
Db	1593	TGTAAAGGTCTTAAATATATGAAACGATATTTGATTAACCTGCTTGTGAATTTTAACTCA	1652
OY	1965	GAAAGCATTTGACTAATCAAGGATTTGGGCACTTTTCTTTTGGCACTTAAATCTGAGAT	2024
Db	1653	GAAAGCATTTGACAAATCAAGGATTTGGGCACTTTTCTTTTGGCACTTAAATCTGAGAT	1712
OY	2025	GCACATATAAACAGTTAGCCAGAGGTTTGGCTGTGTTTGTAGATCTATTTGCTGTCAAG	2084
Db	1713	GCACATATAAAGCTGTCAGAGGTTTGGCTGTGTTTGTAGATCTATTTGCTGTCCGTCCTG	1772
OY	2085	TGGATGTATTTTGAAGCACTGGAATAGCCAGTGAAGCAATGCAAAAGCTCATTAATT	2144
Db	1773	TGGATGTATCTGAAGCACTGGAACAGCAAGTGAAGCCATGGAAGGCTCATTAACCT	1832
OY	2145	AACTGACATTTCTCAAAACGAGAGGAAGATGATAACAAAGGTAACAGATGAATTTTT	2204
Db	1833	AAAGCAATCTCTTAAGCAGAGAAAGAAAGATGACACAAAGGTAACAGATGAATTTTT	1892
OY	2205	AGTTGAGCAATAGAGCGACAGATTTTCATGATGCTCTACAGAGGCTTGTCTCTCT	2264

Db	1893	GGTTGAACGATGTGAGACAGCCGACCTTCATGGATGCTTTTSCAGGGTTCCTGTCCTCT	1952
Oy	2265	AAACCCGCTCATCAACTAGGAACCTCAGGCTTAAAGAGTGAATTAATGCTTCG	2334
Db	1953	GAATCTGCTCACCACCTAGGAACCTCAGGCTTAAAGAGTGAATTAATGCTTCG	2012
Oy	2335	AAAAAGCCACTGTGTGGTAATTTGGGAACCCAGACATCATGTCAAGATTACTGTTCA	2384
Db	2013	AAAAAGCCACTGTGTGGTAATTTGGGAACCCAGACATCATGTCAAGATTACTGTTCA	2072
Oy	2385	GAACAAATGAGTCTCTTTAAAAATGGGAGATGATTTACGGCMAGATATGCTAACACTTCA	2444
Db	2073	GAACAAATGAGTCTCTTTAAAAATGGGAGATGATTTACGGCMAGATATGTTAACCTTCA	2132
Oy	2445	AATTAATTCGTATTATGCAAAAATATCTGGCAAAATCAAGATCTTGATCTTGGAAATGTTAC	2504
Db	2133	GATCATCCGAATCATGTAGAAACATCTTGGCAAAACCAAGGCTTGAACCTTGGCATGTCAAC	2192
Oy	2505	TTATGTGTTGTCGTCAATCCGATGACTGTGTGGGACTTAATTAAGGTGTGGCAATTTCA	2564
Db	2193	TTATGTGTTGTCGTCAATCCGATGACTGTGTGGGCTCATCGAGGTGTGGAAACCTCTCA	2252
Oy	2565	CACATTAATATGCAATTTCAATGCAAAAGCGGCTTGAAGGTGCACTGACATTTCAACACCA	2624
Db	2253	CACATCATGCAAAATTCAGTGCAGAAAGAGGCTGMAAGGCGCTGTGACATTTCAACACCA	2312
Oy	2625	CACACTACATGAGTGGCTCAAAAGCAGAAACAAAGGAAATATATATGATCAGCATTA	2684
Db	2313	CACACTACATGATGGCTTCAAGGACAAAGAAACAGGCGGAATATATGATCAGCATTA	2372
Oy	2685	CTGTGTTTACAAGTTCATGTGTGTGATCTGTGTAGTACCTTCAATTTTGGAAATTTGAGA	2744
Db	2373	CTGTGTTTACAAGTTCATGTGTGTGATCTGTGTAGTACCTTCAATTTTGGAAATTTGAGA	2432
Oy	2745	TGCTCACAATATGTAACATTCATGTGAAAGACGATGCAACCTGTTTCAATATGAAATTTGG	2804
Db	2433	CCGGCACAACGACAACTCAATGTGAAAGATGACGCAACACTGTTTCATATTAAGATTTTGG	2492
Oy	2805	ACACTTTTGGATTCAGAAAGAAATTTGGTTTAAACGGAACGTGTGCACTTGT	2864
Db	2493	GCACCTTTTGGATTCAGAAAGAAATTTGGTTTAAACGGAACGTGTGTGCACTTGT	2552
Oy	2865	TTTGACACAGGATTTCTTAATAGTATTAAGAGACCCCAAGATGCAACAAAGCAG	2924
Db	2553	CTTGACACAGGATTTCTTGATTTGATTAAGAGGAGCAACAGATGACACAAAGCAG	2612
Oy	2925	AGAAATTTGAGAGTTTCAGAGATGTGTTTCAAGGCTTAATCTAGCTAATTTGACAGCATGC	2984
Db	2613	AGAAATTTGAGAGTTTCAGAGATGTGTTTCAAGGCTTAATCTAGCATTTGCGCAGCATGC	2672
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Db	2673	CAATCTCTTCAATAATTTTTCATAGATGTGTGGCTGTGGAATGCGAATCTACATC	2732
Oy	3045	TTTGATGACATTTGACATATTCGAAAGACCCAGCTTATGATATTAACATGAGCAAGGCG	3104
Db	2733	TTTGATGACATTTGACATATTCGAAAGACCTTAGCTTGTGAACAACTGACGAAAGGCG	2792
Oy	3105	TTTGAGTATTTTCATGAAACAAATGGAATGATGACATCATGTGTGCTGACAAACAAAT	3164
Db	2793	TTTGAGTATTTTCATGAAACAAATGGAATGATGACATCATGTGTGCTGACGACAAACAAAT	2852
Oy	3165	GGATTTGATCTTCCACACATTAATAACGACATGCAATTTGAATGAAAGATTAACCTAGAAAT	3224
Db	2853	GGATTTGATCTTCCACACATTAATAACGACATGCAATTTGAATGAAAGATGAGGCTGAGACTG	2912
Oy	3225	GAAGGCTCAGCTTGACACATGACCTGTTAATTAACCTGACGAGGCAAGACGAT	3284
Db	2913	CGAGCTGAGCTCCGAGCTTCTCCACTGCA-TGGCAGTGAAGTGGCAGCAGGCAAGGCAATG--	2969
Oy	3285	TGCATAGAAATTCGACATCCATGAACAGCATTTAGATTTTACAGCAAGAACAGAAATTAATA	3344

Db	2970	---	GGATGGGATGGCAGCTGCGAAGCAACATTAGACTGTGAGCAAGAACTTAACCAAG	3028
Qy	3345	TACTATATTAATTAAATATGTAAACGCAACAGCGTTGTATAGCACTTAACCTGTTCA	3404	TTCACTTAA
Db	3027	TGCTTAAATTAATGGAACACTGTACACGACAGCGGTTGTATAGCAC-TAAACTGATTTA	3085	TTTCAAAA
Qy	3405	TTTCAAAA	3412	TTTCAAAA
Db	3086	TTTCAAAA	3093	TTTCAAAA
RESULT 2				
LOCUS	B0228953			
DEFINITION	AGENCOURT_7572613 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6044713			
ACCESSION	B0228953			
VERSION	B0228953.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 872)			
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: csapbs-remail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
	DNA sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLN at:			
	http://image.llnl.gov			
	Plate: L14M13287 row: m column: 02			
	High quality sequence stop: 648.			
FEATURES				
Source	Location/Qualifiers			
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	/organism="Homo sapiens"			
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	/db_xref="taxon:9606"			
	/clone="IMAGE:6044713"			
	/label_type="embryonal carcinoma, cell line"			
	/tissue="DH10B (phage-resistant)"			
	/lab_host="NIH MGC 92"			
	/note="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI;			
	Site 2: SalI; Cloned unidirectionally; oligo-dT primed.			
	Average insert size 2.5 Kb. Library enriched for			
	full-length clones and constructed by Life Technologies.			
	Note: this is a NIH_MGC Library."			
BASE COUNT	265 a	166 c	186 g	255 t
ORIGIN				
Query Match	23.6%	Score 806;	DB 13;	Length 872;
Best Local Similarity	97.9%	Pred. NO. 5.6e-163;		
Matches 848;	Conservative 0;	Mismatches 15;	Indels 3;	Gaps 3;
Qy	1190	CTCGGCGTGCAGACTTTGACCTTTCATCTTGTCTGTAAAGGCCGAAGGCTGCTAAG	1249	TTTCAAAA
Db	1	CTCGTGCCTGCAGACTTTGACCTTTCATCTTGTCTGTAAAGGCCGAAGGCTGCTAAG	60	TTTCAAAA
Qy	1250	AGGAACACTGTCCATTTGCGATGGGGAATATTAACCTTTGATTACACAGACTCTAG	1309	TTTCAAAA
Db	61	AGGAACACTGTCCATTTGCGATGGGGAATATTAACCTTTGATTACACAGACTCTAG	120	TTTCAAAA
Qy	1310	TATCTGAAAAATGCGCTTTGAATCTTTGGCCAGTACTCATGATGTAGAGATTGCTGA	1365	TTTCAAAA
Db	121	TATCTGAAAAATGCGCTTTGAATCTTTGGCCAGTACTCATGATGTAGAGATTGCTGA	180	TTTCAAAA
Qy	1370	AACCTATGCGTTACTGAGATCAATCAATTAAGAACTCCATGCTTAAGATTGAGT	1429	TTTCAAAA

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT							
Dp	181	ACCCTATGGGTACTGCATCAAAATCCAAATAAAGAAATCCATGCTTAGAGTTGGAGT	240																
Qy	1430	TTGACTGGTTCAGAGAGTGTGTAAAGTTCCAGATATGTCAGTATGTGAAGAGCATGCCA	14899																
Dp	241	TTGACTGGTTCAGAGAGTGTGTAAAGTTCCAGATATGTCAGTATGTGAAGAGCATGCCA	300																
Qy	1490	ATTGAGTGTATCCCGAAGAGCAGGATTTTAGCTATTCGCCACGACGACGTAGTAACGAC	15449																
Dp	301	ATTGAGTGTATCCCGAAGAGCAGGATTTTAGCTATTCGCCACGACGACGTAGTAACGAC	360																
Qy	1550	TAGCTAGAGACAATGAATTAAGGAAAAATGACAAAGAACAGCTCAAGCAATTTCTACAC	16099																
Dp	361	TAGCTAGAGACAATGAATTAAGGAAAAATGACAAAGAACAGCTCAAGCAATTTCTACAC	420																
Qy	1610	GAGATCTCTCTCTGAAATCACTGACGAGGAAAGATTTTCTATGGAGTCACGACACT	16699																
Dp	421	GAGATCTCTCTCTGAAATCACTGACGAGGAAAGATTTTCTATGGAGTCACGACACT	480																
Qy	1670	ATTGTGTACTATCCCGAAATTCCTACCAAATGCTTGTGTCTGTTAAATGCAATCTA	17299																
Dp	481	ATTGTGTACTATCCCGAAATTCCTACCAAATGCTTGTGTCTGTTAAATGCAATCTA	540																
Qy	1730	GAGATGAAGTAGCCACAGATGTATTGCTGTGTAAGAATTTGSCCTCAATCAAACTGAC	17899																
Dp	541	GAGATGAAGTAGCCACAGATGTATTGCTGTGTAAGAATTTGSCCTCAATCAAACTGAC	600																
Qy	1790	AGGCTATGAACTTCTTGAGCTGATATTAATCCCAATCTTATGTGTGAGTTTGCTGTTG	18499																
Dp	601	AGGCTATGAACTTCTTGAGCTGATATTAATCCCAATCTTATGTGTGAGTTTGCTGTTG	660																
Qy	1850	GGTGCCTTGAAAAATTTTAACGATGACAACTTCTGAGTATTAATCAGTACTAC	19099																
Dp	661	GGTGCCTTG-AAAAATTTTAACGATGACAACTTCTGAGTATTAATCAGTACTAC	719																
Qy	1910	AGGTCCTAAATATGAAACAATATTGGATTAATGCTTGTGAGATTTTCTGAAAGAAAG	19699																
Dp	720	AGGTCCTAAATATGAAACAATATTGGATTAATGCTTGTGAGATTTTCTGAA-AAAAG	778																
Qy	1970	CATTGACTAATCAAGAGATTGGGCACTTTTCTTTT-GGCATTTTAAATTGAGATGCAC	2028																
Dp	779	CATTGACTAATCAAGAGATTGGGCACTTTTCTTTTGGGCTTTTAAACCTGAATGCC	838																
Qy	2029	AATTAACAGTTAGCCAGAGTTTG	2054																
Dp	839	CATTAACCGTTAACCCAAAGTTTG	864																
RESULT 3																			
LOCUS	AL706270	750 bp	mRNA	linear	EST 22-MAR-2002														
DEFINITION	DKFZp860163_r1 686 (synonym: hicc3) Homo sapiens cDNA clone																		
ACCESSION	DKFZp860163.5	mRNA sequence.																	
VERSION	AL706270																		
KEYWORDS	AL706270.1	GI:19689625																	
SOURCE	EST																		
ORGANISM	Homo sapiens (human)																		
REFERENCE	Homo sapiens																		
AUTHORS	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.																		
	1 (bases 1 to 750)																		
	Duesterhoeft, A., Lauber, J., Mewes, H. W., Gassenhuber, J. and Wiemann																		
	, S.																		

This clone (DKFZp686C016) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp6860163"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlec3)"
/notes="vector: pTribEX2; Site_1: S11A; Site_2: S11B;
cDNA-collection"
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BASE COUNT	227 a	147 c	165 g	208 t	3 others
ORIGIN					

Query Match	21.7%	Score 739.4;	DB 9;	Length 750;
Best Local Similarity	99.5%	Pred. No. 1.2e-148;		
Matches 740; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1090	GGAGAACCCCTATGAGCAAAATGTGAACACTGAAGAGTAACTGTCTCAATCCCAAGTGG	1143
Dp	1	GNAGAACCCCTATGTGNCMAATGTGAACACTGAAGAGTAACTGTCTCAATCCCAAGTGG	60
QY	1150	AATGAATGCTGAATTTATGATATATATACATTCCTGATCTTCCCTCGGCTGCTGCATTTGGC	1209
Dp	61	AATGAATGCTGAATTTATGATATATATACATTCCTGATCTTCCCTCGGCTGCTGCATTTGGC	120
QY	1210	CTTTCCATTTGCTCTGTITAAAGGCCGAAGGGGTGCTAAAGAGCAACTGTCTCATTTGGCA	1268
Dp	121	CTTTCCATTTGCTCTGTITAAAGGCCGAAGGGGTGCTAAAGAGCAACTGTCTCATTTGGCA	180
QY	1270	TGGGGAATATAAATCTGTGTGATTACACAGACACTGTAGATGTGGAAAAATGGCTTTG	1328
Dp	181	TGGGGAATATAAATCTGTGTGATTACACAGACACTGTAGATGTGGAAAAATGGCTTTG	240
QY	1330	AATCTTTGGCCAGTACCTCATGATATTAGAAATTTGCTGAACCCCTATTGGTGTACTGGA	1389
Dp	241	AATCTTTGGCCAGTACCTCATGATATTAGAAATTTGCTGAACCCCTATTGGTGTACTGGA	300
QY	1390	TCAATTCCAATTAAGAAACTCCATGCTTTAGATTGAATTTGACTGTTCCAGCAGTGTG	1448
Dp	301	TCAATTCCAATTAAGAAACTCCATGCTTTAGATTGAATTTGACTGTTCCAGCAGTGTG	360
QY	1450	GTAAGTTCCCAAGATATGTCAGTATTTAAAGACATCCCAATTGGTCTGTATCCCGAGAA	1509
Dp	361	GTAAGTTCCCAAGATATGTCAGTATTTAAAGACATCCCAATTGGTCTGTATCCCGAGAA	420
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Dp	421	GCAGAGATTACCTATTTCCCAAGCACTGAGTAAACAGTACAGTACGTAGAGCAATGAATTA	480
QY	1570	AGGGAATAATGACAAAGAACAGCTCAAGCAATTTCTACAGCAGATCCCTCTCTGAAATC	1629
Dp	481	AGGGAATAATGACAAAGAACAGCTCAAGCAATTTCTACAGCAGATCCCTCTCTGAAATC	540
QY	1630	ACTGAGCAGGAAAGATTTTCTATGTGAGTCAACAGACATATGTGTACTATATCCCGAA	1689
Dp	541	ACTGAGCAGGAAAGATTTTCTATGTGAGTCAACAGACATATGTGTACTATATCCCGAA	600
QY	1690	ATTCTACCCCAATTTGCTCTGTGCTGTAAATGGAATTTCAAGATGAAAGTACGCCAGATG	1749
Dp	601	ATTCTACCCCAATTTGCTCTGTGCTGTAAATGGAATTTCAAGATGAAAGTACGCCAGATG	660
QY	1750	TATTGCTTTGTAAAGATTTGGCCTTCCATCAAACTGAACAGGCTATGAACTTTCTGGAC	1809
Dp	661	TATTGCTTTGTAAAGATTTGGCCTTCCATCAAACTGAACAGGCTATGAACTTTCTGGAC	720
QY	1810	TGTATATTAACCAAGTCTATGTGTT	1813
Dp	721	TGTATATTAACCAAGTCTATGTGTT	744

RESULT 4					
LOCUS	BM470620				
DEFINITION	BM470620	1063 bp	RNA	linear	EST 05-FEB-2002
	AGENCOURT_66463064	NIH_MGC_71	Homo sapiens	cdna clone	IMAGE:553478

ACCESSION	BM470620	
VERSION	BM470620.1	GI:18519662
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 1063)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .1063

Site_2: SalI, Cloned unidirectionally. Primer: Oligo dr
Average insert size 2.1 kb. "

Query Match	21.2%	Score 722;	DB 12;	Length 1063;
Best Local Similarity	96.7%	Pred. No. 7.7e-145;		
Matches 768; Conservative	0;	Mismatches 22;	Indels 4;	Gaps 3

Qy	883	TTTCGAACGTGCAGATCGCATCTCTTTTAAACAATGCATCTTATCTCAGAGGCATTTCCAGAGCT	942
Db	12	TATGTGCACCCCGCGCTCCGGTTTAAATGCATCTTATTCGACAGCCATTTCCAGAGCT	71
Qy	943	ACACCATAATATGAATGGAGAAACATCTCAAAAAATCCCTTTGGGTTATAAATAGAGCACTC	1002
Db	72	ACACCATAATATGAATGGAGAAACATCTCAAAAAATCCCTTTGGGTTATAAATAGAGCACTC	131
Qy	1003	AGATAAATAATTCCTTTGTCGACCTAGCTGAATCTAAATTTGGAGACATTTGACAAGATT	1062
Db	132	AGAAATAAAAAATTCCTTTGTCGACCTAGCTGAATGTAAATATTTGGAGACATTTGATATATC	191
Qy	1063	TATGTTGGAAACAGGTATCTACATGAGAGAAACCCCTTATGTGACAAATGTGAACACTGAA	1122
Db	192	TATGTTGGAAACAGGTATCTACATGAGAGAAACCCCTTATGTGACAAATGTGAACACTGAA	251
Qy	1123	AGAGTACCTTGTTCCATCCCAAGTGGAAATGGCTGAATATATGATATATACATTCCCT	1182
Db	252	AGAGTACCTTGTTCCATCCCAAGTGGAAATGGCTGAATATATGATATATACATTCCCT	311
Qy	1183	GATCTTCCTGCTGCTGCTGCACTTTGGCTTTGCATTGCTCTGTAAAGGCCGGAAGAGGT	1242
Db	312	GATCTTCCTGCTGCTGCTGCACTTTGGCTTTGCATTGCTCTGTAAAGGCCGGAAGAGGT	371

QY 1243 GCTAAGAGAACTGCTTCATTGGCATGGGAATATATACTTTGATTACAGAC 1302
 DB 372 GCTAAGAGAACTGCTTCATTGGCATGGGAATATATACTTTGATTACAGAC 431
 QY 1303 ACTAGATCTGAAAAATGGCTTTGAATCTTTGGCAGATACCTCATGATTTGAGAT 1362
 DB 432 ACTAGATCTGAAAAATGGCTTTGAATCTTTGGCAGATACCTCATGATTTGAGAT 491
 QY 1363 TTGCTGAACCTTATTTGTTGTTAGTATGATCAATCAATTAAGAACTCATGCTTAGAG 1422
 DB 492 TTGCTGAACCTTATTTGTTGTTAGTATGATCAATCAATTAAGAACTCATGCTTAGAG 551
 QY 1423 TTGAGATTGACTGTTAGAGAGTGTGTAAAGTTCCAGATATGTCATGATTTGAGAG 1482
 DB 552 TTGAGATTGACTGTTAGAGAGTGTGTAAAGTTCCAGATATGTCATGATTTGAGAG 611
 QY 1483 CATGCAATTGGTCTGTATCCGGAAGACAGATTATTAATTCCTCCAGCAGACTGAGT 1542
 DB 612 CATGCAATTGGTCTGTATCCGGAAGACAGATTATTAATTCCTCCAGCAGACTGAGT 671
 QY 1543 AACAGACTAGCTAGAGACATGAAATTAAGGAAATGACAAAGAACAGCTCAAGCAATT 1602
 DB 672 AACAGACTAGCTAGAGACATGAAATTAAGGAAATGACAAAGAACAGCTCAAGCAATT 731
 QY 1603 TCTACAGAGATCTCTCTCTGAAA--TCACTAGACA-GGAGAAAGATTTTCTATGG-AG 1658
 DB 732 TCTACAGAGATCTCTCTCTGAAAATCACTGAGACAGGAGAAAGATTTTCTATGGAG 791
 QY 1659 TCACAGACACTATT 1672
 DB 792 TCACAGACCTATT 805

RESULT 5
 LOCUS BX437220 834 bp mRNA linear EST 15-MAY-2003
 DEFINITION BX437220 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YF10
 ACCESSION BX437220
 VERSION BX437220.1 GI:30781556
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 834)
 Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1992.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0CAP005YF10&cluster=1992.f. Contact :
 Peng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0CAP005YF10.
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 /mol_type="mRNA"
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 /clone="CS0CAP005YF10"
 /issue_type="THYMUS"
 /clone_lib="Homo sapiens THYMUS"
 /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector."

FEATURES
 SOURCE

BASE COUNT 256 a 152 c 184 g 241 t 1 others
 ORIGIN
 Query Match 21.1%; Score 719.4; DB 13; Length 834;
 Best Local Similarity 98.9%; Pred. No. 2.6e-144;
 Matches 723; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1742 CCCAGATGATTTGCTTGTAAAGATTTGCGCTCAATCAAACTGAACAGAGCTATGAGAC 1801
 DB 104 CACAGATGATTTGCTTGTAAAGATTTGCGCTCAATCAAACTGAACAGAGCTATGAGAC 163
 QY 1802 TTCTGACTGATTAATCCAGATTCATAGGTTGAGGTTTGTCTGCTTGGTGGAAA 1861
 DB 164 TTCTGACTGATTAATCCAGATTCATAGGTTGAGGTTTGTCTGCTTGGTGGAAA 223
 QY 1862 AATTTTAAGAGATGAACAACTTTCAGATTTAATTCAGCTAGTACAGTCTTAAT 1921
 DB 224 AATTTTAAGAGATGAACAACTTTCAGATTTAATTCAGCTAGTACAGTCTTAAT 283
 QY 1922 ATGACATATTTTGATTAATCTGCTTGTGAGATTTTACTGAAGAAAGCATTAATC 1981
 DB 284 ATGACATATTTTGATTAATCTGCTTGTGAGATTTTACTGAAGAAAGCATTAATC 343
 QY 1982 AAAGATTTGGCACTTTTCTTTTGGCATTAAATCTGATGACATTAACAGTTA 2041
 DB 344 AAAGATTTGGCACTTTTCTTTTGGCATTAAATCTGATGACATTAACAGTTA 403
 QY 2042 GCCAGAGTTTGGCTGCTTGTGAGATTCATTTGCTGATGATGATGATGATGATGATG 2101
 DB 404 GCCAGAGTTTGGCTGCTTGTGAGATTCATTTGCTGATGATGATGATGATGATGATG 463
 QY 2102 ACCGATATAGCAAGTGCAGCAATGGAAGCTCAATTAATTAATCACTGATTTCTCAAC 2161
 DB 464 ACCGATATAGCAAGTGCAGCAATGGAAGCTCAATTAATTAATCACTGATTTCTCAAC 523
 QY 2162 AGGAGAGAAAGATGAACACAAAGGTACAGATGAAGTTTGTAGTTGACCAATGAGGC 2221
 DB 524 AGGAGAGAAAGATGAACACAAAGGTACAGATGAAGTTTGTAGTTGACCAATGAGGC 583
 QY 2222 GACCAATTTTCATGAGATGAGCCCTCAGAGGCTTGTGCTCTCTCAAACTGCTCATCAAC 2281
 DB 584 GACCAATTTTCATGAGATGAGCCCTCAGAGGCTTGTGCTCTCTCAAACTGCTCATCAAC 643
 QY 2282 TAGCAAACTCAGAGCTTAAAGATGCTGAATTAATGCTTGTGCAAAAAGGCCACTGNGT 2341
 DB 644 TAGCAAACTCAGAGCTTAAAGATGCTGAATTAATGCTTGTGCAAAAAGGCCACTGNGT 703
 QY 2342 TGAATTGGAGAAACCCAGACATCATGTCAAGTTACTGTTTCAGAACATGAGATCATCT 2401
 DB 704 TGAATTGGAGAAACCCAGACATCATGTCAAGTTACTGTTTCAGAACATGAGATCATCT 763
 QY 2402 TTTAAATTTGGGATGATTTACGGCAGATATGCTAACACTTCAATTTATTTGATATG 2461
 DB 764 TTTAAATTTGGGATGATTTACGGCAGATATGCTAACACTTCAATTTATTTGATATG 823
 QY 2462 AAAATATCTGG 2472
 DB 824 AAAATATCTGG 834

RESULT 6
 LOCUS BU167122 883 bp mRNA linear EST 04-SEP-2002
 DEFINITION BU167122 AGENCOURT_7958965 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163350
 ACCESSION BU167122
 VERSION BU167122.1 GI:22681087
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 883)
 NIH-MGC <http://mgc.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L14M13518 row: m column: 23
 High quality sequence stop: 555.
 Location/Qualifiers

FEATURES

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 Average insert size 2 kb. Library constructed by Life
 Technologies."
 BASE COUNT 272 a 161 c 189 g 261 t

Query Match 19.9%; Score 678.8; DB 13; Length 883;
 Best Local Similarity 93.0%; Pred. No. 1.5e-135;
 Matches 722; Conservative 0; Mismatches 52; Indels 2; Gaps 1;

682 AAAACATGAAAGTATGTTGCTATCATCTGAACAAATTAAATCTGTGTTTGAATATCAG 741
 1 ATTAACGAGATATGTTGCTATCTCTGAACAACTAAATCTGTGTTTGAATATCAG 60
 742 GGCAGATCACTTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 801
 61 GGCAGATCACTTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 802 AGTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
 121 AGTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 862 ATGCGTAAAGAAAGCCTTTATCTCAATGCGCAATGAGCTGTTTACATGCAATCTTAT 921
 181 ATGCGTAAAGAAAGCCTTTATCTCAATGCGCAATGAGCTGTTTACATGCAATCTTAT 240
 922 TCAGAGCGATTTCCACAGCTACACATATATGATGATGATGATGATGATGATGATGATGATGAT 981
 241 TCAGAGCGATTTCCACAGCTACACATATATGATGATGATGATGATGATGATGATGATGATGAT 300
 982 TGGGTATTAATAGAGCACTCAGATTAATAATCTTTGTGCAACTACAGTGAATCTPAAT 1041
 301 TGGGTATTAATAGAGCACTCAGATTAATAATCTTTGTGCAACTACAGTGAATCTPAAT 360
 1042 ATTGAGACATGACAGATTTATGTTGAAACAGATCTACAGATGAGAGAGAACCTTTA 1101
 361 ATTGAGACATGATTAAGATCTATGTTGAAACAGATCTACAGATGAGAGAGAACCTTTA 420
 1102 TGGAGAACTGTAACAGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
 421 TGGAGAACTGTAACAGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 1162 AATTATGATATATACATCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1221
 481 AATTATGATATATACATCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 1222 TCTGTAAAGCGGAAAGGCTGCTAAAGAGAACTCTGTCATGCGATGAGGAGAAATATA 1281

Db 541 TCTGTAAAGCGGAAAGGCTGCTAAAGAGAACTCTGTCATGCGATGAGGAGAAATATA 600
 Qy 1282 AACTGTTGATATACAGACACTAGATCTGAGAAATAGGCTTTGAATCTTTGGCCA 1341
 Db 601 AACTGTTGATATACAGACACTAGATCTGAGAAATAGGCTTTGAATCTTTGGCCA 660
 Qy 1342 GATCTGATGATATGAGATTTGCTGAACCC--TATGCTGTTACTGATCAATTCGA 1399
 Db 661 GATCTGATGATATGAGATTTGCTGAACCCCTATTTGCTGTTACTGAGATCAAAATCC 720
 Qy 1400 ATTAAGAACTCCATCTTGAAGTTGAGTTGATGATGATGATGATGATGATGATGATGATGAT 1455
 Db 721 AATTAAGAACTCCATCTGCTGCTTGAAGTTGAGATGAGATGATGATGATGATGATGATGATGAT 776

RESULT 7

EX437219/c 827 bp mRNA linear EST 15-MAY-2003
 LOCUS BX437219 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YF10
 DEFINITION 3-PRIME, mRNA sequence.
 ACCESSION BX437219
 VERSION BX437219.1 GI:30779545
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 827)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1992.f For
 more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0CAP005YF10&pic=cluster=1992.f>. Contact :
 Feng Liang Email: liang@life.techn.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0CAP005YF10

FEATURES

source

1. 827
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 /clone="CS0CAP005YF10"
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 with a NotI-oligo (dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT 232 a 150 c 138 g 302 t 5 others

Query Match 19.9%; Score 678.2; DB 13; Length 827;
 Best Local Similarity 99.3%; Pred. No. 2e-135;
 Matches 702; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

2708 GATACGTGTAGTACTCTTCAATTTGGGAATTTGGAATGTCACATTAATACATATAGG 2767
 827 GATACGTGTAGTACTCTTCAATTTGGGAATTTGGAATGTCACATTAATACATATAGG 768
 Qy 2768 TGAAGACAGTGAACACTGTTTCATATATGATTTTGGACACTTTTGGATCAAGAGA 2827
 Db 767 TGAAGACAGTGAACACTGTTTCATATATGATTTTGGACACTTTTGGATCAAGAGA 708
 Qy 2828 AAAAATTTGGTATTAAGAGAAAGCTGTCATTTGTCACAGATTTCTTAATAG 2887

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Db      707  AAAATTGGTTATTAACGAGACGTGTCCATTGTTTTCACACAGGATTTCTTAATAG 648
Qy      2888 TGATTAGTAAAGAGCCCAAGATGCAACAAAGAGAAATTTAGAGTTTCAGAGAGA 2947
Db      647  TGATTAGTAAAGAGCCCAAGATGCAACAAAGAGAAATTTAGAGTTTCAGAGAGA 588
Qy      2948 TGTGTTACAGGCTTATCTAGCTATTGACACGATGCCAATCTCTTCAATAATCTTTCT 3007
Db      587  TGTGTTACAGGCTTATCTAGCTATTGACACGATGCCAATCTCTTCAATAATCTTTCT 528
Qy      3008 CAATGAGCTTGGCTCGGAATGCGAAGATCAATCTTTGATGACATTCATACATTC 3067
Db      527  CAATGAGCTTGGCTCGGAATGCGAAGATCAATCTTTGATGACATTCATACATTC 468
Qy      3068 GAAAGACCTTAGCTTATGATTAACCTGACAGAGGCTTTGAGTATTTCAAGAACAA 3127
Db      467  GAAAGACCTTAGCTTATGATTAACCTGACAGAGGCTTTGAGTATTTCAAGAACAA 408
Qy      3128 TGAATGATGACATCATGCTGCTGACACAAATAATGATTCATTCACACAAATTA 3187
Db      407  TGAATGATGACATCATGCTGCTGACACAAATAATGATTCATTCACACAAATTA 348
Qy      3188 AACGATGATGATGACATGCTGCTGACACAAATAATGATTCATTCACACAAATTA 3246
Db      347  AACGATGATGATGACATGCTGCTGACACAAATAATGATTCATTCACACAAATTA 288
Qy      3247 ACTGACCTGTTAATTAATCTCTGACAGGCAAGCCGATTCATGATGATGATGATGAT 3306
Db      287  ACTGACCTGTTAATTAATCTCTGACAGGCAAGCCGATTCATGATGATGATGATGAT 228
Qy      3307 TGAACAGCATTTAG-ATTACAGCAAGAACAGAAATTAATATCTATTAATTAATATG 3365
Db      227  TGAACAGCATTTAG-ATTACAGCAAGAACAGAAATTAATATCTATTAATTAATATG 168
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RESULT 8
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LOCUS DEFINITION 602543009P1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4665482 5'
mRNA sequence.
ACCESSION BG497751 GI:13459268
VERSION BG497751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 753)
NIH-MGC http://mgs.nci.nih.gov/.
REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapds-remail.nih.gov
COMMENT Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1471 row: a column: 03
High quality sequence, stop: 649.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4665482"
/tissue_type="adenocarcinoma"

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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccggcgcc); Site 2: SfiI (ggcattatggcc)
); Double-stranded cDNA was prepared from cell line RNA.
5', and 3' adaptors were used in cloning as follows: 5'
sequence: 5'-ATTCTAGAGGCGGAGCGGCTGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 241 a 136 c 176 g 200 t
ORIGIN

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Query Match 19.5%; Score 666; DB 10; Length 753;
Best Local Similarity 97.0%; Pred. No. 8.3e-133;
Matches 733; Conservative 0; Mismatches 15; Indels 8; Gaps 5;

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Qy      2080 GCATGTGGATGATATTGAAGCACCTGAATAGGCAATCGAGGCAATGAGAAAGCTCAT 2139
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Qy      2140 AACTTAACTGACATTTCTGAACAGAGAGAGAGAGATGAAACACAAAAGTACAGATGAAG 2199
Db      61  AACTTAACTGACATTTCTGAACAGAGAGAGAGAGATGAAACACAAAAGTACAGATGAAG 120
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Qy      2260 CCTCTAAACCTGCTCATCACTAGAGAAACCTCAGGCTTAAAGATGTCGAAATGATGCT 2319
Db      181  CCTCTAAACCTGCTCATCACTAGAGAAACCTCAGGCTTAAAGATGTCGAAATGATGCT 240
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Db      361  CTTCAAAATTAATGATATGAGAAATATCTGCAAAATCAAGGCTTGTATCTTCGATG 420
Qy      2500 TTACTTATGTTGTCTGCAATCGGTGACTGTGTGGACTTATGAGGTGTGCGAAT 2559
Db      421  TTACTTATGTTGTCTGCAATCGGTGACTGTGTGGACTTATGAGGTGTGCGAAT 480
Qy      2560 TCTCAGCATTTATGCAAAATTCAGTGCMAAGGGGCTTGAAGAGTGCATGCGATCAAC 2619
Db      481  TCTCAGCATTTATGCAAAATTCAGTGCMAAGGGGCTTGAAGAGTGCATGCGATCAAC 540
Qy      2620 AGCACACACTATCATGCTGCTCAAAAGACAAAGAAAGAGAAATATATGATGACGCC 2679
Db      541  AGCACACACTATCATGCTGCTCAAAAGACAAAGAAAGAGAAATATATGATGACGCC 600
Qy      2680 ATTGACCTGTTTACAGTTGATGCTGCTGATCTGATGCTGATCTTCAATTT--TGGGAA 2737
Db      601  ATTGACCTGTTTACAGTTGATGCTGCTGATCTGATGCTGATCTTCAATTTGCGGGAAT 660
Qy      2738 TTGAGATGCTGCAATAG-TAAATCATAT-GGTGAAGAGATGACACACTGTTTCATAT 2795
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Qy      2796 AGATTTTGAACATTTTGGATCAACAAGAGAAAA 2831
Db      720  AGATTTTGG--ACATTTGGATCAACAAGAGAAAA 752

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RESULT 9
 CB23732 854 bp mRNA linear EST 10-APR-2003
 LOCUS
 DEFINITION
 CB23732 UI-M-FYO-cdv-21-0-UI.r1 NIH_BMAP_FYO Mus musculus cDNA clone
 IMAGE: 6844054 5', mRNA sequence.
 ACCESSION
 CB23732.1 GI:29780874
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 854)
 TITLE
 JOURNAL
 COMMENT
 Unpublished
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.

FEATURES

Location/Qualifiers
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http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: PYX-5.
 Location/Qualifiers
 1. 809
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 /mol_type="mRNA"
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 /issue_type="whole brain"
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 /lab_host="DH10B (T1 phage resistant)"
 /clone_11b="NH BMAP F00"
 /note="Organ: Brain; Vector: PYX-Asc; Site:1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGCC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., Program coordinator."

BASE COUNT 248 a 173 c 179 g 206 t 3 others
 ORIGIN

Query Match 18.6% Score 633; DB 14; Length 809;
 Best Local Similarity 87.1% Pred. No. 1.1e-125;
 Matches 704; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

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 1 TCACCTCTGCAACAGAACTTTTCTTACATTTCTGAAGTGTACCAAGAGAGAG 60
 237 GGAAGAAATTTTGTATGAAACAGACGCTTGTGATCTTGGCTTTTCAACATTTT 296
 61 GGAAGAAATTTTGTATGAAACAGACGCTTGTGATCTTGGCTTTTCAACATTTT 120
 297 AAAAGTAATGAAACAGACGCTTGTGATCTTGGCTTTTCAACATTTT 356
 121 AAAAGTAATGAAACAGACGCTTGTGATCTTGGCTTTTCAACATTTT 180
 357 TGCTATCGGCAATGCGAGTGTGCAATTTGATATGTTAAAGATCTGAGTACAGACTT 416
 181 TGTTATTTGGCATGCGAGTGTGCAATTTGATATGTTAAAGATCTGAGTACAGACTT 240
 417 CCGAAGAAATTTTCTTAAATGTTTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 476
 241 TCGAAGAAATTTTCTTAAATGTTTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 300
 477 TCAATAGAGCAATGATCTTAAATGTTTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 536
 301 TCAATAGAGCAATGATCTTAAATGTTTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 360
 537 GCACATATATATATATATGATGAGGCAATATATATGATGATGATGATGATGATGATGATG 596
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 421 TCCAAATATATATATGATGAGGCAATATATATGATGATGATGATGATGATGATGATGATGATG 480
 657 AGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 716
 481 AGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

QY 717 AAAACTCTGTGTTTAAATATATGAGGCAAGTACATTTTAAAGTGTGATGATGATG 776
 DB 541 GAAACTCTGTGTTTAAATATATGAGGCAAGTACATTTTAAAGTGTGATGATGATG 600
 QY 777 ATACTCTGTAAGAAATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 836
 DB 601 ATACTCTGTAAGAAATATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 837 TGGAGAGATGCCCAATTTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 896
 DB 661 GGGAGAGATGCCCAATTTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 719
 QY 897 GGAAGTGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 956
 DB 720 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779
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RESULT 11
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 DEFINITION
 ACCESSION AUI29890
 VERSION AUI29890.1 GI.10990244
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
 Yamamoto.J., Nakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
 Isogai.T.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 HRI human cDNA project
 Unpublished
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
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 /note="Vector: pMB18SPJ3; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 232 a 133 c 160 g 219 t 9 others
 ORIGIN

Query Match 17.9% Score 612; DB 9; Length 753;
 Best Local Similarity 97.4% Pred. No. 3.7e-121;
 Matches 662; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 762 GTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
 DB 1 GTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 822 AACCTGTATATGCTTGGAGATGCCCAATTTGAAGATGATGCTTAAGAAAGCCTTTA 881

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Db      61 AACCTGATATATCTGGGAGATGCCCAATTGATGTTATGCTAAAGAAAGCCTTA 120
QY      882 TTCTCACTGCGCAATGAGACTGTTTACATGCCATCTTATTCAGACGATTTCCACAGC 941
Db      121 TTCTCACTGCGCAATGAGACTGTTTACATGCCATCTTATTCAGACGATTTCCACAGC 180
QY      942 TACACCATATATGATGAGAAACATCTACAAAATCCCTTGGGTTATATAATAGAGACT 1001
Db      181 TACACCATATATGATGAGAAACATCTACAAAATCCCTTGGGTTATATAATAGAGACT 240
QY      1002 CAGATATAAAATCTTGTGCAACCTACAGTGAATCTTAATATTCAGACATTCAGAAAT 1061
Db      241 CAGATATAAAATCTTGTGCAACCTACAGTGAATCTTAATATTCAGACATTCAGAAAT 300
QY      1062 TTATGTTGCAACAGATATCTACATGAGAGAGAACCTTATGTGACATGTGAACACTCA 1121
Db      301 CTATGTTGCAACAGATATCTACATGAGAGAGAACCTTATGTGACATGTGAACACTCA 360
QY      1122 AAGAGTACCTTGTTCACATCCAGGTGAAATGAATGGCTGAATATGATATATACATTC 1181
Db      361 AAGAGTACCTTGTTCACATCCAGGTGAAATGAATGGCTGAATATGATATATACATTC 420
QY      1182 TGAATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
Db      421 TGAATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY      1242 TGCTAAAGAGAACACTGCTCATGTCATGGAGGAAATATTAACCTGTTGATTAACAGA 1301
Db      481 TGCTAAAGAGAACACTGCTCATGTCATGGAGGAAATATTAACCTGTTGATTAACAGA 540
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QY      1361 ATTTCGTGAACCTT-ATGCTGTACTGATTCAAATTCAAA-TAAGAAATCCATGCTT 1418
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QY      1419 AGAG-TTGGAGTTGACTGG 1437
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RESULT 12
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 DEFINITION
 BM986382
 SUBMIT alpha, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
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 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 833)
 Malek,R.U., Cho,J., Lee,Y., Karamycheva,S., Parvizli,B., Pertea,G.,
 Sultana,R., Teal,J., White,J., Quackenbush,J. and Lee,N.H.
 Generation of ESTs from a rat multiple tissue survey
 Unpublished
 Other ESTs: EST445877 EST345567
 Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 This clone is available through the ATCC, contact the ATCC
 tel#703-365-2700 for further information
 Seq primer: M13 reverse.

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FEATURES
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                /note="Vector: pT73Pac; Site 1: EcoRI, Site 2: NotI;
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                libraries, and Bento Soares normalized libraries of ovary,
                brain, kidney, liver, placenta, lung, embryo, skeletal
                muscle, spleen, heart"
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    Matches 668; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
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    QY      249 CCAGATTTTATGATGATGCTTTCAGAGGCTTTCCTGCTCTTAAATCTGCTATCACTA 308
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    QY      309 GGAACCTGAGGCTTAAAGAGTGTCAATTAATGCTTCTGCAAAAAGGCACTGTGGT 368
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    QY      669 AAGAGCAAGAAACAAAGGCGAGATATATGAGCAGCATGACCTGTTTACAGCTTCATG 728
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    QY      729 GCTGATACTGTGTAGCTACCTTCAATTTTGGAAATGAGATGTCACAAATGTAACATC 788
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RESULT	13
CBS20825	
LOCUS	
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ACCESSION	IMAGE: 6841250 5' , mRNA sequence.
VERSION	CBS20825
KEYWORDS	CBS20825.1 GI:29354180
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
TISSUE	Mus musculus
REFERENCE	Eutharyota; Metazoa; Chordata; Craniolata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 759) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS	Unpublished
JOURNAL	Contact: Robert Strauszberg, Ph.D.
COMMENT	Email: cgsapbs@email.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousef1.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer:	PYX-5.

FEATURES	Location/Qualifiers
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BASE COUNT      232 a      161 c      168 g      197 t      1 others
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6841250"
/tissue_type="whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NH BMAP GH0"
/name="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chan, Ph.D.,
program coordinator."

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	Query Match	17.8%	Score 607.8	DB 14	Length 759
	Best Local Similarity	88.3%	Pred. No. 3e-120		
	Matches	671	Conservative	0	Mismatches 89; Indels 1; Gaps 1;
QY	1397	CAAAATAAGAAACCTCATGCTTAGAGTTGGAGTTGACTGTTCAGCAGTGTGTAAGT	1456		
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QY	1457	TCCGAGATATATCAGTGAATTGAAGCGATGCGCAATTGGTCTGTATCCCGAAGACGAGAT	1516		
Db	61	TTCCAGCATGTCTGTGATCGAAGAAACATGCCAATGTGTCGTGTCGAGAAAGCTGGAT	120		
QY	1517	TTAGTATTTCCACGCGAGACTAGTAACAGACTGTAGAGACACATGAATTAAGGAAA	1576		
Db	121	TCAGTATCTCCCATACAGACCTGAGTAACAGACTGTAGCCAGAGACATAGATTAAGAGAAA	180		
QY	1577	ATGACAAAGAACGCTCAAAGCAATTTCTACACGAGATCTCTCTGAAATCACTGAGC	1638		

Db	181	ATGACAGAGGAACAGCTCCGAGCACTTTGCACCCGGGAGCCACATATCTGAATCACTGAAC	240
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Db	241	AMGAGAAAGACTTCCTATGAGGCCACGAGACACTACGCTAGACTATTCCTGAAATCCTAC	300
OY	1697	CCAAATTGCTCTGCTCGTTAAATGGAATCTTGAGATGAAGTAGCCAGATGATTTGCT	1756
Db	301	CCAAATTGCTTCTGTCTGTCAAGTGAATTCGAGACGGAAGTGGCCCAATGACTACTCT	360
OY	1757	TGCTAAAGATTTGGCCTCCAAATCAAACTGAGACGCTATGAACTTCTGACTGTAA TT	1816
Db	361	TAGTAAAGATTTGGCCTCCAAATCAAACTGAGACGCTATGAACTTCTGACTGTAA CT	420
OY	1817	ACCGAGATCTATGCTCGAGGTTTGTCTGTTGGTGCTTGGAAAAATATTTAACAGATG	1876
Db	421	ATCCGAGATCTATGCTCGAGGTTTGTCTGTTGGTGCTTGGAAAAATATTTAACAGATG	480
OY	1877	ACAAACTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAATATGAAACAATTTTGG	1936
Db	481	ACAAACTTCTCAGTACCTCAATTCACCTGTACAGGCTTTAAATAATGAAACAATTTTGG	540
OY	1937	ATAACTGCTGTGAGATTTTAACTGAGAGGAAGCATTTGACTAAATCAAGAGTTGGCACT	1996
Db	541	ATAACTGCTGTGAGATTTTAACTGAGAGGAAGCATTTGACTAAATCAAGAGTTGGCACT	600
OY	1997	TTTTCTTTGGCATTTAAATCTGAGATGCACAATAAACAAGTTAGCCAGAGTTTGGCC	2056
Db	601	TTTTCTTTGGCATTTAAATCTGAGATGCACAATAAACAAGTTAGCCAGAGTTTGGCC	660
OY	2057	TGCTTTTGGAGTCCATATGTCGAGCATGAGGAGTGTATTTGGAAGCACCTGATATGAGCAAG	2116
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RESULT 14
B0852815
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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B0852815 789 bp mRNA linear EST 16-OCT-2002
 AGENCOURT_10444521 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6619356
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 B0852815
 B0852815.1 GI:24037779
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 Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 789)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Straube, Ph.D.
 Email: cgabs-remail.nih.gov
 Issue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L10W2867 row: 1 column: 12
 High quality sequence stop: 653.
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/lab_host="DH10B (T1 phage-resistant)"
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/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site: 1:
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3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT      297 a      128 c      149 g      214 t      1 others
ORIGIN
Query Match      17.8%; Score 607.2; DB 13; Length 789;
Best Local Similarity 99.2%; Pred. No. 4e-120; 3; Indels 2; Gaps 2;
Matches 631; Conservative 0; Mismatches 3;

QY      2779 GGAACAAGTGTTCATATAGATTGTCACACTTTTGATCCAGAGAGAAAAATTTGGT 2838
DB      3 GGCACACTGTTTCATATAGATTGTCACACTTTTGATCCAGAGAGAAAAATTTGGT 62
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DB      63 TATTAACGAGAACGTGTGCTATTGTTTGCACAGGATTCTTAAATAGTATTAGTAA 122
QY      2899 GGAGCCCAAGATGCACAAGACAGAGATTGAGAGGTTTAGAGAGATGCTTCAAG 2958
DB      123 GGAGCCCAAGATGCACAAGACAGAGATTGAGAGGTTTAGAGAGATGCTTCAAG 182
QY      2959 GCTTATCTAGTATTGTCAGCAGATGCCAATCTCTTCAATTAATCTTTTCAATGATGCT 3018
DB      183 GCTTATCTAGTATTGTCAGCAGATGCCAATCTCTTCAATTAATCTTTTCAATGATGCT 242
QY      3019 GGCTCTGGAATGCGAGAACTACTTTTGGATGACATGTCATACATTGGAAGACCTTA 3078
DB      243 GGCTCTGGAATGCGAGAACTACTTTTGGATGACATGTCATACATTGGAAGACCTTA 302
QY      3079 GCGTTGATTAACCTGAGCAGAGAGGCTTTGGATTTTCAATGAACAAATGATGATGTA 3138
DB      303 GCGTTGATTAACCTGAGCAGAGAGGCTTTGGATTTTCAATGAACAAATGATGATGTA 362
QY      3139 CATCATGTGTGCTGACCAACAAATAATGATGGATCTTCACACAAATTAACAGCATGCA 3198
DB      363 CATCATGTGTGCTGACCAACAAATAATGATGGATCTTCACACAAATTAACAGCATGCA 422
QY      3199 TTGAACCTG-AAAGATACTGAGAAAAATGAAGCTCACTCTGACACTACCTGACTGTT 3257
DB      423 TTGAACCTGAAAAAGATACTGAGAAAAATGAAGCTCACTCTGAGATCCACACTGACTGTT 482
QY      3258 AATTAATCTCAGAGAGCAAAAGACCGTTCATGAGAAATTCACAAATCCATGAAACACATT 3317
DB      483 AATTAATCTCAGAGAGCAAAAGACCGTTCATGAGAAATTCACAAATCCATGAAACACATT 542
QY      3318 AG-ATTACAGCAAGAACAGAAATAATACTATATATTAATTAATATGTAACGCAAC 3376
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QY      3377 AGGTTTGATAGCACTTAACTAGTTCATTTCAAAA 3412
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RESULT 15
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LOCUS      UI-M-Fyo-ctf-g-j-12-0-UI.r1 NIH_BMAP_Fyo Mus musculus cDNA clone
DEFINITION: IMAGE: 6854605 5', mRNA sequence.
ACCESSION      CD349473
VERSION      CD349473.1 GI:31140988
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/
AUTHORS      1 (bases 1 to 785)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-remail.nih.gov
      Tissue Procurement: Dr. Jim Lin, University of Iowa
      cDNA library preparation: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Distribution: Distribution information can be found at
      http://genome.iowa.edu/distribution/mousefl.html
      This clone was contributed by the Brain Molecular Anatomy Project
      (BMAP)
Seq primer: pyx-5.
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/notes="Organ: Brain; Vector: pyx-Asc; Site: 1: EcoR I;
Site: 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AAGCGAGACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
program coordinator."
BASE COUNT      238 a      169 c      172 g      203 t      3 others
ORIGIN
Query Match      17.7%; Score 603.6; DB 14; Length 785;
Best Local Similarity 96.7%; Pred. No. 2.4e-119;
Matches 674; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

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DB      61 GTTATTGAACCAAGTAGCAACCGTGAAGAAAGATCCATATGAGAAATTTGTTGCT 120
QY      361 ATCGGCATCCAGTGTGCGAATTTGATATGATTAAAGATCTGAAGTACAGAGCTTCCGA 420
DB      121 ATTCGCATCCAGTGTGCGAATTTGATATGATTAAAGATCTGAAGTACAGAGCTTCCGA 180
QY      421 AGAAATATTTCTAAATGTTTGTAAAGAGGTGTGATCTTAAGGATTTTAATCACTCAT 480
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QY      481 AGTAGAGCAATATATGTCTATCCGACATGTAGATCTTCAACAGAGCTGCAAGAC 540
DB      241 AGCAGAGCAATATATGTCTATCCGACATGTAGATCTTCAACAGAGCTGCAAGAC 600
QY      541 ATATATTAATTAATTTGATAGAGCCAAATTAATAGTGTGATTTGGGTAAATGTTCTCA 600

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QY 601 AATATGACAAGCAGAGATATCTGTGAAAAATCAACCATGACTGTGCGAACAAGTA 660
Db 361 AACACAGACAAAGCAGAGATACCTGTGAATCATATGACTGTGCGAAGCAAGTC 420
QY 661 ATTGCTGAGCAATCAGGAAAAAACTAGAAGTGTGCTATCATCTGAACAATTAAA 720
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QY 721 CTCTGTGTTTAAATATCAGGGCAATGATTTTAAAGTGTGATGTGATGAATAC 780
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QY 841 AGGATGCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAACTGCCAATGGAC 900
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QY 961 GAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGATATAAAATCTT 1017
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Job time : 4536.51 secs

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Db	241	GAATTTTGTGTAACAAGACGACTTTGTGATCTTGCGCTTTTTCACCACTTTTAAAA	300
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Qy	841	AGGATGCCCAATTTGAAGATGATGCTAAAGAAAGCTTTATTTCTCAACTGCCAATG	900
Db	841	AGGATGCCCAATTTGAAGATGATGCTAAAGAAAGCTTTATTTCTCAACTGCCAATG	900
Qy	901	TGTTTTACAAATGCCATTTATTTCCAGAGCAATTTCCACAGCTAACCAATATGAAATG	960
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Qy	1381	GTTACTGATCAAAATCCAAATTAAGAAACCTCATGCTTAGAGTTGAGATTTGACTGGTTC	1440
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QY 2461 GAAATATCTGGCAAAATCAAGGCTTATCTTGGAAATGTTACTTATGCTGCTGCA 2520
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RESULT 2
US-09-764-877-3796/c
; Sequence 3796, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antihodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3796
; LENGTH: 4074
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TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1934)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3796

Query Match
Best Local Similarity 98.6%; Pred. No. 8e-105;
Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 2931 TGAGAGTTTCAGAGATGTGTTTACAAAGCTTATCTAGTATTGACAGATGCCAATCT 2990
DB 3417 TTAAGGTTTCAGAGATGTGTTTACAAAGCTTATCTAGTATTGACAGATGCCAATCT 3358
QY 2991 CTTCAATTAATCTTTTCCATATGATGCTGCTGCTGGAATGCCGAATCAATCTTTTGA 3050
DB 3357 CTTCAATTAATCTTTTCCATATGATGCTGCTGCTGGAATGCCGAATCAATCTTTTGA 3050
QY 3051 TGACATTGCAATACATTCGAAGAACCCTAGCCTTAGATTAATCTGACAGCAAGAGCCTTTGA 3110
DB 3297 TGACATTGCAATACATTCGAAGAACCCTAGCCTTAGATTAATCTGACAGCAAGAGCCTTTGA 3238
QY 3111 GTAATTCATGAACCAATGAATGATGATGATGATGATGATGATGATGATGATGATG 3170
DB 3237 GTAATTCATGAACCAATGAATGATGATGATGATGATGATGATGATGATGATGATG 3178
QY 3171 GATCTTCACACAAATTAACAGCATGATGATGATGATGATGATGATGATGATGATGATG 3229
DB 3177 GATCTTCACACAAATTAACAGCATGATGATGATGATGATGATGATGATGATGATGATG 3118
QY 3230 CTCACCTGGAACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3289
DB 3117 CTCACCTGGAACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3058
QY 3290 AGGAATTCGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3348
DB 3057 AGGAATTCGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2998
QY 3349 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3408
DB 2997 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2938
QY 3409 AAAA 3412
DB 2937 AAAA 2934

RESULT 3
US-09-814-353-19587
; Sequence 19587, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
```

PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 19587
LENGTH: 3777
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 3772..3773, 3774, 3775, 3776, 3777
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-19587

Query Match 12.9%; Score 441; DB 12; Length 3777;
Best Local Similarity 50.2%; Pred. No. 5,1e-102;
Matches 1567; Conservative 0; Mismatches 1450; Indels 106; Gaps 15;

QY 58 ATCTAGTGAATGTTTACTACCAATGGAATGATGACTTATAGATGCTCCGTGAG 117
DB 426 ATACTGTGATTTCTTTTCCCTGCTGATTTATATCCAGTTGAGGTACTCGGGA 485
QY 118 GCTCATTTAGTACTATTAAGCATGACTATTTTAAAGCAAGAAATACCTCTCAT 177
DB 486 GCTACCAATTTCTATATTAAGCATGATTTTGAAGCAAGTTCACAATTCACATGTC 545
QY 178 CAATCTTCTCAAGATGAACTTTCTTACATTTTCTGAAGTGTACCAAGAACAGAAAG 237
DB 546 AACCTCTTATGATATGATGCTCTATATGTTTGCATGTGAAATCAGACTGCTGTAT 605
QY 238 GAAGAATTTTGTGTAAGAAACAGACTTTGTATCTTCCGCTTTTCAACATTTT 297
DB 606 GAGAGAGCTGAAATGAAACAGAACTCTGTGATGACACCTTTTCTCCAGTCTC 665
QY 298 AAAGTATGACCAAGTACGACACCGTGAAGAAAGATCTCAATCCAGAAATGCTTT 357
DB 666 AAATTAGACAAAGATTTGACCCAGGGGAAAA--ATGAGCTCAAAAATTTGAGTTC 722
QY 358 GCTATGCGCATGCGAGTGGCAATTTGATGTTGTTAAAGATCTGAAAGTACAGACTTC 417
DB 723 CTATAGAAAGGCTGCTGATGAAATTTGATCTTGAAGGATCTGAAAGTAAATGAAAT 782
QY 418 CGAAGAAATTTCTTAATGTTTGAAGAGCTGTGATCTTAGGATCTTAATTCCT 477
DB 783 CGAAGAAATGCGCAATTCAGCA-----GAAAAAATCTCTGCA 824
QY 478 CATGTGAGCAATGTATGTCTATCCGACATGTAGATCTTCAACAGAGCTGCCAAG 537
DB 825 CTGTGGATTTGTCTTGATGACTGTGCTAAACAAACATATCCACAGACATGAACA 884
QY 538 CACATATATATTAATGATAGAGGCCAATTAATAGTGTGTTGGTAAATGTTCT 597
DB 885 TCCATCCCTGAAACCTTAGAATTAATTTATGGGGAAGCTCATCTGCTGTTGAT 944
QY 598 CCAATATATGACAGACAGAACTATCTGAAAAATCAACATGACTGTGCTCCAGAAC 657
DB 945 TTGAAAACTGCCGAGAGCTTTTACGTTTCAAGTGTCTCTAATATGAATCTATCAA 1004
QY 658 GTAATGTGTAAGCAATCAGAAAAAACTAGAAATATGTTGCTATCTTGAACAAT 717
DB 1005 GTAATGATTTGGCAATC---CAAAAAGTGTGACTATTCATGGGAAGAAAGTGAAGT 1061
QY 718 AAATCTGTGTTTGAATATCAGGGCAAGTACATTTTAAAGTGTGAGTGTGAAG 777
DB 1062 AGCCCTATGATATG-----TGTGCAAGTCAAGGGGAGAGTGA 1103
QY 778 TACTTCTAGAAAAATATCTCTGAGTCAATATAGTATATAGAGCTGTATATGCTT 837
DB 1104 TATGTTTTGGTGTATCATCCATTAATTCAGTTTCCAGTATATCCGAAATGTGTATGAC 1163
QY 838 GGGAGATGCCCAATTTGAGAT-----GATGGCTAAAGAAAGCTTTATTTCAATGCTC 892
DB 1164 AGACCCCTGCCCCATTTTATCTTGTGGAATGCTGCAAGATCAAGAAATGTATGAACA 1223

QY 893 CAATGACTGTTTATACATGCCATCTTATTCAGAGCAATTTCCACAGTACACATATA 952
DB 1224 GAATGATTCATAGAGCTGCCATTAATGAAATTCATCTATCTTCTTCCATTA 1283
QY 953 TGAATGAGAAACATCTCAAAAATCCCTTTGGCTTATTAATAGACCTAGAAATAAA 1012
DB 1284 CCACCAAGAAACACCAATTAATTTCTCAAGTTTGGGAAATTAACAACCTTTCCAAAT 1343
QY 1013 TTCTTGTGCAACCTAGTAATCTAAATTTGAGACATTTGCAAGATTTATGTTGA 1072
DB 1344 GTCTTGTGTAAGGAA--ATTAATTTAACAAGAACTGTAAGAGTTCAATGTCAGG 1401
QY 1073 CAGTATCTACCATGAGAGAAACCTTATGTA---CAATGTGAACCTCAAGAGTAC 1129
DB 1402 CTGCTCTTTTCAATGTAGTACAGCTCCTGTGTAAGCAATGTAAGTCAAGAGTAC 1461
QY 1130 CTGTTCCAAATCCAGGTGAATGATGCTGTAATTTGATATATACATTTCTGATCTC 1189
DB 1462 GGAATAATGATCATATTTGGAATGAAACACATGGAATTTGATTAATTTGTGACTTAC 1521
QY 1190 CTGCTGCTGCTGACTTGTGCTTTCATTT-----GCTGTGTAAGGCGGAAAGGTG 1244
DB 1522 CAAGATGCTCAATTAATGTTTGTGCTGTTATGCAAGTTTGAATPAAGTAAACGAGA 1581
QY 1245 TAAAGAGAACTGTCAT-----TGCATGGGAAATATTAACCTGTTTG 1291
DB 1582 AATCAAGAAACATTAATCCCTTAATATGACACATCAAGAAAGCGAAAGTGC 1641
QY 1292 ATTAACAGCACTCTAGATCTGAAAAATGCTTTGAATCTTTGGCCAGTACCTATG 1351
DB 1642 ATTAATCTGTAGGTGGGTAAATACATGTTTGTGCTTAAGGCAATTTAGAACTG 1701
QY 1352 GATTAGAAGATTTTGTAACCCATTTGTTGATGCTGATCAATCCAAATPAAGAACTC 1411
DB 1702 GAGACATTAATTAACAGCTGCTCTTCAATTTCTGATGAACTGGAAGAAATGTGATC 1761
QY 1412 CATGCTTAGAGTTGAGTTTGAAGTGTGACAGAGTGTGAAGTTCCAGATATGCTAG 1471
DB 1762 CAATGGAACTGTTCAACAAACAAATCCATATCTGAAATGCAAGCTTGCATGTTAAT 1821
QY 1472 TGATGAGACATGCCAATGCTCTGTATCCGAGAGAGCAATTTAGCTATTTCCAG 1531
DB 1822 TTCAGAGAAATAAAAACAACCTTAATTAATCCCTCTCGATTAAGATTAAGAAAG 1881
QY 1532 CAGACCTAGTAACAGCTAGTGAAGACAAATGAATTAAGGAAATGACAAAGAACAG 1591
DB 1882 CAGCTGATTTGCAAGAGTGAATGCTAATGTCTAATGTCAGAGTGAAGAAAGTTTC 1941
QY 1592 -----TCAAGCAATTTCTACAGAGATCTCTCTGAAATCACTGACAGAGAG 1642
DB 1942 TTCTGTATGAAAGAAATCTTGAAGAGGATCTCCTGTCTCAACTGTGTGAAATGAA 2001
QY 1643 AAGATTTCTATGAGTCAAGAC---ACTATGTGTACTATCCCGAAATTTCAACCA 1699
DB 2002 TGATCTTAATTTGGAATTTGCGCAAGACGCGAGAGATTTCCCAATTCATCGCAA 2061
QY 1700 AATTGCTTCTGTCTGTTAAATGGAATTTGAAATGAATGAAGCCAGATGTATGCTGG 1759
DB 2062 AATTACGTGTCAATCAAGTGAATTAACCTTAGAGTGTGCTCAGCTTCAGGCGTGC 2121
QY 1760 TAAAGATTTGCGCTCCCAATCAAACTGAAACAGGCTATGAACTTGTGAACTGTAATTAC 1819
DB 2122 TTCAAGATTTGGCTTAACCTCCCCCGGAGAGGCTTGAAGCTTGTGAACTTCACTATC 2181
QY 1820 CAGATCTATGTTTGAAGTTTGTGTTGTTGCTTGAAGAAATTTAACAAGATGACA 1879
DB 2182 CAGACAGTACGTTGGAATATGCTGTAGCTGCTG---CGACAGATGAGTGAAG 2238
QY 1880 AACTTTCTAGTATTTAATCAGTACTACAGGCTCAAAATTAATGAACAATATTTGATA 1939
DB 2239 AACTTCTCAATATCTTTTCAACACTGATGCAAGTGTAAATGTAGGCTTTTCTTGATTT 2298

QY 1940 ACTGCTTGAGATTTTCTAGTGAAGAAAGCATTCATCAATCAAGATTGGGCACTTT 1999
 Db 2299 GTGCCCTCTAGATCTCTATTTAGAAAGACATGTGTAATCGAGGATAGGGCAGTTTC 2358
 QY 2000 TCTTTGGCATTTAAATCTGAGATGCAATTAATAACGTTAGCCAGAGTTGGCCGC 2059
 Db 2259 TATTTGGCATCTTAGTCAGAGAGTGCATTTCCGTGCTCTCAGTACAAATTTGGTGTCA 2418
 QY 2060 TTTTGAATCCTATTTGTCGTCATGTGGATGTATTTGAAACACCTGAATAGGCAATCG 2119
 Db 2419 TCCTTGAAGCATCTGCCGGGAGTGTGGGCAATGAAAGTCTTTCTTAGCAGAGTTG 2478
 QY 2120 AGGCAATGAAAAGCTCTTACTTACTGACATTTCTCAACAGAGAGAGAGATGAAA 2179
 Db 2479 AAGACCTCAATTAATTAATACTTAATTAATCAATCAATGCGCTGAAGTTAA 2538
 QY 2180 CACAAAAGCTACAGTGAAGTTTATGTAGAGCAATAGAGCCAGCCGATTTCTAGATG 2239
 Db 2539 ACAAGCCAAAGGAAAGAGGCGCATGCACTCTGTTAAACAGAGTCTTACCGGAG 2598
 QY 2240 CCTTACAGAGGCTGCTGCTCTCTTAAACCTGCTCACTCACTAGAAAACCTCAGGCTTA 2299
 Db 2599 CCTCTGACCTGACAGTCAACCCCTGAACCCATGTTATCTCTCAGAACTCTATGTTG 2658
 QY 2300 AAGAGTGCATTAATGCTCTTCTGCAAAAAGGCCACTGTGTTGAATTTGGAGAACCCAG 2359
 Db 2659 AAAAGTCAATATACATGATTCGAAAATGAAGCTTTGTGGCTGATATACATATCAAG 2718
 QY 2360 ACATCATGTACAGATTAAGTCTGTTTGAAGCAATAGATCATCTTTAAATAGGGATGATT 2419
 Db 2719 TATTTGTAGAGATTCAGT-----TGAAGTGAATTTTAAATGGTATGATT 2766
 QY 2420 TACGCAAGATATGCTAACACTTCAAAATTTATGTTATTTGAAGAAATATCTGCAAAATC 2479
 Db 2767 TAGACACAGATATTTGACACTCCAAATGTGCGCTGATGAGATTTACTCTGGAAGAGAG 2826
 QY 2480 AAGGCTTGAATCTTGAATGTTTACCTTATGTTGCTGTCTCAATGCGTACTGTGTGGAC 2539
 Db 2827 CTGGTTTGAATCTTGGATGTGGATGTGCTTATGGCTGTTAGCAACGAGATGGCTGGCC 2886
 QY 2540 TTATTTAGTGTGTCGCAATTTCTACATATTAATGCAATTTCAATGCAAGAGCGGC---T 2586
 Db 2887 TCATTGAAGTGTGAGACCTCTGAACCAATGTGTCATTCAGCTGAACAGTAGCATG 2946
 QY 2597 TGAAGGTGCACTGCACTTCAACAGCACAACACTACATACAGTGTGCTGAAAGACAAGACA 2656
 Db 2947 TGGGTGTGCAAGAGCTTCAACAAAGATGCCCTTCTGAACTGTCTTAAAGAAATACACT 3006
 QY 2657 AAGAGAAATATATGATGACAGCCATGACCTGTTTACAGCTTCAATGTGTGATCTGTG 2716
 Db 3007 CTGGGAGATGACCTGACCGAGCCATGAGCAATTTACATGCTCTGTGTGGCTACTGTG 3066
 QY 2717 TAGTACTTCAATTTTGGGAATTTGAGATGTCACATAGTACATCATGTGTGAAGAGC 2776
 Db 3067 TAGGTTTCTTATGCTTGGGATTTGGTACAGACATAGTCAACATCATGTGTCAAAAAA 3126
 QY 2777 ATGCAAACTGTTTCAATATAGATTTTGGACCTTTTGGATTCACAAAGAAAAAATTTG 2836
 Db 3127 CTGGCCAGCTCTTCCACATTTGACTTTGACATTTCTTGAATTTCAAAATCTAAGTTTG 3186
 QY 2837 GTATATAACAGAGACGTGTGCACTTTTGGACAGATTTTGAATAGTGTAGT 2896
 Db 3187 GCATTAAGAGAGAGAGTGTGCTTTATTTCTTACCTATGATTTTCAATGTCTATTAAC 3246
 QY 2897 AAGAGCCCAAGATGACAAAGACAGAGATTTGAGAGTTTCAAGAGATGTGTACA 2956
 Db 3247 AAGG-----AAAAACGAAATACAGAAAAGTTTGGCCGCTTCGCGCAGTGTGTAGG 3300
 QY 2957 AGGCTTATAGCTATTCAGACAGATCCAAATCTTCAATAAATCTTTCTCAATGATGTC 3016
 Db 3301 ATGATATCTGATTTTACAGACGAGATGGAAATCTTCTCAATCACTCTTTTGGCGCTGATGT 3360
 QY 3017 TTGGCTCTGAAATGCCAGAACTACAAATCTTTTATGATGATGTGATACATTCGAAAGACC 3076

Db 3361 TGACTGAGGAGCTTCCGAACTCACATCACTCAAGATATATACATCTTAAAGACTCTC 3420
 QY 3077 TAGCTTAGATTAATAACAGACCAAGAGGCTTTGGAGTATTTCAAGAAACAATGATGATG 3136
 Db 3421 TTGCATTAAGGAAAGAGTGAAGAAAGAGCACTCAAAACAGTTTAAGCAAAAATTTGATAGG 3480
 QY 3137 CAC 3139
 Db 3481 CGC 3483
 RESULT 4
 US-09-352-2439
 ; Sequence 2439, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathalagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; FILE REFERENCE: 16511.006/37-21 (10298)C
 ; CURRENT FILING DATE: US/09/960.352
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 2439
 ; LENGTH: 412
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 11-LIB3058-019-Q1-K1-C11
 US-09-352-2439
 Query Match 11.2%; Score 380.6; DB 10; Length 412;
 Best Local Similarity 95.4%; Pred. No. 4.1e-87;
 Matches 392; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1355 TAGAAGATTTGCTGAACCCCTATTTGTTGTTACTGATCGATCAAAATCCAAATTAAGAAACCTCCAT 1414
 Db 2 TAGAAGATTTGCTGAACCCCTATTTGTTGTTACTGATCGATCAAAATCCAAATTAAGAAACCTCCAT 61
 QY 1415 GCTTAGATTTGAGATTTGACTGCTGTTCAAGAGTGTGTTAAAGTCCAGATATGTCAGTGA 1474
 Db 62 GTTTAGATTTGAGATTTGACTGCTGTTCAAGAGTGTGTTAAAGTCCAGATATGTCAGTGA 121
 QY 1475 TTGAAGAGATGCAATTTGCTGTATCCCGAGAGCAGATTTAGCTATTCCACAGCAG 1534
 Db 122 TTGAAGAGATGCAATTTGCTGTATCCCGAGAGCAGATTTAGCTATTCCACAGCAG 181
 QY 1535 GATGTAGTAAACAGACTAGCTAGAGACATGAAATTAAGGAAAAATGCAAAAGAACAGCTCA 1594
 Db 182 GACTGAGTAAACAGACTAGCTAGAGACATGAAATTAAGGAAAAATGCAAAAGAACAGCTCC 241
 QY 1595 AAGCAATTTCTACAGAGATCTCTCTCTGAAATGCACTGAGCAGAGAAAGATTTCTCTAT 1654
 Db 242 GAGCAATTTCTACAGAGATCTCTCTCTGAAATGCACTGAGCAGAGAAAGATTTCTCTAT 301
 QY 1655 GAGTCACAGACACTATTGTGTATCTATCCCGAAATTTCTACCAATTTGCTGTCTG 1714
 Db 302 GAGTCACAGACACTATTGTGTATCTATCCCGAAATTTCTACCAATTTGCTGTCTG 361
 QY 1715 TTTAAATGGAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1765
 Db 362 TTTAAATGGAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 412
 RESULT 5
 US-10-162-160-2
 ; Sequence 2, Application US/10162160
 ; Publication No. US20030099627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Hasedroeck, Bart

APPLICANT: Waterfield, Michael D.
 TITLE OF INVENTION: No. US2003009627A1 Lipid Kinase
 FILE REFERENCE: 2332-1-002
 CURRENT APPLICATION NUMBER: US/10/162,160
 PRIOR FILING DATE: 2002-06-03
 PRIOR APPLICATION NUMBER: US/09/194,640
 PRIOR FILING DATE: 1998-12-01
 PRIOR APPLICATION NUMBER: 9611460.8
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 3387
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-162-160-2

Query Match 9.7%; Score 329.8; DB 14; Length 3387;
 Best Local Similarity 53.2%; Pred. No. 1.7e-73;
 Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

1682 TCCCGGAATCTCTCCCAATTTGCTCTGTCTTTAATTTGAATTTCTAGATGATGATG 1741
 1625 TCCCGGAGCGCTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1684
 1742 CCCGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1801
 1685 CCCGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1744
 1802 TTTCTGATGATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 1861
 1745 TGTCTGATGATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 1804
 1862 AATATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 1921
 1805 AATATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 1861
 1922 ATGAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 1981
 1862 ACGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1921
 1982 AAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2041
 1922 GCAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
 2042 GCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2101
 1982 CCGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2041
 2102 ACGTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2161
 2042 TGTCTGATGATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 2101
 2162 AGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2221
 2102 TGACCTCTCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 2161
 2222 GACGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2281
 2162 AGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2221
 2282 TAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2341
 2222 TGGCTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2281
 2342 TGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2401
 2282 TCATGATCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 2341
 2402 TTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2461
 2333 TTAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2392

2462 AAAATATCTGCAAAATCAAGCTCTGATCTTTGATTTGATTTGATTTGATTTGATTT 2521
 2393 ACGTCTCTGGAAG 2452
 2522 TCGTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2581
 2453 CCGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2512
 2582 A---GTGCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2641
 2513 AACTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2572
 2639 GGTCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2698
 2573 GGTCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2632
 2699 CATGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2758
 2633 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2692
 2759 ACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2818
 2693 ACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2752
 2819 ACAAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2878
 2753 ATTCAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2812
 2879 TCTTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2938
 2813 TGTCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2866
 2939 TTTCAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2998
 2867 TCGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2926
 2999 ATCTTTCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3058
 2927 ACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2986
 3059 CATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3118
 2987 AGTATCTCAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3046
 3119 TGAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3178
 3047 GAGTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3106
 3179 ACA 3181
 3107 ACA 3109

RESULT 6
 US-10-337-192-1
 Sequence 1, Application US/10337192
 Publication No. US2003019521A1
 GENERAL INFORMATION:
 APPLICANT: SABHU, Chanchal et al.
 TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
 FILE REFERENCE: 27866/39033
 CURRENT APPLICATION NUMBER: US/10/337,192
 PRIOR FILING DATE: 2003-01-06
 PRIOR APPLICATION NUMBER: 60/159,655
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 60/238,057
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 5220
 TYPE: DNA
 ORGANISM: Human p110delta complete cDNA

[illegible]

Db	2888	ACATCATGATCCGAGAGAGTGGCGAGCTGTTCCACATTGATTTTGGGCACTTTCTGGGGA	2947
Oy	2819	ACAGAAGAAAAATTTGGTTATTAACGAGAACGTGGCCATTGTTTGACACAGATT	2878
Db	2948	ATTTCAGAGACCCAAATTGGGAATCAACCCGCGAGCGCTGTGCCATTCATCTCCACCTATGACT	3007
Oy	2879	TCTTAATAGTGATTAAGTAAGGAGCCCAAGATGCACAAAAGACAAAGAAATTGAGAGGT	2939
Db	3008	TTGTCCATGTGTATTCAGACAGG-----GAAAGCTAATTAATAGTACAGAAATTTAAGCGT	3061
Oy	2939	TTTCAGAGATGTGTACAGAGCTTTATGTAGCTATTTCAGACAGCATGCCATCTCTTCAATA	2998
Db	3062	TCCGGGGCTACTGTGAAGAGGCTCAACACATCTCGGGCGCCAGGGGCTTCTTCTCCGC	3121
Oy	2999	ATCTTTTCTCAATGATGCTTGCTGTCTGGAATGCCAAGCTAACAATCTTTTGATACATGG	3058
Db	3122	ACCTCTTTGCTTCCTATCGGGCGCGCAAGCCCTGCTGAGCTGACTGCCAAGACATCC	3181
Oy	3059	CATCATTTCCGAAAGACCCCTAGCCCTTAATATAAACTGAGCAAGAGCGCTTGGAGTATTCA	3118
Db	3182	AGTATCTCAAGAGCTCCCTGCGACTGCGGAGAAACAGAGAGAGGACCTGAAGACATTCC	3241
Oy	3119	TGAACAACAATGAATGATGACATCATGATGGCTGCGACACAACAAAATGATGGATCTTCC	3178
Db	3242	GAGTGAAGTTTAACGAAGACCCCTCCCTGAGAGCTGGAACCAAGTAACTCGCTGGCGCC	3301
Oy	3179	ACA 3181	
Db	3302	ACA 3304	

RESULT 8

US-09-918-995-23649

Sequence 23649, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918, 995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235, 076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 23649

LENGTH: 483

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-23649

Query Match	8.9%; Score 304; DB 11; Length 483;
Best Local Similarity	93.9%; Pred. No. 2,1e-67;
Matches 338; Conservative 0; Mismatches 20; Indels 2; Gaps 2;	

Oy	3055	ATTGCATACATTGGAAGACCCCTAGCCTTAGATATAAACTGAGCAAGAGGCTTTGGAGTAT	3114
Db	2	ATTGAACGTTTTCGCGGACCTCGGCGACGAGATATAAATGAGCAAGAGGCTCTGGAGTAT	61
Oy	3115	TTTCATGAACAAATGATGATGATGACATCATCATGTGTGCTGCGACACAAAAATGATTTGGATC	3174
Db	62	TTTCATGAACAAATGATGATGATGACATCATCATGTGTGCTGCGACACAAAAATGATTTGGATC	121
Oy	3175	TTTCACACAATTAACAGCATGTCATTGAACGTG-AAAGATTAATGAGAAAAATGAAAGCTCA	3233
Db	122	TTTCACACAATTAACAGCATGTCATTGAACGTGAAABAAATTAATGAGAAAAATGAAAGCTCA	181
Oy	3234	CTCTGACACTACACTGCACCTGTTAATTAACCTCTCAGCAGGCAAGACCGATTTGCATAGGA	3293
Db	182	CTCTGGAATTCACACTGCACCTGTTAATTAACCTCTCAGCAGGCAAGACCGATTTGCATAGGA	241
Oy	3294	ATTGCAACAATTCATGAACAGCATTAAG-ATTTCAGCGCAAGAGCAAGAAATTAATATCTATAT	3352

Db 242 ATTGCACAAATCCATGAAACAGCATTAATTTACAGCAAGAAATTAATAATCTATAT 301
QY 3353 AATTTAAATATATGATTAACGCAACAGGGTTGTAGACTTAACATGATTCATTTCAAA 3412
Db 302 AATTTAAATATATGATTAACGCAACAGGGTTGTAGACTTAACATGATTCATTTCAAA 361

RESULT 9
US-10-101-235A-3
; Sequence 3, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCR
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; NUMBER OF SEQ. ID NOS: 9
; SOFTWARE: Paceseq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-235A-3

Query Match 8.7%; Score 295.6; DB 12; Length 3342;
Best Local Similarity 52.6%; Pred. No. 9.9e-65;
Matches 855; Conservative 0; Mismatches 724; Indels 45; Gaps 8;

QY 1586 AACAGCTCAAGCAATTTCTACAGAGATCTCTCTGMAATCAGTACAGAGAGAAAG 1645
Db 1655 AGCAATGGAGGCGATATAGCACTGATCCACTTAACCTCTACAGCAGAGAGCAAG 1714
QY 1646 ATTTCTATGAGTCAAGACACTATGTGTAATCTATCCCGAATTTCTACCCMAATTCG 1705
Db 1715 AATTCCTCTGCGATTTTNGATAGCAAGCCTTAAGCAACCCMAAGCATATCTTAAGCTAT 1774
QY 1706 TTCTGTCTGTTAAATGGAATTTAGAGATGAAGTACCCAGATGATTCCTTG----- 1758
Db 1775 TTAGTTCAGTGAATGGGACAGCAAGAAATGTGGCAAAACATPACCAATTTGTGSCA 1834
QY 1759 -----GTAAAAGATGGCGCTCCATCAACCTGAAACAGGCTATGGAATCTTGACT 1810
Db 1835 GAAGGGAAGTCTGGATCAAGTGTGATGTGGGTTAAACAATCAGCTCTTGACT 1894
QY 1811 GTATTACCCAGATCTATGATGATGAGGTTTGTGCTTGGTCTGTAATAATATTTAA 1870
Db 1895 GCAATCTCTAGATGAAATGTAAGACCATTTGAGTTCAAGATTCGAGAGC---TTGG 1951
QY 1871 CAGATGCAAACTTTCTCAGTATTTAATCAGTAGTACAGGTCCTAAAAATATGACAAAT 1930
Db 1952 AGAGCATGATGTTCTGCAATTAATCTTCAATATGTCAGGCTGTGAATTTGACCAT 2011
QY 1931 ATTGGATTAATCTGCTGTGAGATTTTACTGAAAGAAAGCATGACTAATCAAGAGTTG 1990
Db 2012 ACCATGATAGCGCCCTTGCCAGATTTCTGCTGAAGCGTGTGTTAAGAAACAAAAGATTG 2071
QY 1991 GGCACCTTTTCTTTGGCATTTAAATCTGAGAT---GCACATTAACAGTTAGCCAGA 2047
Db 2072 GTCACTTTTGTGTTGGTCTTGAGAGTGAAGTAGATAGCCAGTCAAGACATATAGAGAA 2131
QY 2048 GGTTCGCTGCTGCTTTGAGAGTCTAATGTGCTGATGTGGAGTGTATTTGAAGCACTGA 2107
Db 2132 GGTTCGCTGATCTCTGGAAGCTATCTGAGGGGCTGTGGCAAGCCATGCTGACAGACT 2191
QY 2108 ATAGGCAAGTGAAGCAATGAAAGCTCATTAATCTTAATGAGATTTCTCAAGAGAGA 2167
Db 2192 TTACCAACAAAGTCCAAAGTAATGAGATGTTAACAAGATCACTTGTATTTAAATGCG 2251

QY 2168 GGAGAGTGAACACAAAAGGTACAGATGAAGTTTACTGTAGCAAAATGAGGCGACG 2227
Db 2252 TCTCTCTGTAAGAAATGATGAGTCACTCCCAATTTATTTACAACTTTAAACAAAGCTTG 2311
QY 2228 ATTTCAATG-----GATGCCCTACAGGCGCTGTGCTCTCTCTAAACCCCTGCTCATG 2278
Db 2312 AAAACCTGAGAAATTTCTCAATCCCGAAAGCTTTAGAGTTTCCATATGATCTTGAGCTGA 2371
QY 2279 AACTAGAAACCTCAGGCTTTAAAGAGTGTGAATTTATGTTCTTGTGCAAAAAGGCCACTGT 2338
Db 2372 AAGCAGAGAGCGCTGCGCAATTTGAAATGTAAGTATAGGCTCTCAAGAAAACCACTAT 2431
QY 2339 GGTGAATTTGGAGAACCAAGACATCATGTCAAGTTACTGTTTCAGAAACATGAGATCA 2398
Db 2432 GGCTGAGTTTAAATGTGCGGATCTTA---CAGCCCTATCAAAATGAACAAATGGAATTA 2488
QY 2339 TCTTTAAATGGGAGTGAATTTAGCGGCAAGATATGCTAACCTCAATTAATCTGATTA 2458
Db 2489 TCTTTAAACATGTGTGATGATCTGGCGCAAGACATGCTTTATTTACAGATTTACGAATCA 2548
QY 2459 TGGAAATATCTGCAAAATCAAGTCTTGATCTTGAATGTTACCTTATGTTGTCTGT 2518
Db 2549 TGAAGTCTATTTGGGAGACTGAATCTTTGATCTATGCTCTCCCATATGTTGATTCATTT 2608
QY 2519 CAATCGTGAAGTGTGGGACTTATGAGGTGTGGCAATTTCTCACTATTTATGCAAA 2578
Db 2609 CAATCGTGAAGTGTGGGACTTATGAGGTGTGGCAATTTCTCACTATTTATGCAAA 2668
QY 2579 TTCAATGCAAGGCGCTTGAAGGTGCACTGTGACATTTCAACAGCCACACACTATCATAGT 2638
Db 2669 TTAG---CAAAACAGTGTGGGACACGAGACATTTAAAGTGAAGTCTTAATCACT 2725
QY 2639 GGCTCAAGACAGAAAC---AAGGAGAAATATATATGATGAGCGCATTTGACTTTACAC 2695
Db 2726 GGCTCAAGAAATATCCCTACTGAAGAAAGTTTACAGCAGAGTGGAGAAATTTGTT 2785
QY 2696 GTTCATGTGTGATATCTGTATAGTACTTCAATTTTGGAAATGAGATGTCACAAAT 2755
Db 2786 ATTCCTGTGAGGCTACTGTGTGGCAACCTTTGTTCTGGAAATGAGCGACAGACAAATG 2845
QY 2756 GTAACTATGTGTGAAGAGAGTGAACACTGTTTATATAGATTTTGAACATTTTGG 2815
Db 2846 ACAATATATGATCACCGAGACAGAAACCTATTTATATGACTTCGGGCAATTTCTG 2905
QY 2816 ATCAAGAAAGAAATTTGTTATTAACGAGAGGTGCGCAATTTGTTGACAGAG 2875
Db 2906 GGAATTAACAAGTTTCTGGGCAATTAATTAAGAGAGTGCATTTTGTCTAAACCTG 2965
QY 2876 ATTTCTTAATAGATTAATTAAGAGCCCAAGATGCAACAAAGACAGAAATTTGAGA 2935
Db 2966 ACTTCCCTTTGTGAGT-----GGAACCTGTGAAAGAAAGACAGGCCACACTTCAGA 3019
QY 2936 GGTTCAGAGATGTGTACAGGCTTATTTACTATTTGACAGCATGCCAATCTCTTCA 2995
Db 3020 AATTTAGGACATCTGTGTTAAGGCTTATCTACCCCTTGTCTACACAAACCTCTGA 3079
QY 2996 TAAATCTTTCTGAATGATGCTGTGCTGTGAATGCGAGAACTACATCTTTGATGACA 3055
Db 3080 TCAATCTGTTCTCATGATGCTGATGACAGAAATGCCCCAGTTAACAAGAAAGACACA 3139
QY 3056 TTGCATACATTTGAAAGACCTTAGCTTAGATTAATCTGAGCAAGAGGCTTTGAGATTT 3115
Db 3140 TTGAATATATCCGGAGATGCCCTCAAGTGGGAAATATGAGGAGATGCTAAAGATAT 3199
QY 3116 TCATGAAACAAATGAATGATGACATCATGTGTGCTGTGACAAACAAATGATTTGATCT 3175
Db 3200 TTCTTGATCAGATCGAAGTTTGAAGACAAAGATGAGACTGTGCAAGTTAATTTGTTTC 3259
QY 3176 TCCA 3179
Db 3260 TAQA 3263

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RESULT 10
US-10-092-219-1
; Sequence 1, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domain, Jan
; TITLE OF INVENTION: No. US20020115114A1el Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092.219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

Query Match      6.5%; Score 223; DB 13; Length 5061;
Best Local Similarity 49.3%; Pred. No. 5.5e-46;
Matches 806; Conservative 0; Mismatches 790; Indels 39; Gaps 7;

Dy 1566 ATTAAGGAAATGACAAAGAAAGCTCAAGCAATTTCTACAGAGATCCTCTCTGA 1625
Dy 2598 ACTAGAGATGATATATAAGGAAACCTTCTGATATCTTCAATAAGCTCATCACTGG 2657
Dy 1626 AATCACTGAGCAGAGAAAGATTTTCTATGAGTCACAGACACTTTGTAACTATCCC 1685
Dy 2658 ACTTCTTAAAGAAATTAAGCTTTTATGGAAGAAAGCTTATTTCTTCAAAACACC 2717
Dy 1686 CGAAATCTACCCAAATGCTCTGTCTGTATTAATGAAATCTAGAGATGAAGGCCA 1745
Dy 2718 AATTTGCTCTCTAAATATTAGCAAGCGCCCAACTGAAATGGGTAATCTTGCCAA 2777
Dy 1746 GATGATTCCTTGGTAAAGATTTGGCTTCAATCAACCTGAACGGCTATGAACTCT 1805
Dy 2778 AACTTACTCATGCTTCCACAGTGGCTGCAATTTGACCTCAATTTGATTGGAACCTT 2837
Dy 1806 GGACTGTAAATACCCAGATCCTATGTTGAGATTTTCTGTGCGTCTTGGAAATA 1865
Dy 2838 TGATTCAAATTTTGCTGATCAGAAAGTAAGATCCTTACGTG---GACCTGGATTGAGGC 2894
Dy 1866 TTTAACAGATGACAAACTTCTCAGTATTTAATTCAGTATGAGTACAGGTCTCTAAATATGA 1925
Dy 2895 CATTAGTATGATGATGCTAACAGATCTTCTTCCACAGTTTGTACAAAGCTTTGAATATGA 2954
Dy 1926 ACAATATTTGATTAACCTGCTGTGAGATTTTACTGAAAGAAAGATTTGATCAAG 1985
Dy 2955 AATTACTTGAATAGTATTAATGATGCAATTCCTTTTGTCCAGGGGATTGGGAAATATCCA 3014
Dy 1986 GATTGGGCACTTTTCTTTGGCATTTAAATCTGAGATGCAATTAATAAGTATGAGCA 2045
Dy 3015 GATGACACACATTTATATATGCTTCTTCAAAAGATCCCTGCAATGATGACAGTTTATGAC 3074
Dy 2046 GAGGTTTGCCCTGCTTTTGGAGTCTTATGTCGTGATGATGAGATGATTTGAAGCACT 2105
Dy 3075 CCGATACGAAATGTTTGG-----GTGCTCTCTGCTCAGTGAAGGAAAGACACTT 3126
Dy 2106 GAATGAGCAAGTCAGGCAATGGAAGAAAGCTCATTTAACTTAACTGACATTTCTCAACAGGA 2165
Dy 3127 AGAGAAAGAACTTTAAACAGACGAACCTTGTACAGCTTTTGAAGGAGATGACAGAAAAA 3186

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Dy 2166 GAGGAAGATGAAACAAAGGTACAGATGAAGTTTATGTTGACAAATGAGCGACC 2225
Dy 3187 GTAAGCAGGCTAGTGATACAGCCAGACAGTGTGTTCTCCAAAGAACT-ATGGAACAGAT 3245
Dy 2226 AGATTTATGATGCCCTTACAGGCTTGCTGTCTCTCCCTAAACCTGCTCATCACTAGG 2285
Dy 3246 ACAGTCTTTTTCAGAAATTAATGCGCTCTCTCCCTCAAGCCAAAGCTTATGTCGAAA 3305
Dy 2286 AAACCTCAGGCTTAAAGATGCGAATTAATGCTCTGCAAAAAGGCACTGTGTGAA 2345
Dy 3306 AGAATTAATATTAATGATGATGCTTCTTCAAGTTCATTAAGTGTGCTCCCTAAAGTAC 3365
Dy 2346 TTGGGAGAACCCAGACATCATGTCAGATTAAGTCTTCAAGACAAATGATCATCTTTAA 2405
Dy 3366 AATGTGAATGCTGACCCCTGAGGAG-----AAGAAATTAATGTCATGTTTAA 3413
Dy 2406 AATGGGATGATTTAGGCAAGATATGCTTAACACTTCAATTAATGCTTATGAAAA 2465
Dy 3414 GGTGTGAAGATCTTGAGCAAGATATGTTAGCTTTACAGATGATTAAGATTAAGTATGATGA 3473
Dy 2466 TATCTGCAAAATCAAGGTCTTGATCTTCAATGTTTACCTTATGTTGTCTGTCATCGG 2525
Dy 3474 GATCTGCTTAAAGAAAGACTAGATCTGAGATGATGATTTTCAAAAGTCTCTCAACGCG 3533
Dy 2526 TGACTGTGAGGACTTATTAATGAGTGTGCGAAATTTCTCAACATTAATGCAATTCAGTG 2585
Dy 3534 CAGAGATCGAGGACTGTGAGGCTGTTCTGCTCCGATACCTCAGAAATCCAGAT 3593
Dy 2586 CAAGCGGCTTGAAGAGTGCACCTGCACTTCAACAGCCACACACTACATAGGCTCAA 2645
Dy 3594 GGAATATGATGTCAGAGATCTTTAAAGATTAACCACTTGCAGAGTGGCTAAG---AA 3650
Dy 2646 AGACAAAGAAAGAAATATATATGATGAGCAGCTTACCTGTTTACAGTTTATGCTG 2705
Dy 3651 ATACATTCCTCTGAAGAAATATGAAGGCTTCAAGAACTTATCATTCCTGTGC 3710
Dy 2706 TGATATCTGTATGATCTTCACTTATTTGGAAATTTGAGATGTCACAAATGATCAT 2765
Dy 3711 TGATATCTGTATGATCTTCACTTATTTGGAAATTTGAGATGTCACAAATGATCAT 3770
Dy 2766 GGTAAAGAGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATGTCAGAA 2825
Dy 3771 GCTTGAGAGCAGGGAACATGTTTCAATGATTTGAAAGTTTGGAGATGACACA 3830
Dy 2826 GAAATAATTTGTTATTAACAGAAAGTGTGCAATTTGTTTGGACAGATTTCTTAAT 2885
Dy 3831 GATGTTGGCAGCTTCAAAAGGATTCGGGCTCTTTGTGCTGACCTGATATGAGATA 3890
Dy 2886 AGTATTAATGAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAAGGTTTCAAGA 2945
Dy 3891 TGTCAATTAATGGGGGTGA-----AAAGCCACCATTCGTTTCAAGTTGTTGGA 3941
Dy 2946 GATGTTTACAAAGCTTATCTAGTATTTGCAACAGATGCCAATCTCTCATTAATCTTT 3005
Dy 3942 CCTGTGCTGTCAGGCTTCAAACTTGATTAAGAAACAAACAACTTTTCTTAACTCTCT 4001
Dy 3006 CTCAATGATGCTGCTGCTGGAATGCCAGAACTCAATCTTTGATGACATTTGATCAT 3065
Dy 4002 TTCACTGATGATCTTCTTCAAGGTTTACCAAGAACTTACAAATTTGAATATGCT 4061
Dy 3066 TCGAAGACCTTACCTTATGATTAACACTGAGCAAGAGCTTTGAGATTTTCAATGAACA 3125
Dy 4062 TAGAGATGACATTCACCCCAAACTACAGAGCGCAGAAAGCT---ACAATTTCTTACTAG 4118
Dy 3126 AATGAATGATGACATATGATGCTGAGCAACAAATGATTTGATTTGATCTTCCACAAAT 3185
Dy 4119 GCTTATTAATGAATCAAGTTTGGAAAGCAATTCGACAAAGTTTAACTTTCATTAACAACCT 4178
Dy 3186 TAAACAGATGATTT 3200
Dy 4179 TGCTGAGCTTCTGTTT 4193

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RESULT 11
US-10-027-632-213996
; Sequence 213996, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213996
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213996

Query Match
Best Local Similarity 5.1%; Score 173.8; DB 12; Length 1248;
Matches 228; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

QY 1890 GTATTATTCAGCTAGTACAGGCTCTAAATATGAAACAATATTTGGATACTGCTGT 1949
DB 653 GTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
QY 1950 GAGATTTTACTGAGAAAGCATTGA-CTAATCAAGAGATTGGGCACTTTTCTTTGGC 2008
DB 713 CAAGATTATTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 772
QY 2009 ATTAAATCTGAGATGACATTAACAGTTAGCCAGGTTGGCTGCTTTGGAGT 2068
DB 773 CTTTACATCTGAGATGACATTAACAGTTAGCCAGGTTGGCTGCTTTGGAGT 832
QY 2069 CTTATTCGTCGATGCGGATGATTTTGAAGCAGCTGAATAGGCAATGCGAGCAATGG 2128
DB 833 CTTATTCGTCGATGCGGATGATTTTGAAGCAGCTGAATAGGCAATGCGAGCAATGG 892
QY 2129 AAAAGCTCATTACTTACTGACATTTCTCAACAGAGAGAGAGATGAAAACACAAAGG 2188
DB 893 AAAAGCTCATTACTTACTGACATTTCTCAACAGAGAGAGAGATGAAAACACAAAGT 952
QY 2189 T 2189
DB 953 T 953

RESULT 12
US-10-027-632-213996
; Sequence 213996, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
```

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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213996
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213996

Query Match
Best Local Similarity 5.1%; Score 173.8; DB 13; Length 1248;
Matches 228; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

QY 1890 GTATTATTCAGCTAGTACAGGCTCTAAATATGAAACAATATTTGGATACTGCTGT 1949
DB 653 GTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
QY 1950 GAGATTTTACTGAGAAAGCATTGA-CTAATCAAGAGATTGGGCACTTTTCTTTGGC 2008
DB 713 CAAGATTATTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 772
QY 2009 ATTAAATCTGAGATGACATTAACAGTTAGCCAGGTTGGCTGCTTTGGAGT 2068
DB 773 CTTTACATCTGAGATGACATTAACAGTTAGCCAGGTTGGCTGCTTTGGAGT 832
QY 2069 CTTATTCGTCGATGCGGATGATTTTGAAGCAGCTGAATAGGCAATGCGAGCAATGG 2128
DB 833 CTTATTCGTCGATGCGGATGATTTTGAAGCAGCTGAATAGGCAATGCGAGCAATGG 892
QY 2129 AAAAGCTCATTACTTACTGACATTTCTCAACAGAGAGAGATGAAAACACAAAGG 2188
DB 893 AAAAGCTCATTACTTACTGACATTTCTCAACAGAGAGAGATGAAAACACAAAGT 952
QY 2189 T 2189
DB 953 T 953

RESULT 13
US-09-814-353-21472
; Sequence 21472, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elshoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
PRIORITY FILING DATE: 2001-07-31
PRIORITY FILING DATE: 2000-07-31
PRIORITY FILING DATE: 2000-11-02
PRIORITY FILING DATE: 2000-11-02
PRIORITY FILING DATE: 2001-05-11
PRIORITY FILING DATE: 2001-05-11
PRIORITY FILING DATE: 2001-05-15
PRIORITY FILING DATE: 2001-05-15
PRIORITY FILING DATE: 2001-05-22
PRIORITY FILING DATE: 2001-05-22
PRIORITY FILING DATE: 2001-06-06
PRIORITY FILING DATE: 2001-06-06
PRIORITY FILING DATE: 2001-06-13
PRIORITY FILING DATE: 2001-06-13
PRIORITY FILING DATE: 2001-06-19
PRIORITY FILING DATE: 2001-07-09
PRIORITY FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 477
LENGTH: 5990
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477

Query Match 4.9%; Score 168.2; DB 10; Length 5990;
Best Local Similarity 52.5%; Pred. No. 7.2e-32;
Matches 447; Conservative 0; Mismatches 390; Indels 15; Gaps 3;
QY 2241 TTGAATGGGAGAACCCAGATCATGTCAGAGTTACGTGTTGAGAAATGAGATCATC 2400
DB 2988 TTGCCATTGAAGATCATCTTTCATCAATGCTAATCCAAAGGCAAAATATCAGTGTATT 3047
QY 2401 TTTAAATGGGAGATTTAAGGCAAGATATGCTAAACATTCAATTATTCGATTATG 2460
DB 3048 TTTAAGGCCGCGCGAGATCTTCGCGAGATATGCTTGTCTGCAATTATTCAGTGTATG 3107
QY 2461 GAAAAATATCTGGCAAAATCAAGTCTTGATCTTGAATGTTACCTTATGTTGTCTGCA 2520
DB 3108 GACAACTTTGGCTTCAGAGGCGCTCGATATGCAAAATGATCATTTATGATGTCTAGCC 3167
QY 2521 ATGGTGACTGTGGGACTTATGAGGTGTGGCAAAATCTCACTATATGCAATT 2580
DB 3168 ACAGGAAAGGCTCAGAGATTCATAGAGATGTGTCTGATGCTTGAACGTTGCCAAGATC 3227
QY 2581 CAGTCAAAAGCGCGCTTGAAGGTGCACTGCACTGTTCAACAGCCACACATCATCATG 2640
DB 3228 CATCTGCACTCTGGGCTGATAGACCCCTGAAAGAAAACACATCA--AGAACTGGTTC 3284
QY 2641 CTCAAGACAAACAAAGGAAATATATGATGACAGCATTTGACCTGTTTACAGTTCA 2700
DB 3285 AGTCAGACAAACCACTTAAAGGAGATTATGAAAGGCTTGAGAACTTTTTCCTCT 3344
QY 2701 TGTGCTGATATCTGTGATGCTATCTTATTTGGAAATGAGATCGTCAATATGATAC 2760
DB 3345 TGTGCTGCTGT 3404
QY 2761 ATCATGTGAAAGCATGATGACATCTTTCATATAGATTTTGGACACTTTTGGATCAC 2820

DB 3405 ATCATGTGCAAAAGTCAGGCCACATGTTTCATATGACTTTGGAAAATCTTGGGTCAC 3464
QY 2821 AAGAGAAAAAATTTGGTTTAAACGAAACGTTGCTATTTGTTGACACAGATTTTC 2880
DB 3465 GCACAAACATTTGGCGTTATTAAGAGACCGGCTTTTCATTTTACTTCAGAGATG 3524
QY 2881 TTAATAGTATTAAGTAAGAGGCCCAAGAAATGCAAAAGCAAGAAATTTGAGGTTT 2940
DB 3525 GAGTACTTATTTAGCGAGGGTG-----GGAAAAACACAGCATTTTCAAGACTTC 3575
QY 2941 CAGAGATGTGTTACAAAGCTTATCTAGCTATTGACAGCATGCAATCTCTTCATAAT 3000
DB 3576 GTGGAATCTGTCAGAGGCTTCAACATTTGTGGAAGCACAGCCAACTGCTCTGAGC 3635
QY 3001 CTTTTCATAGATGCTGCTGCTGCAATGCGAATACATCTTTGATGATGCA 3060
DB 3636 CTTCTAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3695
QY 3061 TACATGGAAGAACCCCTAGCCTTAGATTAATACTGAGCAAGAGCTTTGAGATTTTCATG 3120
DB 3696 TACGTACAGACATCTCCGGCCAGACAGACAGACCTGGAAGCCAAAGTCAATTTAC 3755
QY 3121 AAACAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
DB 3756 ACAGAGATTAAGCA--GAGTCTGAGGTGCTTCCAGTTAACTGAATTAACCTGATCCAC 3812
QY 3181 ACAATTTAAAG 3192
DB 3813 ACCCTTGACAG 3824

Search completed: November 7, 2003, 13:39:09
Job time : 714.638 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:38:38 ; Search time 155.161 Seconds
(without alignments)
9706.030 Million cell updates/sec

Title: US-09-325-095-32

Perfect score: 3412

Sequence: 1 ATGCTCCAGACATCATC.....TAACTAGTTCATTTCAAA 3412

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues 1139956

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3412	100.0	3412	1	US-08-162-081B-32
2	3412	100.0	3412	2	US-08-162-081B-32
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4	3236.8	94.9	3240	1	US-08-162-081B-34
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6	3236.8	94.9	3240	3	US-09-085-957-34
7	3008.6	88.2	3207	1	US-08-162-081B-35
8	3008.6	88.2	3207	2	US-08-162-081B-35
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28	226.2	6.6	5285	3	US-09-170-996-29	Sequence 29, Appl
29	223	6.5	5061	4	US-09-355-160D-1	Sequence 1, Appl
30	130	3.8	3504	3	US-08-857-076-47	Sequence 47, Appl
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36	90.2	2.6	357	4	US-09-765-298A-13	Sequence 13, Appl
37	70.2	2.1	204	4	US-09-016-434-245	Sequence 245, Appl
38	67	2.0	3252	3	US-09-119-442-1	Sequence 1, Appl
39	67	2.0	3252	3	US-09-677-064-1	Sequence 1, Appl
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41	63.4	1.9	3063	4	US-09-620-312D-474	Sequence 474, Appl
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43	44.8	1.3	381	1	US-08-162-081B-38	Sequence 38, Appl
44	44.8	1.3	381	2	US-08-780-872-38	Sequence 38, Appl
45	44.8	1.3	381	3	US-09-085-957-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-162-081B-32
Sequence 32, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OR INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"
US-08-162-081B-32

Query Match 100.0%; Score 3412; DB 1; Length 3412;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCCCTCCAGACATCATAGGTGAACCTGGGGGCACTCCACTGATGCCCCCAAGAAC 60

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RESULT 2
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; Sequence 32, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Orsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/SB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3304
; OTHER INFORMATION: /standard_name= "CDS"
US-08-780-872-32

Query Match 100.0%; Score 3412; DB 2; Length 3412;
Best local Similarity 100.0%; Pred. No. 0;
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1321 ATGCTTTGATATCTTTGGCCAGTACTCATGATTAAGAAATTTGCTGAACCTATTGGT 1380
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DB 1381 GTTACTGATCAAAATCCAAATTAAGAACTCCATGCTTGAAGTGAAGTTTGACTGCTTC 1440
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Qy 2401 TTTAAATATGGAGATGATTTTACGGCAAGATATGCTTAACTCTTCAATATTCGATTTATG 2460
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Qy 2521 ATCGTGAATGTTGGGACTTATTAAGTGTGCGAAATTTCTCACTATTTATGCAAAAT 2580
Db 2521 ATCGTGAATGTTGGGACTTATTAAGTGTGCGAAATTTCTCACTATTTATGCAAAAT 2580
Qy 2581 CAGTGAAGAGCGGCTTGAAGAGTGCATGCACTTCAACGCCACACACTACTCATCATG 2640
Db 2581 CAGTGAAGAGCGGCTTGAAGAGTGCATGCACTTCAACGCCACACACTACTCATCATG 2640
Qy 2641 CTCAAAGACAAGAACAAAGAGAAATATATGATGCAAGCCATGACCTGTTTACACGTTCA 2700
Db 2641 CTCAAAGACAAGAACAAAGAGAAATATATGATGCAAGCCATGACCTGTTTACACGTTCA 2700
Qy 2701 TGTGCTGATATCTGTGATGCTTCACTTTTGGGAATGAGATGCTTCAATATGATAC 2760
Db 2701 TGTGCTGATATCTGTGATGCTTCACTTTTGGGAATGAGATGCTTCAATATGATAC 2760
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Qy 3001 CTTTCTCATGATGCTGCTGCTGGAATGCCGAATCTAATCTTTTGTATGATTCGAC 3060
Db 3001 CTTTCTCATGATGCTGCTGCTGGAATGCCGAATCTAATCTTTTGTATGATTCGAC 3060
Qy 3061 TACATTCGAAAGAGCCTAGCCTTAGATTAATCTAGACCAAGAGCTTGGAGTATTCATG 3120
Db 3061 TACATTCGAAAGAGCCTAGCCTTAGATTAATCTAGACCAAGAGCTTGGAGTATTCATG 3120
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Qy 3241 CACTACACTGCACTGTTTAAATCTCTACAGAGCAAGACCGATGATGAGATTCAC 3300
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RESULT 3
US-09-957-32
; Sequence 32, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Oren; Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ. ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name= "CDS"
US-09-085-957-32
Query Match 100.0%; Score 3412; DB 3; Length 3412;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	12	ACATTAGACGATATBACCAAGCAACTATTTTAAAGACAAGAAAATACCCTCGATCAA	180
Db	121	ACATTAGACGATATBACCAAGCAACTATTTTAAAGACAAGAAAATACCCTCGATCAA	180
OY	181	CTTCCTCAAGATGATCTCTTACATCTTCGTAAAGTGTGTACCAAGACGAAGAGGAA	240
Db	181	CTTCCTCAAGATGATCTCTTACATCTTCGTAAAGTGTGTACCAAGACGAAGAGGAA	240
OY	241	GAAATTTTGTATGAAACAAAGCGACTTTGTGATCTTCGGCTTTTCAACCATTTTAA	300
Db	241	GAAATTTTGTATGAAACAAAGCGACTTTGTGATCTTCGGCTTTTCAACCATTTTAA	300
OY	301	GTAATGTGAACAGTAGGCAACCGGAAGAAAAGATCCCATTCGAGAAATGTGTTGCT	360
Db	301	GTAATGTGAACAGTAGGCAACCGGAAGAAAAGATCCCATTCGAGAAATGTGTTGCT	360
OY	361	ATCGGCAACGAGTGTGCGAATTTGATATGCTTAAAGATCCGTGAAGTACAGAGCTTCGA	420
Db	361	ATCGGCAACGAGTGTGCGAATTTGATATGCTTAAAGATCCGTGAAGTACAGAGCTTCGA	420
OY	421	AGAAATATCTTAAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAAATTCACCTCAT	480
Db	421	AGAAATATCTTAAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAAATTCACCTCAT	480
OY	481	AGTAGAGCAATGTATGCTATACCCGCAATGTAGAACTTTACAGAGACCTGCCAAAGAC	540
Db	481	AGTAGAGCAATGTATGCTATACCCGCAATGTAGAACTTTACAGAGACCTGCCAAAGAC	540
OY	541	ATATATATTAATTAATGGATAGAGGCCAATAATAGTGGTAAATAGTTTCTTCCA	600
Db	541	ATATATATTAATTAATGGATAGAGGCCAATAATAGTGGTAAATAGTTTCTTCCA	600
OY	601	AATAATGACAAAGCAGAGATATCTGTGAAATCAAACATGACTGTGTGCCAAACAAGTA	660
Db	601	AATAATGACAAAGCAGAGATATCTGTGAAATCAAACATGACTGTGTGCCAAACAAGTA	660
OY	661	ATTGCTGAAGCAATAGGAAAAAACTAGAAATATGTGTCATATCTGAACATTTAAA	720
Db	661	ATTGCTGAAGCAATAGGAAAAAACTAGAAATATGTGTCATATCTGAACATTTAAA	720
OY	721	CTCTGTGTTTAGAATATCAGGGCAAGTATCTTTAAAGTGTGAGTGTGATGATAC	780
Db	721	CTCTGTGTTTAGAATATCAGGGCAAGTATCTTTAAAGTGTGAGTGTGATGATAC	780
OY	781	TTCTTAGAAAAATATCTCTGAGTCAGTATAAGATATAGAACTGTATATATGCTGGG	840
Db	781	TTCTTAGAAAAATATCTCTGAGTCAGTATAAGATATAGAACTGTATATATGCTGGG	840
OY	841	AGGATGCCCAATTTTAAAGATGTGCTTAAGAAAGCCTTATCTCAACCTGCCAATGAC	900
Db	841	AGGATGCCCAATTTTAAAGATGTGCTTAAGAAAGCCTTATCTCAACCTGCCAATGAC	900
OY	901	TGTTTTCAAATGCCATCTTATTCAGAGCGCATTTTCCAGCTCAACCATATATGAAATGA	960
Db	901	TGTTTTCAAATGCCATCTTATTCAGAGCGCATTTTCCAGCTCAACCATATATGAAATGA	960
OY	961	GAAACATCTACAAAATCCCTTTGGGTTTAAATAGAGACTCAGAAATAAAAATCTTTGT	1020
Db	961	GAAACATCTACAAAATCCCTTTGGGTTTAAATAGAGACTCAGAAATAAAAATCTTTGT	1020
OY	1021	GCAACCTACGTCGATCTTAATTTGAGACATTTTCAAGCTCAACCATATATGAAATGTC	1080
Db	1021	GCAACCTACGTCGATCTTAATTTGAGACATTTTCAAGCTCAACCATATATGAAATGTC	1080
OY	1081	TACCAATGAGAGAACCCCTTATGTACATGTGAACCTCAAGAGTACTTGTTCAT	1140
Db	1081	TACCAATGAGAGAACCCCTTATGTACATGTGAACCTCAAGAGTACTTGTTCAT	1140
OY	1141	CCCAAGTGAATGATGCTGAATATATATATATATATATATATATATATATATATATAT	1200
Db	1141	CCCAAGTGAATGATGCTGAATATATATATATATATATATATATATATATATATATAT	1200
OY	1201	CGACTTGCTTTCAATTTGCTCTGTAAAGGCCGAAAGGCTTAAAGAGACACTGT	1260

Db	1201	CGACTTTGCGCTTTCGATTGCTCGTTAAAGCGCAAGGCTGCTAAAGGAACA	1260
Qy	1261	CCATTGGCATGGGAAATATPAACTTGTTGATTACACACACTCTAGTATCTG	1320
Db	1261	CCATTGGCATGGGAAATATPAACTTGTTGATTACACACACTCTAGTATCTG	1320
Qy	1321	ATGGCTTGAATCTTTTGGCCAGTACCTCATGATTTGGAATTTGCTGAAC	1380
Db	1321	ATGGCTTGAATCTTTTGGCCAGTACCTCATGATTTGGAATTTGCTGAAC	1380
Qy	1381	GTTACTGGATCAATCCAAATPAAAGAACTCAATGCTTAGAGTTGACTG	1440
Db	1381	GTTACTGGATCAATCCAAATPAAAGAACTCAATGCTTAGAGTTGACTG	1440
Qy	1441	AGCAGTGTGTAAGTTCCAGATATGTCAATGATTAAGAGATGCGCAAT	1500
Db	1441	AGCAGTGTGTAAGTTCCAGATATGTCAATGATTAAGAGATGCGCAAT	1500
Qy	1501	TCCCGAAGACGAGATTACCTATTCGCCAGCAGAGCTGAGTAAACGAT	1560
Db	1501	TCCCGAAGACGAGATTACCTATTCGCCAGCAGAGCTGAGTAAACGAT	1560
Qy	1561	AATGATTTAAGGGAATGACAAAGAACAGCTCAAGCAATTTCTACAGCA	1620
Db	1561	AATGATTTAAGGGAATGACAAAGAACAGCTCAAGCAATTTCTACAGCA	1620
Qy	1621	TTGGAATCACTGAGCAGAGAAAGATTTCTATGAGTCAACACATATG	1680
Db	1621	TTGGAATCACTGAGCAGAGAAAGATTTCTATGAGTCAACACATATG	1680
Qy	1681	ATCCCGCAATTTCAACCAATTCCTCTCTGTTAAAGAAATCTAAGAT	1740
Db	1681	ATCCCGCAATTTCAACCAATTCCTCTCTGTTAAAGAAATCTAAGAT	1740
Qy	1741	GCCCAAGTATTCCTGGTAAAAAGATTGGCTCCATCAAACTGAAAGG	1800
Db	1741	GCCCAAGTATTCCTGGTAAAAAGATTGGCTCCATCAAACTGAAAGG	1800
Qy	1801	CTTCTGACCTGTAAATTAACCAAGATCTATGAGTTTGCTGTGGTG	1860
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Qy	1861	AAATATTTAACAGATGACAACTTCTCAGTATTTATCAGCTAGTACAG	1920
Db	1861	AAATATTTAACAGATGACAACTTCTCAGTATTTATCAGCTAGTACAG	1920
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Db	1921	TATGACAAATTTGGATACCTGCTGTGAGATTTTACTGAAGAAAGCAT	1980
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Db	1981	CAAGGATTTGGGACCTTTTCTTTGGCATTTAAATCTGAGATGCAAT	2040
Qy	2041	AGCCAGAGGTTGGCCCTTGCTTTGGAGTCCATATGTGTCATGTGGAG	2100
Db	2041	AGCCAGAGGTTGGCCCTTGCTTTGGAGTCCATATGTGTCATGTGGAG	2100
Qy	2101	CACCTGAATAGGCAAGTCGAGGCAATGAAAGCTCATTAACCTTGA	2160
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGAAAGCTCATTAACCTTGA	2160
Qy	2161	CAGAGAGAGAGATGAAACAAAGATACAGATGAAGTTTATGTCAAAT	2220
Db	2161	CAGAGAGAGAGATGAAACAAAGATACAGATGAAGTTTATGTCAAAT	2220
Qy	2221	CGACCAATTTCAATGATGCCCTACAGGCTTGCTCTCTCTAAACCTG	2280
Db	2221	CGACCAATTTCAATGATGCCCTACAGGCTTGCTCTCTCTCTAAACCTG	2280
Qy	2281	CTAGGAACCTCAGGCTTAAAGAGTGTGCAATTAATCTTCTGGAAGG	2340
Db	2281	CTAGGAACCTCAGGCTTAAAGAGTGTGCAATTAATCTTCTGGAAGG	2340

Dp	2281	TTAGGAACCTCAGGCTTTAAAAGTGTGAATTAGTCTTCTGCAAAAAGGCACCTGGG	2349
Qy	2341	TTGAATTGGGAAACCCGACATCATGTCAAGATTCTGTTTCGAACAAATGAGATCATC	2400
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Dp	2401	TTTAAAAATGGGGATGATTTCGGCAATATATGCTTAACACTTCAATTATTCGATTATG	2466
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Dp	2461	GAAATATCTGSCAAATCAAGGTCCTTGATCTTCGATGTTACCTTATAGTGTCTGTCA	2520
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Dp	2521	ATCGGTGACTGTGTGGACCTTATATGAGGTGGCGAAATTTCTCACACTATATGCAATT	2580
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Qy	2701	TGTGCTGGATACGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAAC	2768
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Dp	2821	AAGAGAGAAAAATTTGGTTATTAACGAAAGCGTGGCACTTGGTTTACACAGATTC	2880
Qy	2881	TTAATAGTATTAGTAAAGAGCCCAAGATGCAAAAGACAGATTTGAGAGCTT	2940
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Qy	2941	CAGAGATGTGTACAGGCTTATTTAGCTATTGCAACGATGCCAATCTCTTATTAAT	3000
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Dp	3001	CTTTTCTGAATGATGCTGGCTGTGGAAATGCGAAGATCAACATCTTTGATGACATTGCA	3068
Qy	3061	TACATTGGAAGAAGCCCTAGCTTGAATTAACACTGACAAAGAGCTTTGAGTATTTCTATG	3120
Dp	3061	TACATTGGAAGAAGCCCTAGCTTGAATTAACACTGACAAAGAGCTTTGAGTATTTCTATG	3120
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Dp	3121	AAACAATGAATGATGCAATCATGTGTGGCTGGAACAACAAAATGATTTGATCTTCCAC	3180
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Dp	3181	ACAAATTAACAGCATGATGGAACCTGAAAGATTAAGTGAAGAAAGTCACTCTGGA	3240
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RESULT 4
US-08-162-081B-34
Sequence 34, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiler, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayotov, George; Volinia,
APPLICANT: Stefano; Gout, Iyvan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-34

Query Match          94.9%; Score 3236.8; DB 1; Length 3240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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Qy      301 GTAATTCAACCGATGAGCAACCGTGAAGAAAGATCTCCATCGAGAAATTTGTTTGCT 360
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Db 301 GTAAATGGAACGAGTAGGCAACCGTAAGAAAGATCCCAATCGAAATGGTTTGCT 360
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Db 361 ATCCGCAATGCCAGTGTGGCAATTTGATATGGTTAAAGATCCGGAAGTACAGACCTCCGA 420
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Db 421 AGAAATATCTTAAATGTTTGTAAAGACCTGTGATCTTAGGATCTTAAATTCACCTCAT 480
Qy 481 AGTAGAGCAATGTATGTATCCGCAATGTAGAAATTTTCAACAGAGCTGCCAAGAC 540
Db 481 AGTAGAGCAATGTATGTATCCGCAATGTAGAAATTTTCAACAGAGCTGCCAAGAC 540
Qy 541 ATATATATATTAATTTGATAGAGGCCAAATATAGTGATTTGGGTAAATGTTTCTCA 600
Db 541 ATATATATATTAATTTGATAGAGGCCAAATATAGTGATTTGGGTAAATGTTTCTCA 600
Qy 601 AATAATGCAAGCAGAGATATCTCTGAAATCAACCAATGACTGTGCGCAAGAACATA 660
Db 601 AATAATGCAAGCAGAGATATCTCTGAAATCAACCAATGACTGTGCGCAAGAACATA 660
Qy 661 ATTGCTGAGCAATCAGAGAAAAAACTTGAAGTATGTTGCTATCATCTGAACAAATTA 720
Db 661 ATTGCTGAGCAATCAGAGAAAAAACTTGAAGTATGTTGCTATCATCTGAACAAATTA 720
Qy 721 CTCTGTGTTTGAATATCAGGGCAAGTACATTTTAAAGTGTGGAATGATGAATAC 780
Db 721 CTCTGTGTTTGAATATCAGGGCAAGTACATTTTAAAGTGTGGAATGATGAATAC 780
Qy 781 TTCTAGAAAAATATCTCTGAGTCAATATATATATAGAAAGCTATATATCTTGG 840
Db 781 TTCTAGAAAAATATCTCTGAGTCAATATATATATAGAAAGCTATATATCTTGG 840
Qy 841 AGGATGCCCAATTTGAAGATGATGCTTAAAGAAAGCTTTATCTCAACTCCCAATGAC 900
Db 841 AGGATGCCCAATTTGAAGATGATGCTTAAAGAAAGCTTTATCTCAACTCCCAATGAC 900
Qy 901 TGTTTTCAATGCAATCTTATTCAGAGAGCAATTTCCAGCTACCAATATATATATGA 960
Db 901 TGTTTTCAATGCAATCTTATTCAGAGAGCAATTTCCAGCTACCAATATATATATGA 960
Qy 961 GAAACATCTCAAAATCCCTTTGGGTTATTAATAGAGCACTCAAAATTAATCTTGT 1020
Db 961 GAAACATCTCAAAATCCCTTTGGGTTATTAATAGAGCACTCAAAATTAATCTTGT 1020
Qy 1021 GCAACCTTATGTAATCTTAAATATTCGAGACATTCGAAAGATTTATGTTGCAACAGTATC 1080
Db 1021 GCAACCTTATGTAATCTTAAATATTCGAGACATTCGAAAGATTTATGTTGCAACAGTATC 1080
Qy 1081 TACATGAGAGGAGAACCTTATGTAATTCGAAAGATTCGAAAGATTTATGTTGCAAT 1140
Db 1081 TACATGAGAGGAGAACCTTATGTAATTCGAAAGATTCGAAAGATTTATGTTGCAAT 1140
Qy 1141 CCCAGTGTGAATGATGCTGAATATATATATATATATATATATATATATATATATAT 1200
Db 1141 CCCAGTGTGAATGATGCTGAATATATATATATATATATATATATATATATATATAT 1200
Qy 1201 CGACTTGGCTTTCCATTTGCTGTGTTAAAGCCGAAAGGGTCTAAAGAGAAACACTGT 1260
Db 1201 CGACTTGGCTTTCCATTTGCTGTGTTAAAGCCGAAAGGGTCTAAAGAGAAACACTGT 1260
Qy 1261 CCATTTGGATGGGAAATATATACTTGTGTTTACACAGACACTCTTATGTTGGA 1320
Db 1261 CCATTTGGATGGGAAATATATACTTGTGTTTACACAGACACTCTTATGTTGGA 1320
Qy 1321 ATGCTTTGAATCTTTGGCAGTACCTCATGATTTAGAGATTTGGCTAAACCTATTGGT 1380
Db 1321 ATGCTTTGAATCTTTGGCAGTACCTCATGATTTAGAGATTTGGCTAAACCTATTGGT 1380
Qy 1381 GTTACTGATCAAAATCCAAATTAAGAAATCCATGCTTATGAGTTGAGCTTGCTC 1440
Db 1381 GTTACTGATCAAAATCCAAATTAAGAAATCCATGCTTATGAGTTGAGCTTGCTC 1440
Qy 1441 AGCAGTGTGTAAAGTTCCAGATATGTCAATATTAAGAGATGCCAATGGTCTGTA 1500
Db 1441 AGCAGTGTGTAAAGTTCCAGATATGTCAATATTAAGAGATGCCAATGGTCTGTA 1500
Qy 1501 TCCGAGAGAGAGATTTAGCTATTCACAGCAGAGCTGATTAACAGATAGTAGAC 1560
Db 1501 TCCGAGAGAGAGATTTAGCTATTCACAGCAGAGCTGATTAACAGATAGTAGAC 1560
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Db 1561 AATGAATTAAGGGAATTAAGCAAAACACTCAAAAGCAATTTCTACAGAGATCCCTC 1620
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Db 1621 TCTGAATTCACAGCAGAGAAAGATTTCTATGAGTCAACAGACACTATTGCTACT 1680
Qy 1681 ATCCCGAAATTTCTACCCAAATTTGCTGTGTTAAATGAAATTTAGAGATGA 1740
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Db 1741 GCCCAGATGTATGCTTGTGTTAAAGATTTGGCTCCAAATCAAACTGAACAGGCTATG 1800
Qy 1801 CTCTGAGCTGTAATTTCCAGATCTATGAGTGTGAGGTTTGTGCTGTGCTGTTG 1860
Db 1801 CTCTGAGCTGTAATTTCCAGATCTATGAGTGTGAGGTTTGTGCTGTGCTGTTG 1860
Qy 1861 AATATTTTAAACAGTACAAATCTTCTAGTATTTAATCAGCTAGTACAGTCTTAA 1920
Db 1861 AATATTTTAAACAGTACAAATCTTCTAGTATTTAATCAGCTAGTACAGTCTTAA 1920
Qy 1921 TATGAACAATTTTGTGTAATCTGTTGAGATTTTATCAAGAAAGATTAATCA 1980
Db 1921 TATGAACAATTTTGTGTAATCTGTTGAGATTTTATCAAGAAAGATTAATCA 1980
Qy 1981 CAAGAGATGGGCACTTTTCTTTGAGCAATTTAAATCTGAGATGCAATTAACAGT 2040
Db 1981 CAAGAGATGGGCACTTTTCTTTGAGCAATTTAAATCTGAGATGCAATTAACAGT 2040
Qy 2041 AGCCAGAGGTTTGGCTTTTGTGAGTCTATGTCGATGAGATGTAATTTGAAG 2100
Db 2041 AGCCAGAGGTTTGGCTTTTGTGAGTCTATGTCGATGAGATGTAATTTGAAG 2100
Qy 2101 CACTGATATGAGCAAGTCTGAGGCAATGGAAGAACTCTTAACTTAACTGATCTTAA 2160
Db 2101 CACTGATATGAGCAAGTCTGAGGCAATGGAAGAACTCTTAACTTAACTGATCTTAA 2160
Qy 2161 CAGGAGAGAGAGATGAACACAAAGAGTACAGTGAATTTTATGTTGAGCAAAATGAG 2220
Db 2161 CAGGAGAGAGAGATGAACACAAAGAGTACAGTGAATTTTATGTTGAGCAAAATGAG 2220
Qy 2221 CGACCAATTTCAATGATGCTTACAGGGCTTGTGCTCTCTTAAACCTGCTCATCA 2280
Db 2221 CGACCAATTTCAATGATGCTTACAGGGCTTGTGCTCTCTTAAACCTGCTCATCA 2280
Qy 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGAATTTATGCTTCTGCAAAAAGCCACTGTG 2340
Db 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGAATTTATGCTTCTGCAAAAAGCCACTGTG 2340
Qy 2341 TTGAATTTGGAGAACCCAGACATCATGCTAGATTAAGTTTCAAGAAATGAGATATC 2400
Db 2341 TTGAATTTGGAGAACCCAGACATCATGCTAGATTAAGTTTCAAGAAATGAGATATC 2400
Qy 2401 TTTAAATATGGGATGATTTACGGCAAGATATGCTTAACTTAAATTTTGTATATG 2460
Db 2401 TTTAAATATGGGATGATTTACGGCAAGATATGCTTAACTTAAATTTTGTATATG 2460
Qy 2461 GAAATATCTGAGCAAAATCAAGGCTTGTGATCTTGAATGTTTACCTTATGTTGCTCA 2520
Db 2461 GAAATATCTGAGCAAAATCAAGGCTTGTGATCTTGAATGTTTACCTTATGTTGCTCA 2520

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Db	661	ATTGCTGAAGCAATAGAGAAAAAACTGAAAGTATGTTGGCTATCATCTGAAACATTTAA	720
OY	721	CTGCTGTTTTAGAAATATCAGGGCAAGTAACATTTTAAAAAGTGTGAGTGAATAC	780
Db	721	CTGCTGTTTTAGAAATATCAGGGCAAGTAACATTTTAAAAAGTGTGAGTGAATAC	780
OY	781	TTCTCAGAAAAATATCCTCTGAGTCAGTATAGATATATAGAACCTGTATATGCTTGG	840
Db	781	TTCTCAGAAAAATATCCTCTGAGTCAGTATAGATATATAGAACCTGTATATGCTTGG	840
OY	841	AGGATGCCCAATTTGAAAGTATGAGCTTAAGAAAGCCTTATCTCAACTGCCAATGCAC	900
Db	841	AGGATGCCCAATTTGAAAGTATGAGCTTAAGAAAGCCTTATCTCAACTGCCAATGCAC	900
OY	901	TGTTTTCAATAGCCATCTTATTTCCAGAGCAATTCACAGGTAACCAATATAGATGGA	960
Db	901	TGTTTTCAATAGCCATCTTATTTCCAGAGCAATTCACAGGTAACCAATATAGATGGA	960
OY	961	GAAACATCTACAAAAATCCCTTTGGGTATTAATAAGACACTAGAAATTAATTTCTTGT	1020
Db	961	GAAACATCTACAAAAATCCCTTTGGGTATTAATAAGACACTAGAAATTAATTTCTTGT	1020
OY	1021	GOAACCTAAGTGAATCTAAATATTCGAGACATTCGAAAGATTTATGTTGCAACAGTATC	1080
Db	1021	GCAACCTAAGTGAATCTAAATATTCGAGACATTCGAAAGATTTATGTTGCAACAGTATC	1080
OY	1081	TACCAATGAGAGAACCCCTTAATGTGACAAATGTGAACATCAAAAGATACCTTGTTCCAT	1140
Db	1081	TACCAATGAGAGAACCCCTTAATGTGACAAATGTGAACATCAAAAGATACCTTGTTCCAT	1140
OY	1141	CCCAAGTGAATGATGAGCTGATATATATATATCATTCCTGATCTTCTCGTGCTGCT	1200
Db	1141	CCCAAGTGAATGATGAGCTGATATATATATATATCATTCCTGATCTTCTCGTGCTGCT	1200
OY	1201	CGACTTTCCTTCCATTTGCTCTGTAAAGCCGAAAGGGTGCTAAAGGAACACTGT	1260
Db	1201	CGACTTTCCTTCCATTTGCTCTGTAAAGCCGAAAGGGTGCTAAAGGAACACTGT	1260
OY	1261	CCATTGGGATGGGGAATATTAACCTGTTTTGATTAACAAGACACTGTATGATCTGGAA	1320
Db	1261	CCATTGGGATGGGGAATATTAACCTGTTTTGATTAACAAGACACTGTATGATCTGGAA	1320
OY	1321	ATGCGTTTGAATCTTTGGCCAGTACCTCATGGAATTGAGAAATTTGCTAAACCTATTTG	1380
Db	1321	ATGCGTTTGAATCTTTGGCCAGTACCTCATGGAATTGAGAAATTTGCTAAACCTATTTG	1380
OY	1381	GTTACTGATCAAAATCCAAATTAAGAAACTCCATCTTAGAGTTGGAATTTGACTGCTTC	1440
Db	1381	GTTACTGATCAAAATCCAAATTAAGAAACTCCATCTTAGAGTTGGAATTTGACTGCTTC	1440
OY	1441	AGCAGTGTGTAAGTTCCTCAAGTATGTACAGGATTTGAAGACATGCCAATTTGCTGCTA	1500
Db	1441	AGCAGTGTGTAAGTTCCTCAAGTATGTACAGGATTTGAAGACATGCCAATTTGCTGCTA	1500
OY	1501	TCCCGAGAGCAGATTTAGCTATTTCCACGACGAGCTGAGTAAACAGACTAGTAGAGAC	1560
Db	1501	TCCCGAGAGCAGATTTAGCTATTTCCACGACGAGCTGAGTAAACAGACTAGTAGAGAC	1560
OY	1561	AATGAATTAAGGAAAAATGACAAAGACAGCTCAAGCAATTTCTACACGAGATCTCTC	1620
Db	1561	AATGAATTAAGGAAAAATGACAAAGACAGCTCAAGCAATTTCTACACGAGATCTCTC	1620
OY	1621	TCTGAAATCACTGACAGAGAGAAATTTCTATGAGTCAACAGACACTATTTGTAACT	1680
Db	1621	TCTGAAATCACTGACAGAGAGAAATTTCTATGAGTCAACAGACACTATTTGTAACT	1680
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Db	1681	ATCCCGGAAATCTACCCCAAAATGCTCTGCTGTGTAATATGAAATTTAGAGATGAAGTA	1740
OY	1741	GCCCAAGATGATTTGCTTGTGTAAGATTTGGCTCCAACTGAACAGGCTATGGA	1800

Dp	1741	GCCCAAGATGATTTCTGGTAAAGGATTTGGCTTCAATCAAACTGCAAGGCTATGGAA	1800
Qy	1801	CTTCTGACGTGAATTAATACCAGATCCATATGGTTCGAGGTTTGCTGTCCGTCCTTGGAA	1860
Dp	1801	CTTCTGACGTGAATTAATACCAGATCCATATGGTTCGAGGTTTGCTGTCCGTCCTTGGAA	1860
Qy	1861	AAATATTTTAACAGATGACAACTTTCTCAGTATTTAAATTGACGTAGTACAGGTCCTAATA	1920
Dp	1861	AAATATTTTAACAGATGACAACTTTCTCAGTATTTAAATTGACGTAGTACAGGTCCTAATA	1920
Qy	1921	TATGAACAATATTTGGATTAACCTTGCTGTGAGATTTTATCTGAAGAAAGATGACATA	1980
Dp	1921	TATGAACAATATTTGGATTAACCTTGCTGTGAGATTTTATCTGAAGAAAGATGACATA	1980
Qy	1981	CAAGAGATTTGGGCACTTTTCTTTTGGCATTTTAAATCTGAGATGACAAATTAACAAGT	2040
Dp	1981	CAAGAGATTTGGGCACTTTTCTTTTGGCATTTTAAATCTGAGATGACAAATTAACAAGT	2040
Qy	2041	AGCCAGAGTTTGGCCCTGCTTTTGGAGTCCATATGTCGATGATGGAGATGATTTGAAG	2100
Dp	2041	AGCCAGAGTTTGGCCCTGCTTTTGGAGTCCATATGTCGATGATGGAGATGATTTGAAG	2100
Qy	2101	CACCTGAATATAGGCAAGTCGAGGCAATGGAAAAAGCTCATTAACCTTAACCTGACATTCCTAAA	2160
Dp	2101	CACCTGAATATAGGCAAGTCGAGGCAATGGAAAAAGCTCATTAACCTTAACCTGACATTCCTAAA	2160
Qy	2161	CAGAGAGAAAGATGTAAACAACAAGATACAGATGAAGTTTATAGTTGAGCAAAATGAGG	2220
Dp	2161	CAGAGAGAAAGATGTAAACAACAAGATACAGATGAAGTTTATAGTTGAGCAAAATGAGG	2220
Qy	2221	CGACCAGATTTGATGATGATGCCCTTACAGGCGTTGCTGTCTCTCTTAAACCTGCTCATCAA	2280
Dp	2221	CGACCAGATTTGATGATGATGCCCTTACAGGCGTTGCTGTCTCTCTTAAACCTGCTCATCAA	2280
Qy	2281	CTTAGAATACCTCAGGCTTTAAAGAGTGTCCAAATTAATGCTTCTGCAAAAAGGCCATGTGG	2340
Dp	2281	CTTAGAATACCTCAGGCTTTAAAGAGTGTCCAAATTAATGCTTCTGCAAAAAGGCCATGTGG	2340
Qy	2341	TTGAATTTGGGAGAACCCAGACATCATGTCCAGAGTTACTGTTTCGAACATAGATCATC	2400
Dp	2341	TTGAATTTGGGAGAACCCAGACATCATGTCCAGAGTTACTGTTTCGAACATAGATCATC	2400
Qy	2401	TTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAATTTATTCGATATATG	2460
Dp	2401	TTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAATTTATTCGATATATG	2460
Qy	2461	GAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTAACTTATATGTTATGTATG	2520
Dp	2461	GAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTAACTTATATGTTATGTATG	2520
Qy	2521	ATCGGTGACTGTGGGACCTTATGAGTGGTGGTGAATTTCTCACACTATTTATGCAATTT	2580
Dp	2521	ATCGGTGACTGTGGGACCTTATGAGTGGTGGTGAATTTCTCACACTATTTATGCAATTT	2580
Qy	2581	CAGTGCAAAGCGGCTTGAAGGTGCACTCGAGTTTCAACGCCACACACTACATCAGTGG	2640
Dp	2581	CAGTGCAAAGCGGCTTGAAGGTGCACTCGAGTTTCAACGCCACACACTACATCAGTGG	2640
Qy	2641	CTCAAAAGCAAGAACAAAGAGAAATATATGATGACACCATTGACCTGTTTACACGTTC	2700
Dp	2641	CTCAAAAGCAAGAACAAAGAGAAATATATGATGACACCATTGACCTGTTTACACGTTC	2700
Qy	2701	TGTCGTGATATCTGTATGCTACTTCAATTTTGGGAATGGAGATGCTCAATATGATAC	2760
Dp	2701	TGTCGTGATATCTGTATGCTACTTCAATTTTGGGAATGGAGATGCTCAATATGATAC	2760
Qy	2761	ATCATGTGTGAAGAAGCAGATGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Dp	2761	ATCATGTGTGAAGAAGCAGATGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Qy	2821	AAGAAGAAAAATTTGGTATTAACGGAACGTGTGCATTTGTTTGAACACAGGATTTTC	2880

Db 2821 AAGAGAAAAAATTGGTTATTAACGAAGCTGTGCCATTGTTTGGACACAGGATTC 2880
 QY 2881 TTAATGATGATTAAGAGAGCCCAAGAAATGCAACAAGACAAGAAATTTGAGAGTT 2940
 Db 2881 TTATATGATGATTAAGAGAGCCCAAGAAATGCAACAAGACAAGAAATTTGAGAGTT 2940
 QY 2941 CAGAGATGTTTACAAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTCATMAAT 3000
 Db 2941 CAGAGATGTTTACAAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTCATMAAT 3000
 QY 3001 CTTTTCATGATGATGCTGTGCTGGAATGCCGAATACATCTTTTATGATGATGCA 3060
 Db 3001 CTTTTCATGATGATGCTGTGCTGGAATGCCGAATACATCTTTTATGATGATGCA 3060
 QY 3061 TACATTGAAAAGACCTAGCCTTAGATTAATACTGAGCAAGAGCTTTGAGTATTTGATG 3120
 Db 3061 TACATTGAAAAGACCTAGCCTTAGATTAATACTGAGCAAGAGCTTTGAGTATTTGATG 3120
 QY 3121 AAACCAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
 Db 3121 AAACCAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
 QY 3181 ACAATTAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240
 Db 3181 ACAATTAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240

RESULT 6

US-09-085-957-34

Sequence 34, Application US/09085957

Patent No. 6274327

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu

APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter

APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,

APPLICANT: Stefano; Gout, Ivan Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

TITLE OF INVENTION: THEIR PREPARATION AND USE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/085,957

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/780,872

FILING DATE: 09-JAN-1997

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FILING DATE: February 7, 1994

APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993

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INFORMATION FOR SBO ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 3240 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

US-09-085-957-34

Query Match 94.9%; Score 3236.8; DB 3; Length 3240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCTCCAGAACATCATCAGGTGAACCTGTGGGGCATCCATTGAGCCCCCAAGATC 60
 Db 1 ATGCCCTCCAGAACATCATCAGGTGAACCTGTGGGGCATCCATTGAGCCCCCAAGATC 60
 QY 61 CTAGTGAATGTTTACTTACCAATGGAATGATGATGATGATGATGATGATGATGATGATG 120
 Db 61 CTAGTGAATGTTTACTTACCAATGGAATGATGATGATGATGATGATGATGATGATGATG 120
 QY 121 ACATTAGTAACTTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 121 ACATTAGTAACTTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 QY 181 CTTCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
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 Db 661 ATTGCTGAAGCAATCAGAAAAAACTAGAAGTATGCTATCATCTGAACAATTAATA 720
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 Db 721 CTTCTGTTTGAAGAAATCAAGGCAAGTATGATGATGATGATGATGATGATGATGATGATG 780
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 Db 781 TTCTTGAAGAAATATATCTGAGTCAAGTATGATGATGATGATGATGATGATGATGATGATG 840
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 Db 841 AGGATGCCCAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
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Db 1081 TACCATGAGAGAGAACCTTATGTGACATGTGAACCTCAAGAGTACCTGTTCCAT 1140
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Qy 1201 CGACTTGGCCCTTCCATTTGCTGTTAAAGCCGAAAGGGTGCCTAAAGAGAAACATGT 1260
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Qy 1261 CCATTGGCATGGGAAATATATACTGTTGATTACACAGACACTCTATGATCTGAAAA 1320
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Db 1501 TCCCGAGAGAGATTTAGTATTCCTCCAGCAGACTGATTAACAGACTAGTAGAGAC 1560
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Qy 1621 TCTGAATCACTGACGAGAGAAAGATTTCTATGAGAGTCAACAGACTATTTGTAAT 1680
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Db 1681 ATCCCGCAAAATTTACCCAAATGCTTCTGTCTGTTAAATGCAATTTAGAGATGAACTA 1740
Qy 1741 GCCCAGATGTAATTCCTGGTAAAGATTTGGCCTCCAACTCAAGACAGAGCTATGAA 1800
Db 1741 GCCCAGATGTAATTCCTGGTAAAGATTTGGCCTCCAACTCAAGACAGAGCTATGAA 1800
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Db 1801 CTTCTGACGTGTAATTCACAGATCTCTATGCTGAGAGTTCGCTGCTGCTGCTGAA 1860
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Qy 2041 AGCCAGAGTTTGGCTTCTTGGAGTCTATGTCTGATGATGAGATGATTTTGAAG 2100
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Qy 2101 CACCTGATATGAGCAAGTCAGAGCAATGAGAAAGCTCATTAATTAATGATCTTCAAA 2160
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Db 2281 CTAGAGAACTCAGAGCTTAAGAGTGCATTAATGCTTCTGCTGCTGCTGCTGCTGCTGCT 2340
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Db 2341 TTGAATTTGGAGAACCCAGACATCATGTCAGAGTTACTGTTTACAGAACTAGATCATC 2400
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Db 2401 TTTAAAAATGGGATGATTTACGCGCAAGATATGCTAAACCTGAAATTAATTCGTAATAG 2460
Qy 2461 GAAAAATCTGCGCAAAATCAGGCTTGTATCTTCAATGTTACCTTATGCTGCTGCTGCT 2520
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Qy 2821 AAGAGAAAGAAATTTGGTTTAAACGAGAGAGTGTGCTATTTTGAACAGAGATTTG 2880
Db 2821 AAGAGAAAGAAATTTGGTTTAAACGAGAGAGTGTGCTATTTTGAACAGAGATTTG 2880
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Db 2881 TTAATAGATTAAGTAAGAGCCCAAGAAATGACAAAGACAAAGAAATTTGAGAGTTT 2940
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Db 3001 CTTTCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
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Db 3061 TACATTTGAAAGACCTTACCTTATGATTAATTCAGAGCAAGAGCTTTGAGATTTTCATG 3120
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Db 3121 AAACAAATGATGATGATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
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Oy 3181 ACACATTAACAGCATGCATTGACTGAAAGATAA CTGAAAAATGAAAGCTCCTCTCGA 3240
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Db 3181 ACAATTAAACAGCATGCATTGACTGAAAGATAA CTGAAAAATGAAAGCTCCTCTCGA 3240

RESULT 7

US-08-162-0818-35
Sequence 35, Application US/08162081B
Patent No. 5824492

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand,
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayiotou, George; V
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Disquette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paquiniani, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: L0D 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 688-9200
TELEFAX: (412) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-0818-35

Query Match	88.2%	Score 3006.6	DB 1	Length 3207
Best Local Similarly	96.1%	Pred. No. 0		
Matches 3083	Conservative	0	Mismatches 124	Indels 0
				Gaps 0

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QY	1	2	3	4	5																																																																																															

Db		241	GAATTTTGGATGAAACAAGACGACTTTGTACCTTGGGCTTTTTCACCTTTTAA	300
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Db		301	GTAATGGAACGATGAGCAACCGTAGAAGAAAAGATCCTCAATCGAAGAAATGGTTTGT	360
Qy		351	ATCGGCAATGCCAGTGTGCGAATTTTGATATGGTTAAAGATCCTGAAGTACAGACTTCCGA	420
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Qy		421	AGAAATATCTTAATGTTGTGTAAGAAGCTGGATCTTAGAGATCTTAATTCACCTCAT	480
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Qy		481	AGTAGAGCAATGTAATGTCATCCGCAATGTAGATCTTACAGACAGACTGCCAAGAC	540
Db		481	AGTAGAGCAATGTAATGTCATCCGCAATGTAGATCTTACAGACAGACTGCCAAGAC	540
Qy		541	ATATATTAATAATGGATAGAGGCCCAATAATAGTGTGATTTGGGTAAATGTTCTTCCA	600
Db		541	ATATATTAATAATGGATAGAGGCCCAATAATAGTGTGATTTGGGTAAATGTTCTTCCA	600
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Db		661	ATTGCTGAGCAATCAGGAAAAAAACTGAAGTATGTTGCTATCATCTGAACCACTAATA	720
Qy		721	CTGTGTGTTTAGAATATCAGGCGACATCATTTTAAAGTGTGTGAATGTGATGAATAC	780
Db		721	CTGTGTGTTTAGAATATCAGGCGACATCATTTTAAAGTGTGTGAATGTGATGAATAC	780
Qy		781	TTCTCTAGAAAAATATCCTCTGAGTCAAGTATAGATATTAAGAACTGTATATGCTTGGG	840
Db		781	TTCTCTAGAAAAATATCCTCTGAGTCAAGTATAGATATTAAGAACTGTATATGCTTGGG	840
Qy		841	AGGATGCCAATTTGAAGATGATGGCTTAAAGAAAGCCTTTATTTCTCAACTGCCAATGGAC	900
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Qy		961	GAAACATCTACAAAATCCCTTTGGGTTATTAATAGTGCACTCAANATTAATAATCTTTGT	1020
Db		961	GAAACATCTACAAAATCCCTTTGGGTTATTAATAGTGCACTCAANATTAATAATCTTTGT	1020
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Qy		1141	CCAGAGTGAATGAATGGCTGAATTAATATATATCAATTCCTGATCTTCTCGTGTGCT	1200
Db		1141	CCAGAGTGAATGAATGGCTGAATTAATATATATCAATTCCTGATCTTCTCGTGTGCT	1200
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Db		1201	CGACTTTGGCTTTTCATTTGCTCTGTGTAAGAGCCGAAAGGGTGTCTMAAGAGAACACTGT	1266
Qy		1261	CCATTGGCATGGGAAAAATATAACTGTGTTATACACAGACTCTTATGTCTGGAATA	1320
Db		1261	CCATTGGCATGGGAAAAATATAACTGTGTTATACACAGACTCTTATGTCTGGAATA	1320
Qy		1321	ATGGCTTTGAATCTTTGGCCAGTACCTCATGATTAAGAGATTTGCTGAACCTTATGTT	1380

Db 1321 ATGGCTTTGAATCTTTGGCCAGTACTCATGAGCTAGAGAGATTGCTGAACCTTATGCT 1380
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Db 1381 GTTACTGGATCAATCCAAATTAAGAACTCCATGCTTAGATGGAGTTGA CTGGTTC 1440
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Db 1501 TCCCGAGAGAGAGATTAGTATTTCCAGCAGAGACTGAGTAAACAATCTGCTAGAGAC 1560
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Db 1861 AAAATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGTATGACAGTCTCTAAA 1920
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Db 1921 TATGACCAATTTTGGATTAATCTGCTGAGATTTTACTGAGAAAGCAATGACATAT 1980
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Qy 2881 TTAATGATATTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
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Qy 3061 TACATTTGAAAGACCTTACCTTATGATTAATTAATCTGAGCAGAGCTTTGAGATTTGATG 3120
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Db 3121 AAACAAATGATATGATGACATCAGTGTGCTGGAACAAACAAATGATGATGCTTCCAC 3180
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Db 3181 ACAATTAACAGCATGCTTTGAATGA 3207

RESULT 8
US-08-780-872-35
Sequence 35, Application US/08780872
Patent No. 584824
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bales, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Parayotou, George; Volinia,
APPLICANT: Stefano, Gout, Iyan Tatarovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

Db 1681 ATCCCGAAATTCACCCAAATTCCTGCTGTTAAATGAACTCAGAGATGAATA 1740
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 Qy 1801 CTCTGAGCTGTAAATTAACCCAGATCTATGCTGAGGCTTTGCTGTTGGTCTTGAA 1860
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 Qy 2521 ATCGGTGACTGTGTGGACTTATGAGGTGTGCAAAATTCACACTATTAATGCAAT 2580
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 Qy 2581 CAGTCAAGAGGCTTGAAGAGTCACTGCAAGTTTAAAGCACTCATCAGTGG 2640
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Db 2761 ATCATGTGAAAGATGATGCAACTGTTTATATATATTTTGGACACTTTTGGATCAC 2820
 Qy 2821 AAGAGAAAAAATTTGGTTTAAAGAGAACTGTGCTGCTTTTGTGACACAGATTTTC 2880
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 Db 3121 AAACAAATGATGATGACATCATGCTGAGTGGCTGCAACAAATGATGATGCTTCCAC 3180
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 Db 3181 ACAATTAACGACATGCTTGAATGCA 3207

RESULT 9
 US-09-085-957-35
 : Sequence 35, Application US/09085957
 : Patent No. 6274327
 : GENERAL INFORMATION:
 : APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 : APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
 : APPLICANT: Joseph; Otsu, Masayuki; Panayiotou, George; Volinia,
 : APPLICANT: Stefano; Gout, Ivan Tarasovich
 : TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 : TITLE OF INVENTION: THEIR PREPARATION AND USE
 : NUMBER OF SEQUENCES: 50
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Felfe & Lynch
 : STREET: 805 Third Avenue
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10022
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 : COMPUTER: IBM PS/2
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: Wordperfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/085,957
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/780,872
 : FILING DATE: 09-JAN-1997
 : APPLICATION NUMBER: 08/162,081
 : FILING DATE: February 7, 1994
 : APPLICATION NUMBER: PCT/GB93/00761
 : FILING DATE: 13 April 1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Paesqualini, Patricia A.
 : REGISTRATION NUMBER: 34,894
 : REFERENCE/DOCKET NUMBER: LUD 5256
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 688-9200
 : TELEFAX: (212) 838-3884

! INFORMATION FOR SRO ID NO: 35:
! SEQUENCE CHARACTERISTICS:
! LENGTH: 3207 base pairs
! TYPE: nucleic acid
! STRANDEDNESS: single
! TOPOLOGY: linear
US-09-085-957-35

Query Match 88.2%; Score 3008.6; DB 3; length 3207;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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DB 61 CTAGTGAATGTTTACTACCAATGGAATGATGATCTTACGAATGCTCCGGAGAGCT 120
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DB 121 ACATTAGTAATATTAAGCATGAACTATTTAAAGAACAGAAATAACCTCTGCATCAA 180
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 RESULT 10
 US-09-392-350-1
 ; Sequence 1, Application US/09392350
 ; Patent No. 613032
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowser
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 BETA EXPRESSION
 ; FILE REFERENCE: RTS-0075
 ; CURRENT APPLICATION NUMBER: US/09/392,350
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 1
 ; LENGTH: 3213
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3213)
 US-09-392-350-1
 Query Match 13.5%; Score 460.8; DB 3; Length 3213;
 Best Local Similarity 50.4%; Pred. No. 1,9e-118;
 Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;
 Qy 58 ATCTAGTGAATGTTTACTAACCAATGGAATGATGACTTTAGATGCTCCGTGAG 117
 Db 88 ATACCTGTGATTTCCCTTTTGGCCACTGGGATTTATATCCAGTTGGAGTACCTCGGGAA 147
 Qy 118 GCTACATTAGTAACATTAAGACATGAACATTTTAAAGACAAAGAAATACCTCTGCAT 177
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 Qy 178 CAATCTTGAAGATGAATCTTTCTTACATTTTGTGTAAGTGTATCCCAAGACGAAAG 237
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 Qy 298 AAAGTAATGAACAGTAGGCAACCGTGAAGAAAGATCCCAATCGAGAAATGTTT 357
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 Qy 478 CATAGTAGAGCAATGTATGTTTCCGCCCATGTAGATCTTCAACAGAGCTGCCAAG 537
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Qy 838 GGGAGATGCCCAATTTGAAGATGATGCTA---AGAAAGCTTTATTTCAACCTGC 892
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Db 1064 CTGCTCTTTTCAATGACTGAGCTCCTGTGTAACCATGTAACTGAGAGTATCAG 1123
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Db 1901 AACTTCTCAGATTTCTTTTACACATGCTGCAAGTGTAAATATGAGCTTTCTTGATTT 1960
Qy 1940 ACTTGTGTGAGATTTTATCTGAAGAAACATTTGACTAATCAAGAGATTTGGCACTTTT 1999
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 Db 3143 CGCTCAGGAAAGCTGAGCTACTTAAGTGAAGTGGATGGCCACAGATT 3192

RESULT 11
 US-09-194-640A-2
 Sequence 2, Application US/09194640A
 Patent No. 6482623
 GENERAL INFORMATION:
 APPLICANT: Van Hasebreeck, Bart
 APPLICANT: Waterfield, Michael D.
 TITLE OF INVENTION: No. 6482623el Lipid Kinase
 FILE REFERENCE: 2332-1-002
 CURRENT APPLICATION NUMBER: US/09/194.640A
 CURRENT FILING DATE: 1998-12-01
 PRIOR APPLICATION NUMBER: PCT/GB97/01471
 PRIOR FILING DATE: 1997-05-30
 PRIOR APPLICATION NUMBER: 9611460.8
 PRIOR FILING DATE: 1996-06-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 3387
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-194-640A-2

Query Match 9.7%; Score 329.8; DB 4; Length 3387;
 Best Local Similarity 53.2%; Pred. No. 7.1e-82;
 Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

QY 1682 TCCCGAAATCTACCCCAATTTGCTGCTGTTAAATGGAATCTAGATGAAGTAG 1741
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QY 3179 ACA 3181
Db 3107 ACA 3109

RESULT 12
US-09-357-070-1
; Sequence 1, Application US/09357070
; Patent No. 6046049
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 DELTA EXPRESSION
; FILE REFERENCE: RFS-0076
; CURRENT APPLICATION NUMBER: US/09/357,070
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(3313)
US-09-357-070-1

Query Match 9.7%; Score 329.8; DB 3; Length 3868;
Best Local Similarity 53.2%; Pred. No. 7.6e-82;
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

QY 1682 TCCCGGAAATTTACCCAAATTTGCTTCTGTCTGTTAATGGAATTTAGAGATGAATAG 1741
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Db 2058 ACGAGTCTTACTGAGCTGAGAGCTGACCAATTTCTGTGGA-CCGCGCCCTGGCCAAAC 2117
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QY 2342 TGAATTGGAGAACCCAGACATATGTCAGATTACTGTTTCAAGAAATGATGATCATCT 2401
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QY 2402 TTAATAATGGGAGATGATTTACGGCAAGATATGCTTACACTTCAATATATGATTTG 2461
Db 2529 TTAAGAAAGGAGATGATCTCCGCGAGGACATGCTGACCTTGACAGATGATCAGCTCATGG 2588
QY 2462 AAAATATCTGCAAAATCAAGTCTTGTATCTTGTGAAATGTTACCTTATGTTGTCTCA 2521
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QY 2522 TCGTGACTGTGGGACTTATTGAGGTGTGGAATTTCTCACTATTAATGCAATTC 2581
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QY 2582 A---GTCCAAAGCGCTTAAAGTGCACTGCAAGTTCAACAGCCACACTCATAGT 2638
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QY 2699 CATGTGCTGATACTGTGATGCTTCACTTTTGGAAATGAGATGTCACAAATGTA 2758
Db 2829 CTGTGTGCTATTTGTGTGGCCAAATATGTGCTGGGCAATGCGCATGCGCACAGCACA 2888
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Db 3243 GAGTGAAGTTTAAAGAAACCCCTCCGTGAGAGCTGGAACCAAGTGAATGCTGCGCCC 3302
QY 3179 ACA 3181
Db 3303 ACA 3305

RESULT 13

US-08-777-405A-1
Sequence 1, Application US/08777405A
Patent No. 5858753
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekeita, Merl F.
APPLICANT: Holzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..3327
US-08-777-405A-1

Query Match 9.7% Score 329.8; DB 2; Length 5220;
Bee local Similarity 53.2%; Pred. No. 8.8e-82;
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

Qy 1682 TCCCGAATTTCTACCCAAATTTGCTTCTGTGTTAAATGGAATTTCTAGAGTGAATAG 1741
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Qy 1802 TTCTGATGTAATTAACCAATGCTATAGTTTTCAGGTTTGTGCTTGGTGGTCTTGGAAA 1861
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Qy 1862 AATATTTTACAGATGACAACTTTCTCAGTATTTTAAATTCAGCTAGTACAGGCTCTAAAT 1921
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Job time : 169.161 secs

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Qy 2641 CTCAAAAGACAAAGCAAAAGAGAAATATATATGATGACGCACTGACTGTTTACAGTTGA 2700
Db 2641 CTCAAAAGACAAAGCAAAAGAGAAATATATATGATGACGCACTGACTGTTTACAGTTGA 2700
Qy 2701 TGTGCTGATACTGTGTAGTACTTCAATTTTGGCAATTTGAGATGTCACAAATGATTAAC 2760
Db 2701 TGTGCTGATACTGTGTAGTACTTCAATTTTGGCAATTTGAGATGTCACAAATGATTAAC 2760

Qy 2761 ATCATGTGAAAGAGATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC 2820
Db 2761 ATCATGTGAAAGAGATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC 2820
Qy 2821 AAGAAAGAAAATTTGGTTATTAACAGAGACGTGTGCCATTTGTTTGCACAGATTTTC 2880
Db 2821 AAGAAAGAAAATTTGGTTATTAACAGAGACGTGTGCCATTTGTTTGCACAGATTTTC 2880
Qy 2881 TTAATAGATTAAGTAAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Db 2881 TTAATAGATTAAGTAAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Qy 2941 CAGAGATGTGTTCACAGGCTTAATCTAGCTAATTTGCACAGATGCCAATCTCTTCAAAAT 3000
Db 2941 CAGAGATGTGTTCACAGGCTTAATCTAGCTAATTTGCACAGATGCCAATCTCTTCAAAAT 3000
Qy 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTAACATCTTTGATGACATTTGCA 3060
Db 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTAACATCTTTGATGACATTTGCA 3060
Qy 3061 TACATTTGAAGAGCCCTAGCTTATTAACCTGACAAAGAGGCTTTGGAGATTTGATG 3120
Db 3061 TACATTTGAAGAGCCCTAGCTTATTAACCTGACAAAGAGGCTTTGGAGATTTGATG 3120
Qy 3121 AAACAAATGAATGATGACATCATATGCTGCTGACACAAAAATGATTTGATCTTTCAC 3180
Db 3121 AAACAAATGAATGATGACATCATATGCTGCTGACACAAAAATGATTTGATCTTTCAC 3180
Qy 3181 ACAATTTAAACAGCATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3240
Db 3181 ACAATTTAAACAGCATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3240
Qy 3241 CACTACCTGACCTGTTAATTAATCTCTCAGAGGCAAGACGATTTGATGATTTGAC 3300
Db 3241 CACTACCTGACCTGTTAATTAATCTCTCAGAGGCAAGACGATTTGATGATTTGAC 3300
Qy 3301 AATCATGAAACAGCATTTAGATTTACAGCAAGAACAGAAATTAATTAATTAATTAAT 3360
Db 3301 AATCATGAAACAGCATTTAGATTTACAGCAAGAACAGAAATTAATTAATTAATTAAT 3360
Qy 3361 TAAATGTAACCGCAACAGGCTTTGATGACACTTAATGATTTTCAAA 3412
Db 3361 TAAATGTAACCGCAACAGGCTTTGATGACACTTAATGATTTTCAAA 3412
RESULT 2
ABL59523
ID ABL59523 standard, cDNA, 3424 BP.
AC ABL59523;
XX
AC 16-JUL-2002 (first entry)
XX
DT Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
DE Human phosphatidylinositol-3-kinase catalytic alpha; enzyme;
XX
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW Chromosome 3q26.3; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200227028-A1.
XX
PD 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-US30366.
XX
XX 28-SEP-2000; 2000US-0676052.
XX
XX (ATAT-) ATRIRGIN TECHNOLOGIES INC.
XX
XX Skinner MK, Paton JL, Chaudhary J;
PI

XX MFI; 2002-402054/43.
XX Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action -
XX
PS Example 1; Page 82-83; 113pp; English.
XX
XX The present invention describes a method for identifying tumor
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilized on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumor characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention.
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;
Query Match 99.9%; Score 3407.2; DB 24; Length 3424;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGCTCCAGACCATCATCAGGTGAACGTGCGGCGATCCATCTGATGCCCAAGAAATC 60
DB 13 ATGCTCCAGACCATCATCAGGTGAACGTGCGGCGATCCATCTGATGCCCAAGAAATC 72
QY 61 CTAGTGGAAATGTTTACTACCAATGAAATGATGATGATGATGATGATGATGATGATGAT 120
DB 73 CTAGTGGAAATGTTTACTACCAATGAAATGATGATGATGATGATGATGATGATGATGAT 132
QY 121 ACATTGTAATCTAATAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 133 ACATTGTAATCTAATAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192
QY 181 CTCTTTCAGATGATGATCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 193 CTCTTTCAGATGATGATCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 252
QY 241 GAATTTTTTGAAGAAACAGAGACCTTGTGATCTTGGCTTTTCAACATTTTAAATA 300
DB 253 GAATTTTTTGAAGAAACAGAGACCTTGTGATCTTGGCTTTTCAACATTTTAAATA 312
QY 301 GTTAATGAAACAGTGAAGCAAGCTGTAAGAAAGATCTCAATCGAGAAATTTGGTTTGTCT 360
DB 313 GTTAATGAAACAGTGAAGCAAGCTGTAAGAAAGATCTCAATCGAGAAATTTGGTTTGTCT 372
QY 361 ATCGGATGCAAGTGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 373 ATCGGATGCAAGTGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
QY 421 AGAATATTTCTTAATGTTTGAAGAAGCTGTGATCTTAAGGATCTTAATTTCACTCAT 480
DB 433 AGAATATTTCTTAATGTTTGAAGAAGCTGTGATCTTAAGGATCTTAATTTCACTCAT 492
QY 481 AGTAGAGCAATGATGATCTATCGGACATGTAAGATCTTCAACAGAGTGGCAAGAC 540
DB 493 AGTAGAGCAATGATGATCTATCGGACATGTAAGATCTTCAACAGAGTGGCAAGAC 552
QY 541 ATATATTAATTAATTTGATGAGAGCCCAATATATGATGATGATGATGATGATGATGATGAT 600
DB 553 ATATATTAATTAATTTGATGAGAGCCCAATATATGATGATGATGATGATGATGATGATGAT 612
QY 601 AATATATGACAGAGATTAATCTGTAAATTAACCATGACTGTGTGCGAAGCAAGTA 660

DB 613 AATATGACAGAGATTAATCTGTAAATTAACCATGACTGTGTGCGAAGCAAGTA 672
QY 661 ATGCTGAAGCAATCAGAAAAAACTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 673 ATGCTGAAGCAATCAGAAAAAACTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 732
QY 721 CTCTGTGTTTGAATATCAGGCAAGTACATTTTAAAGTGTGATGATGATGATGATGATGAT 780
DB 733 CTCTGTGTTTGAATATCAGGCAAGTACATTTTAAAGTGTGATGATGATGATGATGATGAT 792
QY 781 TTCTTAAGAAAAATATCTCTGTAGTAAATGATATTAAGAAAGCTGTATATGCTTTGGG 840
DB 793 TTCTTAAGAAAAATATCTCTGTAGTAAATGATATTAAGAAAGCTGTATATGCTTTGGG 852
QY 841 AGAGTCCCAATTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 853 AGAGTCCCAATTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
QY 901 TGTTTTACATGCAATCTTATTCAGAGCATTTTCACAGCTACACCATATATGATGATGATGAT 960
DB 913 TGTTTTACATGCAATCTTATTCAGAGCATTTTCACAGCTACACCATATATGATGATGATGAT 972
QY 961 GAAACATCTACAAATTCCTTTGGGTTATTAATTAAGCACTGCAATATTAATTAATTAATTA 1020
DB 973 GAAACATCTACAAATTCCTTTGGGTTATTAATTAAGCACTGCAATATTAATTAATTAATTA 1032
QY 1021 GCACCTACGTAATCTAATAATTTGAGACATTTGACAGATTTATGTTGCAAGCATGATC 1080
DB 1033 GCACCTACGTAATCTAATAATTTGAGACATTTGACAGATTTATGTTGCAAGCATGATC 1092
QY 1081 TACCATGAGAGAAACCTTATGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1093 TACCATGAGAGAAACCTTATGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
QY 1141 CCCAGGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1153 CCCAGGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1212
QY 1201 CGACTTTCCTTTCATTTGCTGTGTAAGAGCCGAAAGGGGCTTAAGAGAGAAACATGCT 1260
DB 1213 CGACTTTCCTTTCATTTGCTGTGTAAGAGCCGAAAGGGGCTTAAGAGAGAAACATGCT 1272
QY 1261 CCATTGGATGAGGAAATATACTTGTGATTAACAGACACTCTAATATCTGAAATA 1320
DB 1273 CCATTGGATGAGGAAATATACTTGTGATTAACAGACACTCTAATATCTGAAATA 1332
QY 1321 ATGCTTTGAATCTTTGGCCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1333 ATGCTTTGAATCTTTGGCCAGTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1392
QY 1381 GTTACTGATCAATCCAAATTAAGAAACCTCATGCTAGAGTTGGAGTTGACTGCTTC 1440
DB 1393 GTTACTGATCAATCCAAATTAAGAAACCTCATGCTAGAGTTGGAGTTGACTGCTTC 1452
QY 1441 AGCAGTGTGTAAGATTTCCAGATATGTCAGTATGTAAGAGCATGCAATTTGTCTGTA 1500
DB 1453 AGCAGTGTGTAAGATTTCCAGATATGTCAGTATGTAAGAGCATGCAATTTGTCTGTA 1512
QY 1501 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGAGCTGATTAACAGACTAGCTAGAGAC 1560
DB 1513 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGAGCTGATTAACAGACTAGCTAGAGAC 1572
QY 1561 AATGAATTAAGGAAAAATGAAGAAAGAGCTCAAGCAATTTTACAGAGATCTCTTC 1620
DB 1573 AATGAATTAAGGAAAAATGAAGAAAGAGCTCAAGCAATTTTACAGAGATCTCTTC 1632
QY 1621 TCTGAATCACTGAGCAGAGAGAAAGATTTCTATGAGATCAAGACACTATTTGTATACT 1680
DB 1633 TCTGAATCACTGAGCAGAGAGAAAGATTTCTATGAGATCAAGACACTATTTGTATACT 1692
QY 1681 ATCCCGAAATTTCAACCAATTTGCTTGTCTGTTAATGAAATTTCTAGAGATGAAATGTA 1740

Db 1693 ATCCCCAAATCTACCCAAATGCTTCTGTCTGTTAAATGGAATCTTAGAGATGAAGTA 1752
 Qy 1741 GCCCAGATGATGTGCTGTAAAGATGAGCTCCCAATCAAACTGAACAGGCTATGGA 1800
 Db 1753 GCCCAGATGATGTGCTGTAAAGATGAGCTCCCAATCAAACTGAACAGGCTATGGA 1812
 Qy 1801 CTTCTGAGCTGTAATTAACCCAGATCTTATGTTGCAAGGTTTGTCTGTTGGTGGAA 1860
 Db 1813 CTTCTGAGCTGTAATTAACCCAGATCTTATGTTGCAAGGTTTGTCTGTTGGTGGAA 1872
 Qy 1861 AAATATTAACAGATGACAAACCTTCTCAGATTTAATTCAGCTAGTACAGGCTCTAA 1920
 Db 1873 AAATATTAACAGATGACAAACCTTCTCAGATTTAATTCAGCTAGTACAGGCTCTAA 1932
 Qy 1921 TATGACAATATTTGGATTAATCTGCTTGTGAGATTTTATCTGAGAAAGCATTTGACTAAT 1980
 Db 1993 TATGACAATATTTGGATTAATCTGCTTGTGAGATTTTATCTGAGAAAGCATTTGACTAAT 1992
 Qy 1991 CAAGGATTTGGGACCTTTTCTTTTGGCATTTAAATCTGAGATGACAAATAAACAGTT 2040
 Db 1993 CAAGGATTTGGGACCTTTTCTTTTGGCATTTAAATCTGAGATGACAAATAAACAGTT 2052
 Qy 2041 AGCCAGATTTGGGCTGCTTTTGGAGTCTTATTTGCTGTCATGTTGGATGATTTGGAAG 2100
 Db 2053 AGCCAGATTTGGGCTGCTTTTGGAGTCTTATTTGCTGTCATGTTGGATGATTTGGAAG 2112
 Qy 2101 CACCTGAATAGGCAAGTGCAGGCAATGGAAGAGCTCATTACTTAATCTGACATTTCTCAA 2160
 Db 2113 CACCTGAATAGGCAAGTGCAGGCAATGGAAGAGCTCATTACTTAATCTGACATTTCTCAA 2172
 Qy 2161 CAGGAGAGAGAGATGAAACACAAAAGGTACAGATGAAGTTTATGTTAGCAAAATGAGG 2220
 Db 2173 CAGGAGAGAGAGATGAAACACAAAAGGTACAGATGAAGTTTATGTTAGCAAAATGAGG 2232
 Qy 2221 CGACCAAGATTTGATGATGATGCTTACAGGCTGCTGCTCTCTAAACCTTCTCATCA 2280
 Db 2233 CGACCAAGATTTGATGATGATGCTTACAGGCTGCTGCTCTCTAAACCTTCTCATCA 2292
 Qy 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGTTCTTCTGCAAAAAGGCACTGGG 2340
 Db 2293 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGTTCTTCTGCAAAAAGGCACTGGG 2352
 Qy 2341 TTGAATTTGGAGAACCCAGACATCATGTCAGAGTTACTGTTTTCAGAAACATGAGATCATC 2400
 Db 2353 TTGAATTTGGAGAACCCAGACATCATGTCAGAGTTACTGTTTTCAGAAACATGAGATCATC 2412
 Qy 2401 TTTAAATTTGGGAGATGATTAAGGCAAGATATGCTTAACCTTGAATTTTGTATATG 2460
 Db 2413 TTTAAATTTGGGAGATGATTAAGGCAAGATATGCTTAACCTTGAATTTTGTATATG 2472
 Qy 2461 GAAATATCTGSCAAATCAAGGCTGTGATCTTTCGAATGTTACCTTATGTTGTCTGTCA 2520
 Db 2473 GAAATATCTGSCAAATCAAGGCTGTGATCTTTCGAATGTTACCTTATGTTGTCTGTCA 2532
 Qy 2521 ATCGGTGACTGTGTGGGACTTTATGAGTGTGTGCGAAATCTCACAATAATTATGCAAAAT 2580
 Db 2533 ATCGGTGACTGTGTGGGACTTTATGAGTGTGTGCGAAATCTCACAATAATTATGCAAAAT 2592
 Qy 2581 CAGTCAAAAGGCTGCTTGAAGGTGACTGCACTTTCACAGGCACTCACTCATGATGG 2640
 Db 2593 CAGTCAAAAGGCTGCTTGAAGGTGACTGCACTTTCACAGGCACTCACTCATGATGG 2652
 Qy 2641 CTCAAAGACAAAGACAAAGGAAATATATATGATGACAGCATGACCTGTTTACAGTTCA 2700
 Db 2653 CTCAAAGACAAAGACAAAGGAAATATATATGATGACAGCATGACCTGTTTACAGTTCA 2712
 Qy 2701 TGTGCTGATACTGTGTAGCTACTTTCATTTTGGAAATGAGATGCTGACAAATAGTAAC 2760
 Db 2713 TGTGCTGATACTGTGTAGCTACTTTCATTTTGGAAATGAGATGCTGACAAATAGTAAC 2772
 Qy 2761 ATCATGTTGAAAGACATGATGACAACTGTTTTCATATATGATTTTGGACATTTTGGATCAC 2820
 Db 2773 ATCATGTTGAAAGACATGATGACAACTGTTTTCATATATGATTTTGGACATTTTGGATCAC 2832

Qy 2821 AAGAGAAAAATTTGTTATTAACAGAACGTGTGCCATTTGTTTGGACACAGATTTTC 2880
 Db 2833 AAGAGAAAAATTTGTTATTAACAGAACGTGTGCCATTTGTTTGGACACAGATTTTC 2892
 Qy 2881 TTAATAGATTTAGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
 Db 2893 TTAATAGATTTAGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2952
 Qy 2941 CAGGAGATGTTTACAGAGCTTATCTAGCTATTTGACAGATGACCAATCTCTTAAT 3000
 Db 2953 CAGGAGATGTTTACAGAGCTTATCTAGCTATTTGACAGATGACCAATCTCTTAAT 3012
 Qy 3001 CTTTTCATGATGCTTGGCTGTGGAATGCGACAACTACAACTTTTGTATGACATTTGCA 3060
 Db 3013 CTTTTCATGATGCTTGGCTGTGGAATGCGACAACTACAACTTTTGTATGACATTTGCA 3072
 Qy 3061 TACATTTGAAAGACCTTACCTTGTAGATTAACCTGACAAAGGCTTTGAGATTTTCATG 3120
 Db 3073 TACATTTGAAAGACCTTACCTTGTAGATTAACCTGACAAAGGCTTTGAGATTTTCATG 3132
 Qy 3121 AAACAAATGATGATGACATCATGCTGCTGGAACAACAAATGATTTGATTTCCAC 3180
 Db 3133 AAACAAATGATGATGACATCATGCTGCTGGAACAACAAATGATTTGATTTCCAC 3192
 Qy 3181 ACAATTTAAACAGATGATGATTAACCTGACAAAGATTACTGAAATGAAAGCTCACTCTGGA 3240
 Db 3193 ACAATTTAAACAGATGATGATTAACCTGACAAAGATTACTGAAATGAAAGCTCACTCTGGA 3252
 Qy 3241 CACTAGCTGCACTGTTATTAATCTCTGACAGGCAAGACGATTTGATAGAAATTTGCAC 3300
 Db 3253 TTTCCACCTGCACTGTTATTAATCTCTGACAGGCAAGACGATTTGATAGAAATTTGCAC 3312
 Qy 3301 AATCATGAAACAGCTTATGATTTACGACAGCAAGAAATTAATATATATTAATTTAA 3360
 Db 3313 AATCATGAAACAGCTTATGATTTACGACAGCAAGAAATTAATATATATTAATTTAA 3372
 Qy 3361 TAATGTTAAACGCAACAGGCTTTGATGACACTTTAACTAGTTCAATTTCAAA 3412
 Db 3373 TAATGTTAAACGCAACAGGCTTTGATGACACTTTAACTAGTTCAATTTCAAA 3424

RESULT 3
 AAS14365
 ID AAS14365 standard; cDNA; 3424 BP.
 XX
 AC AAS14365;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE cDNA encoding human p110alpha isoform of PI3-kinase.
 XX
 KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform;
 KW LAMP-1; cancer; inflammatory disease; ophtalmic disorder; SH3 domain;
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
 KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH CDS
 FT 13..3219
 FT /tag= a
 FT /product= "p110alpha isoform of PI3-kinase"
 XX
 PN W0200185986-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-US15065.
 XX
 PR 10-MAY-2000; 2000US-203346P.
 XX
 PA (ICOS-) ICOS CORP.

XX Sadhu C;
 PT 2002-075252/10.
 DR P-PSDB; AAU09687.
 XX
 PT Identifying a modulator of p10delta polypeptide binding to SH3
 PT domain-containing polypeptides e.g. LASP-1, comprising allowing the
 PT binding partners to interact in the presence and absence of a test
 PT compound

Example 1; Page 55-60; 85bp; English.

XX The present invention relates to identifying a modulator of the
 CC phosphatidylinositol 3-kinase (PI3K; p10delta) enzyme that binds to
 CC the catalytic subunit via a SH3 domain-containing polypeptide such as
 CC LASP-1. Also described are methods of assaying the specific binding
 CC affinity of the PI3-kinase binding partner. Such modulators are useful
 CC for the treatment of diseases characterized by the undesirable or
 CC excessive activity of PI3Kdelta. For example the modulators can be used
 CC for inhibiting the growth or proliferation of cancer cells
 CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
 CC Hodgkin's lymphoma, leukemias), inflammatory diseases (e.g. rheumatoid
 CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
 CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
 CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
 CC dermatoses (e.g. contact dermatitis, central or peripheral nervous
 CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
 CC and Type I diabetes mellitus. The present sequence encodes for human
 CC p10delta isoform of PI3K.

XX Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;

Query Match 99.9%; Score 3407.2; DB 24; Length 3424;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTCCAGACCATCATGAGTGAACCTGTGGGCGATCCACTGTAGCCCCCAAGATC 60
 DB 13 ATGCTCCAGACCATCATGAGTGAACCTGTGGGCGATCCACTGTAGCCCCCAAGATC 72
 QY 61 CTAGTGGAAATGTTTACTACCAATGAAATGATAGTGAATTTAGATGCTCGTAGGCT 120
 DB 73 CTAGTGGAAATGTTTACTACCAATGAAATGATAGTGAATTTAGATGCTCGTAGGCT 132
 QY 121 ACATTGTAATATAAGATGAATATTAAAGAAAGAAATACCTCCATCA 180
 DB 133 ACATTGTAATATAAGATGAATATTAAAGAAAGAAATACCTCCATCA 192
 QY 181 CTTCTTCAAGATGAATCTTACATTTCTTAAGTGTACCCAGAGACAGAAAGGAA 240
 DB 193 CTTCTTCAAGATGAATCTTACATTTCTTAAGTGTACCCAGAGACAGAAAGGAA 252
 QY 241 GAATTTTGAAGAAAGAGAGACTTTGTGATCTTGGCTTTTCAACCATTTTAA 300
 DB 253 GAATTTTGAAGAAAGAGAGACTTTGTGATCTTGGCTTTTCAACCATTTTAA 312
 QY 301 GAATTTGAACAGTAGGCAACCGTGAAGAAAGATCTCAATCGAGAAATTTGTTGCT 360
 DB 313 GAATTTGAACAGTAGGCAACCGTGAAGAAAGATCTCAATCGAGAAATTTGTTGCT 372
 QY 361 ATCGGATCCAGTGTGCAATTTGATATGTTAAAGATCTGAAGTACAGACTTCCGA 420
 DB 373 ATCGGATCCAGTGTGCAATTTGATATGTTAAAGATCTGAAGTACAGACTTCCGA 432
 QY 421 AGAATATTTCTTAATGTTTGAAGAGCTGTGGATCTTAAGGATCTTAATTCACCTCAT 480
 DB 433 AGAATATTTCTTAATGTTTGAAGAGCTGTGGATCTTAAGGATCTTAATTCACCTCAT 492
 QY 481 AGTAGAGCAATGATGTCTATCCGCACTGTAGAAATCTTCAACGAGTGCAGAAAGC 540
 DB 493 AGTAGAGCAATGATGTCTATCCGCACTGTAGAAATCTTCAACGAGTGCAGAAAGC 552

QY 541 ATATATATATTAATTTGGATAGAGCCCAATATAGTGTGATTTGGGTAAATAGTTCTCCA 600
 DB 553 ATATATATATTAATTTGGATAGAGCCCAATATAGTGTGATTTGGGTAAATAGTTCTCCA 612
 QY 601 AATATGAAACAGAGATATCTGTAAATATCAACCATGATGTGTGTCAGAACAGTA 660
 DB 613 AATATGAAACAGAGATATCTGTAAATATCAACCATGATGTGTGTCAGAACAGTA 672
 QY 661 ATTGTGAAGCATGAGGAAAAAACTAGAAATAGTGTCTCATCTGAAATTTAA 720
 DB 673 ATTGTGAAGCATGAGGAAAAAACTAGAAATAGTGTCTCATCTGAAATTTAA 732
 QY 721 CTCTGTGTTTAAATATCGGCAATGATATTTAAAGTGTGTGATGATGAATAC 780
 DB 733 CTCTGTGTTTAAATATCGGCAATGATATTTAAAGTGTGTGATGATGAATAC 792
 QY 781 TTCTTGAAGAAATATCTGTGATGATGATGATGATGATGATGATGATGATGATG 840
 DB 793 TTCTTGAAGAAATATCTGTGATGATGATGATGATGATGATGATGATGATGATG 852
 QY 841 AGGATGCCCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATG 900
 DB 853 AGGATGCCCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATG 912
 QY 901 TGTTTTACATGCAATCTTATTTCAAGAGCATTTTCAAGAGCATATATGATGATG 960
 DB 913 TGTTTTACATGCAATCTTATTTCAAGAGCATTTTCAAGAGCATATATGATGATG 972
 QY 961 GAAACATCTACAAATTCCTTTGGGTATTAATATAGACATCTCAATTAATTTCTTGT 1020
 DB 973 GAAACATCTACAAATTCCTTTGGGTATTAATATAGACATCTCAATTAATTTCTTGT 1032
 QY 1021 GCACCTTACATGCAATCTTATTTCAAGAGCATTTTCAAGAGCATATATGATGATG 1080
 DB 1033 GCACCTTACATGCAATCTTATTTCAAGAGCATTTTCAAGAGCATATATGATGATG 1092
 QY 1081 TACCATGAGAGAAACCTTATGTCAGATGTAACACTCAAGAGTACTTGTTCAT 1140
 DB 1093 TACCATGAGAGAAACCTTATGTCAGATGTAACACTCAAGAGTACTTGTTCAT 1152
 QY 1141 CCCAGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 DB 1153 CCCAGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1212
 QY 1201 CGACTTTCCTTCAATTTGCTGTAAAGGCGAAAGGGGTCTTAAGAGAAACACTGT 1260
 DB 1213 CGACTTTCCTTCAATTTGCTGTAAAGGCGAAAGGGGTCTTAAGAGAAACACTGT 1272
 QY 1261 CCATTGGATGGGAAATATATACTTGTGATTAACAGACACTAGTATCTGAAAA 1320
 DB 1273 CCATTGGATGGGAAATATATACTTGTGATTAACAGACACTAGTATCTGAAAA 1332
 QY 1321 ATGGCTTTGAATCTTTGGCCAGTACTCATGATTTAGAAATTTGCTGAACTTTGCT 1380
 DB 1333 ATGGCTTTGAATCTTTGGCCAGTACTCATGATTTAGAAATTTGCTGAACTTTGCT 1392
 QY 1381 GTTACTGATCAATCCAAATTAAGAAATCTCATGCTTAGAGTTGGAGTTTGACCTGC 1440
 DB 1393 GTTACTGATCAATCCAAATTAAGAAATCTCATGCTTAGAGTTGGAGTTTGACCTGC 1452
 QY 1441 AGCAGTGTGTAAGTTCCAGATATGTCACTGATTTGAAGAGATGCCAATTTGCTGTA 1500
 DB 1453 AGCAGTGTGTAAGTTCCAGATATGTCACTGATTTGAAGAGATGCCAATTTGCTGTA 1512
 QY 1501 TCCGAGAGAGAGATTTAGCTATTTCCAGCAGAGCTGAGTAAACAGCTAGCTAGAGAC 1560
 DB 1513 TCCGAGAGAGAGATTTAGCTATTTCCAGCAGAGCTGAGTAAACAGCTAGCTAGAGAC 1572
 QY 1561 AATGAATTAAGGAAAAAGACAAAGAGAGCTCAAGCAATTTTACACGAGATCTCTC 1620
 DB 1573 AATGAATTAAGGAAAAAGACAAAGAGAGCTCAAGCAATTTTACACGAGATCTCTC 1632
 QY 1621 TCTGAATCACTGAGCAGAGAAAGATTTCTATGAGTCAAGACACTATTTGTACT 1680

Db	1633	TTCTGAATACATGAGCAGGAGAAAGATTTTCTATGGAAGTCAACAACATATGTGTAACT	1692
QY	1681	ATCCCGAAATTTCTAACCCAAATGTCTCTGTCTGTAAATGGAATTTAGAGATGAAGTA	1740
Db	1693	ATCCCGAAATTTCTAACCCAAATGTCTCTGTGTAAATGGAATTTAGAGATGAAGTA	1752
QY	1741	GCCCAAGATGATTTGCTGTGTAAAGATTTGGCTCCATCAAACTTGAAACAGGCTATGGAA	1800
Db	1753	GCCCAAGATGATTTGCTGTGTAAAGATTTGGCTCCAAACCAACCTTGAAACAGGCTATGGAA	1812
QY	1801	CTTCTGCACTGTAAATTAACCAAGATTCATGAGTTGGTGGTGGTGGTGGTGGAA	1860
Db	1813	CTTCTGCACTGTAAATTAACCAAGATTCATGAGTTGGTGGTGGTGGTGGTGGAA	1872
QY	1861	AAATATTTTACAGATGACAAACCTTCTCAGATTTAAATTCAGTCAGTACAGGTCTTAAA	1920
Db	1873	AAATATTTTACAGATGACAAACCTTCTCAGATTTAAATTCAGTCAGTACAGGTCTTAAA	1932
QY	1921	TATGAAACAATTTTGGATATCTTGCTGTGTGATTTTACTGAAAGAAAGCATTAAT	1980
Db	1933	TATGAAACAATTTTGGATATCTTGCTGTGTGATTTTAACTGAAAGAAAGCATTAAT	1992
QY	1981	CAAGGATTTGGGACCTTTTCTTTTGGATTTAAATCTGAGATGACAAATAAACAGTT	2040
Db	1993	CAAGGATTTGGGACCTTTTCTTTTGGATTTAAATCTGAGATGACAAATAAACAGTT	2052
QY	2041	AGCCAGAGGTTTGGCTGCTTTTGGAGTCTTATTTGTCGTGCAATGTGGATTTATTTGAG	2100
Db	2053	AGCCAGAGGTTTGGCTGCTGCTTTTGGAGTCTTATTTGTCGTGCAATGTGGATTTATTTGAG	2112
QY	2101	CACCTGAATAGGCAATGTGAGGCAATGGAAGCTCATTTAATTACTGACATTTCTCAA	2160
Db	2113	CACCTGAATAGGCAATGTGAGGCAATGGAAGCTCATTTAATTACTGACATTTCTCAA	2172
QY	2161	CAGGAGAGGAAGATGAAACAAAGAGGTAAAGATGAACTTTTATGTTAGACAAATAGAG	2220
Db	2173	CAGGAGAGGAAGATGAAACAAAGAGGTAAAGATGAACTTTTATGTTAGACAAATAGAG	2232
QY	2221	CGACCAAGATTTCAATGATGCCCTTACAGGAGCTGCTGTCCTCTTAAACCTGCTCATCAAA	2280
Db	2233	CGACCAAGATTTCAATGATGCCCTTACAGGAGCTGCTGTCCTCTTAAACCTGCTCATCAAA	2292
QY	2281	CTAGGAAACCTCAGGCTTAAAGAGGTGCAATATATGTTCTTGTGCAAAAGGCCACTGTGG	2340
Db	2293	CTAGGAAACCTCAGGCTTAAAGAGGTGCAATATATGTTCTTGTGCAAAAGGCCACTGTGG	2352
QY	2341	TTGATTTGGGAAACCCAGACATCATGTCAGAGTTTACGTTTCAGAGCAATGAGATCATC	2400
Db	2353	TTGATTTGGGAAACCCAGACATCATGTCAGAGTTTACGTTTCAGAGCAATGAGATCATC	2412
QY	2401	TTTAAAAATGGGAGATGATTTTACGGCAAAATATGCTTAACTTCAATTCGTATATG	2460
Db	2413	TTTAAAAATGGGAGATGATTTTACGGCAAAATATGCTTAACTTCAATTCGTATATG	2472
QY	2461	GAATAATATCTGGCAAAATCAAGAGTCTTGATCTTGCAATGTTACCTTATGTTGTCTGTCA	2520
Db	2473	GAATAATATCTGGCAAAATCAAGAGTCTTGATCTTGCAATGTTACCTTATGTTGTCTGTCA	2532
QY	2521	ATCGGTGACTGTGTGGACTTATTTAGAGTGGTGGCAAAATTTCTACACTATTTATGCAATTT	2580
Db	2533	ATCGGTGACTGTGTGGACTTATTTAGAGTGGTGGCAAAATTTCTACACTATTTATGCAATTT	2592
QY	2581	CAGTGCAGAGGCGGCTTGAAAGGTGCACTGCAAGTTCAACAGCAACACTATCAATCAGTGG	2640
Db	2593	CAGTGCAGAGGCGGCTTGAAAGGTGCACTGCAAGTTCAACAGCAACACTATCAATCAGTGG	2652
QY	2641	CTCAAGAGCAAGAACAAAGAGAGAAATATATGATGACAGCATTTGACTTTTACAGTTCA	2700
Db	2653	CTCAAGAGCAAGAACAAAGAGAGAAATATATGATGACAGCATTTGACTTTTACAGTTCA	2712
QY	2701	TGTGCTGGATATCTGTAGCTTCACTTCAATTTTGGAAATTTGAGATGCTCAACATATGTAAC	2760

Accession	Gene	Protein	Function	Location/Qualifiers
Db	2713	TGTCGTGGATACGTGTGAGTACCTTCATTTTGGGAATTGGAGATCGTCACAAATGATAC	2712	
Qy	2761	ATCATGCTGAAGAAGCATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820	
Db	2773	ATCATGCTGAAGAAGCATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2832	
Qy	2821	AAGAAGAAAAAATTTGGTTTATTAACGAGAACGGTGCCTTTGTTTGGACACAGGATTC	2880	
Db	2833	AAGAAGAAAAAATTTGGTTTATTAACGAGAACGGTGCCTTTGTTTGGACACAGGATTC	2892	
Qy	2881	TTAATAGTGAATTAAGGAGCCCAAGAAATGCAAAAGACMAGAGAAATTTGAGAGGTTT	2940	
Db	2893	TTAATAGTGAATTAAGGAGCCCAAGAAATGCAAAAGACMAGAGAAATTTGAGAGGTTT	2952	
Qy	2941	CAGAGATGCTGTTCACAAAGCCTTATCTAGCTATTGACAGCATGCGCAATCTCTTCATTAAT	3000	
Db	2953	CAGAGATGCTGTTCACAAAGCCTTATCTAGCTATTGACAGCATGCGCAATCTCTTCATTAAT	3012	
Qy	3001	CTTTTCTCAATGATGCTTGGGCTCTGGAATGCCAATACAAATCTTTTGAATGACATTGCA	3060	
Db	3013	CTTTTCTCAATGATGCTTGGGCTCTGGAATGCCAATACAAATCTTTTGAATGACATTGCA	3072	
Qy	3061	TACATTGGAAGAGCCCTAGCCTTATGATTAACCTGACAAAGGCTTTGGAGTATTTGATG	3120	
Db	3073	TACATTGGAAGAGCCCTAGCCTTATGATTAACCTGACAAAGGCTTTGGAGTATTTGATG	3132	
Qy	3121	AAACAAATGATATGATGACATCATGTGGCTGGACAAACAAATATGATGATGCTTCAC	3180	
Db	3133	AAACAAATGATATGATGACATCATGTGGCTGGACAAACAAATATGATGATGCTTCAC	3192	
Qy	3181	ACAAATTAACAGCATGCTGATTAAGTGAATGAAATGAAAGCTCAGCTCTGGA	3240	
Db	3193	ACAAATTAACAGCATGCTGATTAAGTGAATGAAATGAAAGCTCAGCTCTGGA	3252	
Qy	3241	CACATCACTGACACTGTTAATTAACCTCAGCAGGCAAGACCGATGATGAGAAATTCGAC	3300	
Db	3253	TTCCACACTGACACTGTTAATTAACCTCAGCAGGCAAGACCGATGATGAGAAATTCGAC	3312	
Qy	3301	AATCCATGAACAGCATTAAGATTTACAGCAAGAACAGAAATTAATACTATATAATTTTAA	3360	
Db	3313	AATCCATGAACAGCATTAAGATTTACAGCAAGAACAGAAATTAATACTATATAATTTTAA	3372	
Qy	3361	TAATGTAAAGCAAAACAGGCTTTGATATGCACTTAATTAAGTTTCAATAAA	3412	
Db	3373	TAATGTAAAGCAAAACAGGCTTTGATATGCACTTAATTAAGTTTCAATAAA	3424	
RESULT 4				
AAQ57012				
ID	AAQ57012 standard; cDNA to mRNA; 3498 BP.			
XX				
AC	AAQ57012;			
XX				
DT	25-MAR-2003 (updated)			
DT	31-AUG-1994 (first entry)			
XX				
DE	Ptdins 3-kinase 110 kD catalytic subunit cDNA.			
XX				
KM	110 kD catalytic subunit; phosphatidylinositol 3-kinase;			
KM	transformation; Schizosaccharomyces pombe; mmt promoter; thiamine;			
KW	Ptdins 3-kinase; assay; detection; cell growth; regulation; cancer;			
KW	blood vessel plaques; ss.			
XX				
OS	Bos taurus.			
XX				
FT	Key			
FT	CDS			
FT	Location/Qualifiers			
FT	1..3207			
FT	/*tag= a			
FT	/product= P110			
XX				
PN	W09403609-A1.			
XX				
PD	17-FEB-1994.			

QY	1621	TCGAAATCACTGACGAGAGAGATTTTCTATGAGCTCAACAACACTATTGTGTAACT	1660
Db	1621	TCTGAAATCACTGAGCAAGCAAGAAATTTTCTGTGAGACCACACACATAATTGTGTAACT	1660
QY	1661	ATCCCCGAAATCTCACCCAAATGTCTGTCTGTCTGTAAATGGAAATCTAGAGATGAAGTA	1740
Db	1661	ATCCCCGAAATCTACCCAAATGTCTGTCTGTCTGTAAATGGAACTTAGAGATGAAGTA	1740
QY	1741	GCCCCAGATGATTTGGCTGTGTAAGAAATGTGGCTCCCAATCAAACTGAAACAGGCTATGGAA	1800
Db	1741	GCTCAGATGTAAGTCTGTGTAAAGATTTGGCTCCCAATCAAACTGAAACAGGCTATGGAG	1800
QY	1801	CTTCTGGAAGCTGTAATTAATCCCAATCTCTATGTTGGAAGTTTGGCTGTGGTGTGGAA	1860
Db	1801	CTTCTGGAAGCTGTAATTAATCCCAATCTCTATGTTGGAAGTTTGGCTGTGGTGTGGAA	1860
QY	1861	AAATATTTAAACGATGACAAACTTCTCAGATATTTAAATTCAGAGTAGTACAGTCCCTAA	1920
Db	1861	AAATATTTAAACGATGACAAACTTCTCAGATATTTAAATTCAGAGTAGTACAGAGTACTAAA	1920
QY	1921	TATGAACAATATTTGGATTAAGTCTGTGTGAGATTTTAACTGAAGAAAGCATTAACATA	1980
Db	1921	TATGAACAATATTTGGATTAAGTCTGTGTGAGATTTTAACTGAAGAAAGCATTAACATA	1980
QY	1961	CAAGAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAATATAAACAGTT	2040
Db	1961	CAAGAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAATATAAACAGTT	2040
QY	2041	AGCCAGAGATTTGGGCTGCTTTTGGAGTCTATTGTCTGCAATGGGATGTATTTGAG	2100
Db	2041	AGTCAAGATTTGGGCTGCTTTTGGAGTCTATTGTCTGCAATGGGATGTATTTGAG	2100
QY	2101	CACCTGAATAGCAAGTGAAGCAATGGAAGCATTAACCTTAACCTGACATTTCTCAA	2160
Db	2101	CACCTTAATAGGCAAGTGAAGCTATGGAAGCATTAACCTTAACCTGACATTTCTCAA	2160
QY	2161	CAGGAGAGAGAGATGAACCAAAAGTACAGATGAAGTTTAAAGTTAGAGCAATAGAG	2220
Db	2161	CAGGAGAGAGAGATGAACCAAAAGTATCAAGATGAAGTTTAAAGTTAGAGCAAAATAGG	2220
QY	2221	CGACAGATTTCAATGATGAGCTTACAGGGCTTGCTGCTCCCTCAAAACCTGCTCATCA	2280
Db	2221	CGACAGATTTCAATGATGAGCTTACAGGGCTTTCTGTCTCTCAAAACCTGCTCATCAG	2280
QY	2281	CTAGGAAACCTTAGGCTTTAAAGATGTGCAATTATGTTCTTGCAGAAAAGGCCACTGTGG	2340
Db	2281	CTGGGAAATCTCAGGCTTGAAGAGGTGCAATTAATGTTCTTGCAGAAAAGGCCACTGTGG	2340
QY	2341	TTGAATTTGGGAAACCCAGACATCATGTCAAGATTAAGTCTTTCAGAAATAGATCATC	2400
Db	2341	TTGAATTTGGGAAACCCAGACATCATGTCAAAATTAAGCTTTCAGAAACAAAGAAATCATC	2400
QY	2401	TTTAAATAATGGGAGATGATTTACGCGAATAATGTCTAACCTTCAAAATTAATTCGATTATG	2460
Db	2401	TTTAAATAATGGGAGATGATTTACGCGAATAATGTCTAACCTTCAAGATTATTCGCAATTATG	2460
QY	2461	GAAATATCTGGCAAAATCAAGGTCCTTGATCTTGCATGTTAACTTAATGTTGTCTGTCA	2520
Db	2461	GAAATATCTGGCAAAATCAAGGTCCTTGATCTTGCATGTTAACTTAATGAGTGTCTGTCA	2520
QY	2521	ATCGGTGACTGTGTGGGCACTTATGAGGTGGTGGGAAATTTCTCAACATTAATAGCAAAAT	2580
Db	2521	ATCGGTGACTGTGTGGGCACTTATGAGGTGGTGGGAAATTTCTCAACATTAATAGCAAGTT	2580
QY	2581	CAGTGCAGAGGCGCTTGAAGAGTGCACTGCAAGTTCAACAGCCACACACTACATCAGTGG	2640
Db	2581	CAGTGTAAAGGCGCTGAAAGGTGCACTGCAAGTTTAAACAGCCACACACTCAATCAAGTGG	2640
QY	2641	CTCAAAAGCAAGAACAAAGAGAGAAATATATGATGCAAGCATTAAGCTGTTTAAACGTTCA	2700
Db	2641	CTCAAAAGCAAGAACAAAGGGGAAATATATGATGCGGCATTCGATTGTTTAAACGATCA	2700

[illegible]


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Db      1501  TCCCGTGAAGCAGATTAGTATTCCTCCAGCAGCTAGTACACTCTACTAGAGC 1560
Qy      1561  ATGAAATTAAGGAAAATGACAAAGAACAGCTCAAAAGCAATTTCTACAGAGATCCTC 1620
Db      1561  ATGAAATTAAGGAAAATGATTAAGAACAGCTCCAGCAATTTGACAGAGATCCTCTA 1620
Qy      1621  TCTGAATCTAGCAGAGAGAAAGATTTCTATGAGAGTCACAGACACTATTGTACT 1680
Db      1621  TCTGAATCTAGCAGAGAGAAAGATTTCTGTGAGGCCACAGACACTATTGTACT 1680
Qy      1681  ATCCCGGAAATCTACCCCAAATTTGCTCTGTCTGTTAAATGGAATCTTGAGATGA 1740
Db      1681  ATCCCGGAAATCTACCCCAAATTTGCTCTGTCTGTTAAATGGAATCTTGAGATGA 1740
Qy      1741  GCCCAGATGATTTGCTGTGTAAGAGATGGCCCTCAATCAAACTTGAAACAGGCTA 1800
Db      1741  GCTCAGATGATGCTGTGTAAGAGATGGCCCTCAATCAAACTTGAAACAGGCTA 1800
Qy      1801  CTCTGGAATGATTAATCCAGATCCTATGCTGAGAGTTTGCTGTTGCTGCTGGA 1860
Db      1801  CTCTGGAATGATTAATCCAGATCCTATGCTGAGAGTTTGCTGTTGCTGCTGGA 1860
Qy      1861  AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAAGTACAGTACTA 1920
Db      1861  AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAAGTACAGTACTA 1920
Qy      1921  TATGAACAATTTGATTAATCTGCTGTGAGATTTTCTGAGAGAAAGCACTTGACT 1980
Db      1921  TATGAACAATTTGATTAATCTGCTGTGAGATTTTCTGAGAGAAAGCACTTGACT 1980
Qy      1981  CAAAGATTTGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGACAAATTAAC 2040
Db      1981  CAAAGATTTGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGACAAATTAAC 2040
Qy      2041  AGCCAGATTTGGCTGCTTTTGGAGTCTATTTGCTGTCATGAGAGATGATTTGA 2100
Db      2041  AGCCAGATTTGGCTGCTTTTGGAGTCTATTTGCTGTCATGAGAGATGATTTGA 2100
Qy      2101  CACCTGAATTAAGCAGTGGAGCAGTGGAAAGCTCATTAATCACTGACATTCCT 2160
Db      2101  CACCTGAATTAAGCAGTGGAGCAGTGGAAAGCTCATTAATCACTGACATTCCT 2160
Qy      2161  CAGAGAGAGAGATGATGAACACAAAGATGACAGATGATTTTATGTTAGCAAT 2220
Db      2161  CAGAGAGAGAGATGATGAACACAAAGATGACAGATGATTTTATGTTAGCAAT 2220
Qy      2221  CGACCAAGATTTATGATGATGCTCTACAGAGGCTTGTCTCTTAAACCTGCT 2280
Db      2221  CGACCAAGATTTATGATGATGCTCTACAGAGGCTTGTCTCTTAAACCTGCT 2280
Qy      2281  CTAGAGAAACCTCAGCTTTAAAGAGTGTCAATTAATGCTTCTGCAAAAAGG 2340
Db      2281  CTAGAGAAACCTCAGCTTTAAAGAGTGTCAATTAATGCTTCTGCAAAAAGG 2340
Qy      2341  TTGAATTTGGGAGAACCCAGACATCATGTCAGATTTACTGTTTCAAGACAT 2400
Db      2341  TTGAATTTGGGAGAACCCAGACATCATGTCAGATTTACTGTTTCAAGACAT 2400
Qy      2401  TTTAAAAATGGGAGATTTTACGGCAGATATGCTAACACTTCAATTAATG 2460
Db      2401  TTTAAAAATGGGAGATTTTACGGCAGATATGCTAACACTTCAATTAATG 2460
Qy      2461  GAAATATCTGGCAAAATCAAGCTCTTGATCTTGCATTTTACCTTAAGTGT 2520
Db      2461  GAAATATCTGGCAAAATCAAGCTCTTGATCTTGCATTTTACCTTAAGTGT 2520
Qy      2521  ATCGGTGACTGTGTGGACTTATGAGGTGTGCAAAATTTCAACATTAATG 2580
Db      2521  ATCGGTGACTGTGTGGACTTATGAGGTGTGCAAAATTTCAACATTAATG 2580
Qy      2581  CAGTCAAAAGCGGCTTGAAGGTGCACTGACGTTCAACAGCAGACATCACT 2640

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Db      2581  CAGTCAAAAGCGGCTTGAAGGTGCACTGACGTTTAAACGCCACACTCCAT 2640
Qy      2641  CTCAAGACCAAGAACAAAGAGAAATATATGATGAGCAGCATGACCTGTTA 2700
Db      2641  CTCAAGACCAAGAACAAAGGGAATATATGATGAGGCGCATGATTTGTTAC 2700
Qy      2701  TGTGCTGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2760
Db      2701  TGTGCTGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2760
Qy      2761  ATCATGTTGAAGAGAGATGACAACTGTTTCAATATAGATTTTGGACACT 2820
Db      2761  ATCATGTTGAAGAGATGACAACTGTTTCAATATAGATTTTGGACACTTT 2820
Qy      2821  AAGAGAAATTTGTTGTTTAAACGAGAGTGTGCCATTTGTTTGAACAGAT 2880
Db      2821  AAGAGAAATTTGTTGTTTAAACGAGAGTGTGCCATTTGTTTGAACAGAT 2880
Qy      2881  TTAATAGTATTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAG 2940
Db      2881  TTAATAGTATTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAG 2940
Qy      2941  CAGAGATGTTGTTAAGGCTTATCTAGCTATTTGACAGCATGCCATCTCT 3000
Db      2941  CAGAGATGTTGTTAAGGCTTATCTAGCTATTTGACAGCATGCCATCTCT 3000
Qy      3001  CTTTCTCAATGATGCTTGGCTGTGAGATGACAGAACTATCTTTGATGAC 3060
Db      3001  CTTTCTCAATGATGCTTGGCTGTGAGATGACAGAACTATCTTTGATGAC 3060
Qy      3061  TACATTCGAAAGACCTTATGATTAATTAATGACAGAGGCTTTGAGAT 3120
Db      3061  TACATTCGAAAGACCTTATGATTAATTAATGACAGAGGCTTTGAGAT 3120
Qy      3121  AAACAAATGATGATGACATCATGCTGCTGAGACAAAGATGATGATCT 3180
Db      3121  AAACAAATGATGATGACATCATGCTGCTGAGACAAAGATGATGATCT 3180
Qy      3181  ACAATTAACAGCATGATGACCTGA 3207
Db      3181  ACAATTAACAGCATGATGACCTGA 3207

RESULT 6
AAA02190
ID AAA02190 standard; cDNA, 741 BP.
XX
XX AAA02190;
AC
XX
XX
DT 19-MAY-2000 (first entry)
XX
XX
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2181.
XX
XX Human; colon cancer; tumour; diagnosis; gene expression product;
XX probe; detection; cancerous state; metastasis; identification;
XX breast cancer; oestrogen receptor-positive breast cancer; therapy;
XX oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX WO958675-A2.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 13-MAY-1999; 99WO-US10602.
PF
XX
XX 14-MAY-1998; 98US-0085426.
PR 15-MAY-1998; 98US-0085537.
PR 15-MAY-1998; 98US-0085696.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.
XX
XX (CHIR ) CHIRON CORP.
PA

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PA (HUSE-) HUSB INC.
XX Williams LT, Escobedo J, Imie MA, Garcia PD, Sudduth-Klinger J,
PI Reinhard C, Giese K, Rendazzo F, Kennedy GC, Pot D, Kassam A,
PI Lamson G, Drmanac R, Dickson M, Drmanac S, Labat I,
PI Leshkowitz D, Kita D, Garcia V, Jones LM, Stache-Crain B,
XX MPI, 2000-126369/11.
XX
XX Polynucleotide library used to determine cancerous states of mammalian
PT cells -
XX
XX Claim 1, page 850, 1097pp, English.
XX
XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC libraries constructed from human colon cancer cell lines. The present
CC invention also describes a method of detecting differentially expressed
CC genes correlated with a cancerous state of a mammalian cell, comprising
CC detecting at least one differentially expressed gene product in a test
CC sample derived from a cell suspected of being cancerous, where detection
CC of the differentially expressed gene product is correlated with a
CC cancerous state of the cell from which the test sample was derived.
CC The polynucleotides sequences can be used in a method for detecting
CC differentially expressed genes correlated with a cancerous state of a
CC mammalian cell. The polynucleotides can also be used as probes for
CC detecting and mapping related genes. They can be used in diagnosis and
CC prognosis of diseases and disorders (e.g. identification of
CC pre-metastatic or metastatic cancerous states, stages of cancer, or
CC responsiveness of cancer to therapy). This is particularly for breast
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC negative breast cancer, lung cancer, and colon cancer.
XX
XX Sequence 741 BP, 221 A, 137 C, 154 G, 208 T, 21 other;
SQ
Query Match 16.5%; Score 564; DB 21; Length 741;
Best Local Similarity 93.0%; Pred. No. 6.3e-138;
Matches 661; Conservative 0; Mismatches 41; Indels 9; Gaps 7;
QY 2182 CAAAGAGTACAGATGAGTATTTAGTGAAGCAATGAGGCGACAG-ATTTCATGATGC 2240.
DB 18 CAAAGAGTACAGATGAGTATTTAGTGAAGCAATGAGGCGACAG-ATTTCATGATGC 77
QY 2241 CCTACGAGGCTTGC-TGTCTCTCTTAACCTCTGCTCATCACTAGAGAACTTACGCTTA 2299
DB 78 TCTACGAGGCTTCTTCTCTCTTAACCTCTGCTCATCACTAGAGAACTTACGCTTGC 137
QY 2300 AAGAGTGTGAATATGATCTTCTGCAAAAAGGCGACCTGTTGATTTGGAGAACCCAG 2359
DB 138 AAGAGTGTGAATATGATCTTCTGCAAAAAGGCGACCTGTTGATTTGGAGAACCCAG 197
QY 2360 ACATCATGTCAAGTACTTCTTCAAGACATGAGATCATCTTTAAAAATGGGATGAT 2419
DB 198 ACATCATGTCAAGTACTTCTTCAAGACATGAGATCATCTTTAAAAATGGGATGAT 257
QY 2420 TACGGCAATATGCTTAACACTTCAAAATTTGTTATGAAAAATATCTGGCAAAATC 2479
DB 258 TACGGCAATATGCTTAACACTTCAAAATTTGTTATGAAAAATATCTGGCAAAATC 317
QY 2480 AAGGTTGATCTGCAATGTAACCTATGCTGTCGTCATCGGTGACCTGTGGGAC 2539
DB 318 AAGGTTGATCTGCAATGTAACCTATGCTGTCGTCATCGGTGACCTGTGGGAC 377
QY 2540 TTATTGAGGTGTCGCAAAATTTCTCACTATTATGCAAAATTCAGTCAAGGCGGCTTA 2599
DB 378 TTATTGAGGTGTCGCAAAATTTCTCACTATTATGCAAAATTCAGTCAAGGCGGCTTA 437
QY 2600 AAGGTCACATGCAATGCAAGGCGACACACTACATGAGTGTCTCAAGCAAGAACAA 2658
DB 438 AAGGTCAC-CTGCAATGCAAGGCGACACACTACATGAGTGTCTCAAGCAAGAACAA 496
QY 2659 GGAGAAATATGATGACGACGATGACCTGTTTAC-CCGTTGATGCTGATATCTGTGT 2717
DB 497 GGAGAAATATGATGACGACGATGACCTGTTTAC-CCGTTGATGCTGATATCTGTGT 556

QY 2718 AGCTACCTTCATTTGG-CAATTGGAGATGTCACAAATGTAACATCATGTTGAAGACG 2776
DB 557 AGCTACCTTCATTTGGCAATTTGGAGATGTCACAAATGTAACATCATGTTGAAGACG 616
QY 2777 ATGCACTGTTTCTAATAGATTTTGGACACTTTTGGATCAAGAGAAAAATTTG 2836
DB 617 ATGCACTGTTTCTAATAGATTTTGGACACTTTTGGATCAAGAGAAAAATTTG 676
QY 2837 GTTATTAACGAGAACGTG---CCATTGTTTGGACAGAGATTCTTA 2884
DB 677 GTTATTAACGAGAACGTTGCTGATTTGTTTGGACAGAGATTCTTA 727
RESULT 7
AAC65690
ID AAC65690 standard; DNA; 3213 BP.
XX
XX AAC65690;
AC
XX 16-FEB-2001 (first entry)
DT
XX
DE Human p13 kinase pllobeta DNA.
XX
XX Human; p13 kinase p110 beta; antisense inhibition; primer; cytostatic;
XX antiinflammatory; antiinfective; ds.
XX
XX Homo sapiens.
XX
XX US6133032-A.
XX
XX 17-OCT-2000.
PD
XX
XX 09-SEP-1999; 99US-0392350.
PF
XX
XX 09-SEP-1999; 99US-0392350.
PR
XX
XX 09-SEP-1999; 99US-0392350.
PX
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Cowser LM,
PI
XX
XX MPI, 2000-686014/67.
DR
XX
XX P-PSDB; AAB11124.
PT
XX
XX Antisense compound 8-30 nucleobases in length targeted to a start codon
PT of the coding region of human p13 kinase pllobeta, useful for
PT inhibiting the expression of the human polynucleotide -
PS
XX
XX Example 1, Column 43-50; 34pp; English.
PS
XX
XX This invention describes a novel antisense compound (I) 8-30 nucleobases
CC in length targeted to a start codon or nucleobases 4-1174 of the coding
CC region of human p13 kinase pllobeta (II), in which (I) specifically
CC hybridizes with and inhibits the expression of (II). The products of the
CC invention have cytostatic, antiinflammatory and antiinfective activity.
CC (I) is useful for inhibiting the expression of (II) in human cells or
CC tissues. The antisense compound can be utilized for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. The
CC antisense compounds may also be useful prophylactically, e.g. to prevent
CC or delay infection, inflammation or tumor formation. The antisense
CC compounds are useful for research and diagnostics, because these
CC compounds hybridize to nucleic acids encoding (II).
XX
XX
SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;
Query Match 13.5%; Score 460.8; DB 21; Length 3213;
Best Local Similarity 50.4%; Pred. No. 1.8e-110;
Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;
QY 58 ATCCAGTGAATGTTTACTACCAATGAGATGATGAGTATGATGCTCGGTAG 117
DB 88 ATCCAGTGAATGTTTCTTTGCTCCACTGGATTTATATTCAGTTGAGGATCTCTGGAA 147

QY 118 GGTACATTAGTACTATTAAGCATGACTATTAAAGAACAAAGAAATACCTCTCAT 177
Db 148 GGTACATTCTTATATATTAAGCATGATGTATGAAAGACAGTACACATTAACCAATGTTCC 207
QY 178 CAACCTCTTCAAGATGAATCTCTTACATTTTGTAGAGTTTACCAGAACACAGAAAG 237
Db 208 AACCTCTTATGATATTTGACTCTCTATGATTTGGATGTGTATGACATCTCTGTAT 267
QY 238 GAAGATTTTTTGATGAAACAAGACGCTTTGTGATCTTGGCTTTTCAACATTTT 297
Db 268 GAGAGGCTTGAAGATGAAGAACAGAGACCTGTGATGTACAGACTTTTCTTCAAGTTC 327
QY 298 AAAGTATTTGAACCAAGTAGCAACCGTGAGAGAAAGATCTTCAATGAGAAATGGTTT 357
Db 328 AAATTAGTACAAAGATGTGATCCAGGGGAAAA--ATTAGACTCAAAAAATTGGAGTC 384
QY 358 GGTATGGGATCCAGTGGCGAATTTGATGTGTTAAAGATCTGAGATACAGACTTC 417
Db 385 CTATTAGGAAAGTCTGATGAATTTGATCTTGAAGATCTGAGATGAATGATTT 444
QY 418 CGAAGAAATATTTCTAATGTTTGTAAAGAGCTGTGATCTTACGGATCTTATTCACCT 477
Db 445 CGAAGAAATATCGGCAATTCAGCGA-----GGAAAAATTCCTGTCA 486
QY 478 CATAGTAGCAATGATGTCTATCCGCACATGTAGAAATCTTCAACAGAGCTGCCAAG 537
Db 487 CTGTGGGATTTGTCTGGATGTGACTGTAAACAAACATATCCACAGAGCATGAACA 546
QY 538 CACATATATTAATTTGGATAGAGCCAAATATATAGTGTATTTGGTATATGTTCT 597
Db 547 TCCATCCCTGAAACCTTGAAGATTAACCTTTATGGGGAAAGCTCATGCTACCTGTCTAT 606
QY 598 CCAATTAATGACAGACAGAAATATCTGAAATCAACCATGACGTGTGCAGAACAA 657
Db 607 TTTGAAATCTGCAGAGCGTGTGTAGCTTTCAAGTGTCTCTATATATGATCTTATCAAA 666
QY 658 GTAAATGCTGAAGCAATCAGAAAAAAACTAGAGATAGTGTCTATCATCTGAACATTA 717
Db 667 GTAAATGAATTTGGCAATC---CAAAAAAGTTGACTATTCATGGAAGGAATGAAGTT 723
QY 718 AAACCTGTGTTTGAATATCAGGCGAAGTACATTTTAAAGTGTGTGATGTATGA 777
Db 724 AGCCCTATGAT-----TATGTGTGCAAGTCAAGCGGAGAGATGAGA 765
QY 778 TACTTCTAGAAAAAATATCTCTGAGTCAATATATATATAGAAAGCTGTATTAATGCTT 837
Db 766 TATGTTTTTGTGATCAATCACTAATTCAGTTCAGTATATCCGAGACTGTGTGATGAAC 825
QY 838 GAGAGGATGCCCAATTTGAGATGATGCTA-----AGAAAGCTTTATTTCTCAACTGC 892
Db 826 AGAGCCCTGCCCCATTTTATACTTGTGGAATGCTGCAGAGATCAAGAAAAATGATGAACA 885
QY 893 CAATGAGACTGTTTACATGCAATGCAATCTTATTCAGAGCGATTTCCACAGCTACACATATA 952
Db 886 GAATGATTTGCCATGAGGCTGCATAATCGAAATTCATCTAATCTTCTCTTCCATTA 945
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QY 1013 TTTCTTTGTGCAACCTAGCGAATCTAAATATTCAGACATATGACAAAGATTTATGTTGCA 1072
Db 1006 GTCTTGTTAAGGAAA--TAACTTAACAGAGAAACCTGTAAGTTCAATGTCAGGG 1063
QY 1073 CAGGATATCTACATGAGAGAAACCTTATGTA---CAATGTGAACACTCAAGAGATAC 1129
Db 1064 CTGGCTTTTCTATGTAAGTCTGAGCTCTGTGTAAACCAATCGTAAGCTCAGAGGTATAG 1123
QY 1130 CTGTTCACATCCAGGTGAGATGAATGCTGAATATATATATATATCTCTGATCTTC 1189
Db 1124 GAAAAAATGATATATTTGGAATGAACACTGGAATTTGATATATTTGTGACTTAC 1183
QY 1190 CTCGTGCTGCTGACTTTGCTTCCATTT-----GCTCTGTATAAGCCGAAAGGCTGC 1244

Db 1184 CAAGATGAGCTCGATTAATGTTTGTGTTATGCAAGTTTGATTAAGTAAACGAAAGA 1243
QY 1245 TAAAGAGGACACTGTCAT-----TGCAATGGGAAATATTAACCTGTG 1291
Db 1244 AATCAAGAAACATATTAATCCCTTAAATATCAACATCAAGAAAGCTGAAAAAGTCC 1303
QY 1292 ATTACACAGACACTAGTATCTGGAATAATGCTTTGATATCTTGGCAGTACCTCATG 1351
Db 1304 ATTATCTGTAGCGTGGGTAATATAGATGTTTTGACTTTAAAGACAAATTTGAACCTG 1363
QY 1352 GATTAGAAATTTGCTGAACCCATTTGGTGTACTGATCAATCCAAATTAAGAACTC 1411
Db 1364 GAGACATATATTAACAGAGCTGTGCTTCAATTTCCGATGAACCTCGAAGAAATGTTGAATC 1423
QY 1412 CATGCTAGAGTTGAGATTTGACTGTGTCAGAGGTGTAAAGTTCCAGATATGTACG 1471
Db 1424 CAATGGAACTGTTCAAACAAATCCATATCTGAAATGCAACAGCTTTGACGTTAAAT 1483
QY 1472 TGATTAAGAGCATCCCAATTTGCTGTATCCCGAAGACAGATTTAGCTATTTCCACG 1531
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QY 1532 CAGACTAGTACAGACTAGCTAGAGCAATGAATTAAGGAAAAATGACAAAGACAGC 1591
Db 1544 CAGCTGAGATTGCAAGCAGTATAGTCTAATGTGTCAAGTCAAGTGGAAAAAGTTTC 1603
QY 1592 -----TCAACCAATTTCTACAGAGATCCCTCTCTGAAATCACTAGACAGAGA 1642
Db 1604 TTCTGTATTTGAATAAAATCTTGAACAGGATCCCTGTCTCACTGTGTGAAAAATGAAA 1663
QY 1643 AAGATTTCTATGAGAGTACAGAC--ACTATGTGTACTATCCCGAAATTTCAACCA 1699
Db 1664 TGTACTTATTTGGACTTTGGCAGACAGACTGCCGAGAAATTTCCACATCACTGCCAA 1723
QY 1700 AATGCTTCTGTCTGTAAATGGAATTTAGAGATGAAGTACCCAGATGATATGCTTGG 1759
Db 1724 AATTACTGCTGCATCAAGTGAATTAACCTGAGAGTGTGTGCTGAGCTTCAGGCGCTGC 1783
QY 1760 TAAAGATTTGCCCTCCATCAAACTGAAACAGGCTATGGAATCTTGAAGCTTAATTAC 1819
Db 1784 TTCAATTTTGGCTTAACCTGCCCCCGGAGGCCCCGTAGACTTCTGAAATTTCAACTATC 1843
QY 1820 CAGATCTATGATTTGAGAGTGTGCTGTGCTGTGGAATAATTTAACAATGAGACA 1879
Db 1844 CAGACAGTACGTTGGAATAATGTCTGTAGCTGTCTG---CGACAGATGAGTGTAGAAG 1900
QY 1901 AACTTCTCAATATCTTTTCAACTGTGCAAGTGTAAATATAGAGCTTTCTTGAAT 1960
Db 1940 ACTTCTGTGAGATTTTATCTGAAGAAAGCATGATCAATCAAAAGATTTGGGCACTTT 1999
QY 1961 GTGCCCTCTTAATCTTATTAAGAAAGCACTGTGTAATCGAGATAGGCGATTC 2020
Db 2000 TCTTTTGCATTTAAATCTGAGATGACAAATTAAGCAAGTGTAGCCAGAGTTTGGCTGC 2059
Db 2021 TATTTTGCATTTTATGTCAGAAATGTCATTTCTGCTGTCTCAATACAAATTTGTGTCA 2080
QY 2060 TTTTGAAGTCTATTTGCTGTCATGTGGAATGTAATTTGACACCTGTAATAGCAAGTGC 2119
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QY 2120 AGGCAATGAAAAAGCTCATTAATTAATCTGATCTCAACAGAGAGAGAAAGATGAAA 2179
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QY 2180 CACAAAGATCAGATGAAGTTTATGTTAGTGAAGCAATAGGAGCAACATTTGATGATG 2239
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QY 2240 CCTTACAGGCTTGTCTCTCTTAAACCTGTCTATCAACTAGAAACCTCAGGCTTA 2299

QY 298 AAAGTAATTGAACCACTAGGCAACCGTGAGAAAAAGATCTCATGCAAAATTTGGTTT 357
DB 328 AAATTAGTGAACAAGATGTGTGACCCAGGGGAAAA---ATTAGACTCAAAAATTTGGAGTC 384
QY 358 GCTATCGGCATGCCAGTGTGGGAATTTGATANGTTAAAGATCCGAGTCAAGACTTC 417
DB 385 CTATAGAAAAAGCTCTGCATGAATTTGATCTTGAAAGATCTGGAAGTAATTAATTT 444
QY 418 CGAAGAAATATTTCTTAATGTTTGTAAAGAGCTGTGATCTTACGATCTTAATTCACCT 477
DB 445 CGAAGAAAAATGCGCAATTCAGCGA-----GGAAAAATCTGTGCA 486
QY 478 CATAGTAGACAATGTATGTCTATCCGCCACATGTAGAAATCTTACCAAGCTGCCAAG 537
DB 487 CTGTGGGATTTGTCTTGATGTGACTGGCTAAAAACAACATATCCACGAGCATGAACCA 546
QY 538 CACATATTAATTAATTTGGATAGAGCCAAATTAATAGTGTGATTTGGGTAAATTTCT 597
DB 547 TCCATCCCTGAAAACTTAGAAGATAACTTTATGGGGAAAGCTCATGTAGCTGTTCAT 606
QY 598 CCAAAATATGACAAGACAGAAAGTATCTGTGAAAAATCAACCATGACTGTGTGCCAGAAC 657
DB 607 TTGAAAATCTGCCAGAGAGCTGTTTAGCTTCAAGTGTCTCTTAATATGAAATCTATCAA 666
QY 658 GTAATGTGTAAGCAATGAGAAAAAACTAGAAAGTATGTGTCTATCATCTGAACAAATTA 717
DB 667 GTAATGAAATGGCAATC---CAAAAAGCTTTGATTAATTCATGGAAGAAAGATGACGTT 723
QY 718 AAATCTGTGTGTTTGAATATCAAGGGCAAGTACATTTTAAAAAGTGTGTGTATGAA 777
DB 724 AGCCCCATGAT-----TATGTGTGCAAGTCAAGGGGAGAGATAGAA 765
QY 778 TACTCTCAGAAAAAATCTCTGTGAGTATAGTATATTAAGAAAGCTGATAATGCTT 837
DB 766 TATGTTTTTGGTATCATCCACTAATTAAGTTCCAGTATATCCGAACTGTGTATGAAAC 825
QY 838 GGGAGAGTCCCAATTTGAAAGATGTGCTA-----AAGAAAGCCTTAATTTCTCACTGC 892
DB 826 AGAGCCCTGCCCATTTTATACTGTGGAAATGCTGCAGATCAAGAAATATGATGAACA 885
QY 893 CAATGAGACTGTTTACATATGCCATTTATTCAGACGCAATTTCCACAGCTACACATATA 952
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DB 1006 GTCTTGTTTAAAGGAAA---TAACTTACACAGAGAAACTGTAAAGTTCAATGCAAGG 1063
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DB 1064 CTGGCTTTTTCATGTAAGTCTGCTGTGTAAAAACATCGTAAGCTCAGAGTATCAG 1123
QY 1130 CTGTTCCAATCCCAAGTGAATGAATGCGTAATTAATGATATATACATCTCTGATCTTC 1189
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DB 1484 TTCAGAAATTAATAAAAAACAACCTTATTAATACCTCCCTTGATATAGTTATGAAAAAG 1543
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QY 1592 -----TCAAGCAATTTCTACAGAGATCTCTCTGGAATCTCAGACAGAGGA 1642
DB 1604 TTCCGTATTTGAAAAAATCTTGACAGAGGATCCCTGTCTCAACTGTGTAAAAATGAAA 1663
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QY 1760 TAAAGATTTGGCTTCCAAATCAAACTGAAACAGGCTATGGAATTTCTGACATGTAATTC 1819
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DB 1844 CAGACCAATAGCTTCGAAGATATGTGTAGGCTGCTG---CGACATAGATGATGAAG 1900
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DB 1901 AACTTCTCAATATCTTTTACATCGTGCAGAGTTAAATATAGAGCTTTCTGTGAT 1960
QY 1940 ACTGTCTTGAGATTTTATCTGAAGAAAGATGACATATCAAGAGATTTGGCACTTT 1999
DB 1961 GTGCCCTCTCTAGATTTCTTATAGAAAGACATTTGTAACTGGAGATGAGGAGTTTC 2020
QY 2000 TCTTTGGCATTTAAATCTGAGATGACAAATTAACAGTAGCAGAGGTTTGGCCCTGC 2059
DB 2021 TATTTTGGCATTTAGTCAAGATGACATTTCTGTCTGTCTGATACAAATTTGCTGCA 2080
QY 2060 TTTTGAATCTTATTTGTGTCATGTGGATGTAATTTGACACCTGATAGGCAAGTCG 2119
DB 2081 TCTTTGAAGCATATGCGCGGGAAGTGTGGGCAATGAAGTCTTTCTAAGCAGGTG 2140
QY 2120 AAGCAATGAAAAAGCTATTAATTAATCTGACATTTCTCAACAGAGAGAAAGATGAAA 2179
DB 2141 AAGCACTCAATTAATTAATAAATTTAAATAGTTTAACTCAAACTAAATGCCGTGAAGTTAA 2200
QY 2180 CAAAAAGGTACAGATGAAGTTTATGTTGACAAATGAGGCGACCAATTTCAATGATG 2239
DB 2201 ACAGAGCCAAAGGAAGAGGCGCATGCAATCTGTTTAAACAGAGTCTTAACGGGAAG 2260
QY 2240 CCTTACAGGGCTGTCTGTCTCTTAAACCTGTCTCATCACTAGAAACCTCAGGCTTA 2299
DB 2261 CCTCTCTGACCTGACGATCACCCCTGAACCAATGTATATCTCTCAGAACTCTATGTTG 2320
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DB 2381 TATTTGTGAGAGATTCAGT-----TGAAGTATTTTAAATAATGATATGAT 2428
QY 2420 TACGGCAGATATCTAACACTTCAAAATTAATGCTATTAAGAAAAATATCTGGCAAAATC 2479

Db	2429	AACGACAGGATATGTGACACTCCAAATGTTGCGCTGTATGATTTACTGTGAAAAG	2489
Qy	2480	AAGGCTTGATTTTGGAACTGTTACTTTATGTTGTCTGTCAAATCGGTGACTGTGGAC	2533
Db	2489	CTGGTTTGGAATCTTTGGATGTTGCTTATGTGCTGTTTAGCAACAGAGATCGCTCTGGCC	2548
Qy	2540	TTATTTAGAGTGGTGGAAATTCACACTATATATGCAATTCGAATTCAGTGCMAAGCGGCGC	2596
Db	2549	TCATTGAAGTTGTGACACTCTTGAAACAAATTTGCTGACCTTCAGCTGAACTAGCAATG	2608
Qy	2597	TGAAAGTGACTGCACTTCAACACGCCACACTACATCAGTGGCTCAAGACAGAAACA	2656
Db	2609	TGGCTGTGACAGCAGCTTTCAACAAAGATGCGCTTCTGAACTGGCTTTAAAGATACAACT	2668
Qy	2657	AAGGAGAAATATATATGACAGCCATTGACCTGTTTACAGCTTCATGTGCTGTATCTGTG	2718
Db	2669	CTGGGGATGACCTGACCGAGCCATTGAGGAATTTACACTGTCCTGTGCTGGCTACTGTG	2728
Qy	2717	TAGCTACCTTCATTTTGGGAATTTGAGATTCGCACAAATAGTAACATCATGTGTGAAGACG	2778
Db	2729	TAGCTTTTATGTCCTTTGGATTTGGTGTGACAGCATATGACAACTATGTGCAAAAAA	2788
Qy	2777	ATGCACACTGTTTCATATAGATTTTGGACCTTTTGGATTCACAAAGAAAAATTTG	2838
Db	2789	CTGGCAGACTCTTCACATTTGACTTTGACATATTTCTTGAATTTCAAATCTAGTTTG	2848
Qy	2837	GTTATTAACGAGAACGTGTGCCATTTGTTTGACACAGGATTTCTTAATAGTATTAAGA	2898
Db	2849	GCATTTAAAGGAGCGAGTGCCTTTTATTTCTTACTATGATTTATTCATGTCATTTCAAC	2908
Qy	2897	AAGGAGCCCAAGATGCAACAAAGAAAGAAATTTGAAGGTTTGAGAGATGTGTCA	2956
Db	2909	AAGGAAAAACAGG-----AAATACAGAAAGTTTGGCCGGTCCGCCAGTGTGTGAGG	2962
Qy	2957	AGGCTTATCTAGCTATTTGACAGCATGCGCAATCTCTCATTAATCTTTCTCAATGATGC	3016
Db	2963	ATGCTATCTGATTTTACAGCGGCAATGGAAATCTTTATCACTCTTTTGCGCTGATGT	3022
Qy	3017	TTGGCTCTGGAATGCGACAACTACATCTTTTGATGACATTTGCATACATTTGAAAGACC	3076
Db	3023	TGACTGCAAGGGCTTCTGAACTCAATCAGTCGAAATATACAGTATCTTAAGGACTCTC	3082
Qy	3077	TAGCTTTGATTAACCTGACCAAGGCTTTGGAGTATTTCAATGAACAAATGAATGATG	3136
Db	3083	TTGCACTTTGGGAAAGATGAGAGACAGCACTCAACAGATTTAAGCAAAAAATTTGATGAGG	3142
Qy	3137	CACATCAATGTGGCTGCAACAAACAAATGATGTGATCTTCCACACCAATT	3186
Db	3143	CGCTCAGGAAAGCTGAGACTACTAAATGTAACTGTATGGCCGACACAGATT	3192
RESULT 9			
AAS14366			
ID	AAS14366 standard; cDNA, 3213 BP.		
XX	AAS14366;		
XX	12-MAR-2002 (first entry)		
XX	cDNA encoding human p110beta isoform of PI3-kinase.		
XX	Human; phosphatidylinositol 3-kinase; PI3K; p110beta isoform;		
KW	LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;		
KW	autoimmune disease; inflammatory bowel disease; bacterial pneumonia;		
KW	Type 1 diabetes mellitus; cytostatic; immunosuppressive; ss.		
XX	Homo sapiens.		
XX	OS		
XX	FH		
XX	FT		
XX	CDS		
XX	Key location/Qualifiers		
XX	1..3213		
XX	/*tag= a		
XX	/product= "p110beta isoform of PI3-kinase"		

Query Match	13.5%	Score 460.8	DB 24	Length 3213
Best Local Similarity	50.4%	Pred. No. 1.8e-110		
Matches 1597	Conservative	0	Mismatches 1467	Indels 106
			Gaps	15
58	ATCTTAGTGGAAATGTTTACTTACTACCAATGGAATGATAGTACTTTTGAATGCTCTCGGTGAG	117		
88	ATACCTGTGGATTTCTTTTGGCCCACTGGGATTTATATATCCAGTTGGAGTACTCTCGGGGA	147		
118	GCTACATTAGTAACATATTAAGCATGACTATTTTAAAGAGCAAGAAATATACCTCTCAT	177		
148	GCTACCATTTCTTATATTTAGCAAGATGTATGGAAGCAAGTTCCACATTTACCAATGTTTC	207		
178	CAACTTCTTCAAGATGATCTTCTTACATTTTCGTAAGTGTATCCCAAGAGCAGAAAGG	237		
208	AACCTCCGTATGATATGACTCCGTATATGTTGGATGTGGAATCAACATCGTGTATAT	267		
238	GAAAGATTTTTTGTATGAAACAGACGACTTTGTGATCTTCGGCTTTTCAACCATTTTAA	297		
268	GAGAGAGCTTGAAAGTGAACACGAAAGACTCTGTATGTACACACCTTTTCTTCCAGTTCTC	327		
298	AAAGTATTTGACACAGTAGAGCAACCGTGAAGAAAGATCCCATTCGAGAAATGGTTT	357		
328	AAATTAGTGACAGAGAGTTGTGACCCAGGGGAAAA--ATTAGACTCAAAAATTTGAGTCC	384		
358	GCTATCGGCATGACAGTGTGCGCAATTTGATATGTTAAAGATTCGTAAGTACAGAGCTTC	417		
385	CTTATAGGAAAAGGTCTGCATGATTTGATTTCTTGAAGATCTCGAAGTAAATGATATTT	444		
418	CGAAGAAATATCTTAAATGTTTGAAGAGCTGTGATCTTAAGGATCTTAATTCACCT	477		
445	CGAAGAAAATGCGCAATTTACAGCA--GGAAGAAATCTGTCA	486		

QY 478 CATAGTAGCATGTATGTCTATCCGCACTGTGAATCTTCAACCGAGCTGCGCAAG 537
Db 487 CTGTGGGATTTGCTCTGGATGAGCTGGCTMAAACCAATATCCACAGAGCATGAACCA 546
QY 538 CACATATATATTAATTTGGATAGAGCCCAATATATGTGTGATTTGGTATATGTTCT 597
Db 547 TCCATCCCTGAAAACCTTAGAAGATTAATCTTATGGGGGAAGACTATCTTACTCTGTCAAT 606
QY 598 CCAATTAATGACAGACAGAGATATCTGAAAATCAACCATGACTGTGTGCGAGAACCA 657
Db 607 TTTGAAAATGCGCAGAGAGCTGTTTAGCTTCAAGTGTCTCTTAATATGAATCTTATCAAA 666
QY 658 GTAATTGCTGAAGCAATCAGAAAAAACTAGAGATGTGCTATCATCTGACAAATTA 717
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Db 724 AGCCCTATGAT-----TATGTGTGCAAGTCAAGCGGAGAGTGA 765
QY 778 TACTTCTAGAAAAATATCTCTGAGTCAGTATAGATATTAAGAAGCTGTATATGCTT 837
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QY 1073 CAGGATCTACCATGAGAGAAACCTTATGTGA--CAATGTGAACACTCAAGAGATAC 1129
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QY 1190 CTCTGTGCTGCACTTGTGCTTTCATTT-----GCTCTGTTAAAGCCGAAAGGCTGC 1244
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QY 1245 TAAAGAGAACACTGTCAAT-----TGGCATGGGGAATATAAATTGTTTG 1291
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Db 1304 ATATATCTGTAGCGTGGGTAATACAGTGTGTTTGACTTTAAAGAACATTTGAGAAC 1363
QY 1352 GATTAGAAATTTGCTGAACCTATTTGGTGTACTGATCAAAATCAATAAAGAAATC 1411
Db 1364 GAGATATATATTAACAGAGCTGTCTTCAATTTCTGATGAATCTCAAGAAATGTTGAATC 1423
QY 1412 CATGCTTGAAGTTGAAGTTTGAAGTTCAGAGTGTGTAAAGTTCCAGATATGTGAG 1471
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QY 1643 AAGATTTCTATGAGAGTCAACAGAC---ACTATGTGTACTATCTCCGCAAAATTCACCA 1699
Db 1664 TGGATCTTATTTGACCTTTGGGACAAAGCTGCGAGAAATTTTCCCAATATCAGTCCAA 1723
QY 1700 AATGCTTCTGTCTGTAAATGGAATTTCTAAGATGAAGTGAAGCCCAATGATATGCTTG 1759
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QY 1760 TAAAGATTTGGCTTCAATCAAACTGAAACAGGCTATGGAATTTCTGACGTAAATTAC 1819
Db 1784 TTCAATTTGGCTTAAACTGCCCCCGGAGGCCCTAGAGCTTCTGGAATTTCAACTATC 1843
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Db 1901 AACTTCTCAATATCTTTTACAACTGTGCAAGTGTAAATTAATGAGCCTTTCTTGAT 1960
QY 1940 ACTGCTGTGAGATTTTACTGAAGAAAGCATGATGATTAATCAAAAGATTTGGGCACTTT 1999
Db 1961 GTGCCCTCTAGATTCCTATTAAGAAAGACATTTGATTCGGAGATGAGGCGATTTC 2020
QY 2000 TCTTTGGCATTTTAAATCTGAGATGACATTAATAACAGTAAAGCAGAGTTTGGCTGC 2059
Db 2021 TATTTTGGCATTTTATGATGACAAAGTGCATTTCTGCTGTCTCAGTAAATTTGTGTCA 2080
QY 2060 TTTTGGACTCTATTTGTCGATGTGGAGTATTTGAAGCACCTGATAGGCAAGTGC 2119
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QY 2120 AGCAATGAAAAGCTCATTTAATTAATGATGATTTCTCAAAACAGACAGAAAGATGAAA 2179
Db 2141 AAGCACTCAATTAATGTTAAACCTTTAATTAATCAATCAATGACCTGGAAGTTAA 2200
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Db 2201 ACAGAGCAAGGAGAGAGGCAATGATCTGTTTAAACAGAGTCTTAACGGGAG 2260
QY 2240 CCTTACAGAGGCTGTCTCTCTTAAACCTGTCTCATCACTAGAAACCTCAGGCTTA 2299
Db 2261 CCTCTCTGACCTGAGTCAACCCCTGAAGCCATGTGTTATCTCTCAGAACTTATGTTG 2320
QY 2300 AAGAGTGTGAATTAATGTTCTTCTCAAAAAGGCACTGTGTGAATTTGGAGAACCCAG 2359
Db 2321 AAAAGTGAATAATGATGATTCAAAATGAAGCCTTTGTGCTGTATACATTAACAAG 2380
QY 2360 ACATCATGCTGAGTACTGTTTCAAGAAATGAGATCATCTTTAAATAATGGGATGAT 2419
Db 2381 TATTTGTGAGATTCAGT-----TGAAGTATTTTAAATATGATATGAT 2428
QY 2420 TACGCAAGATATGCTAACAATTAATTCATATATGAAATATCTGGCAAAATC 2479
Db 2429 TACGACAGGATATTTGACACTCCAAATGTTGCCCTGATGATTTACTCTGGAAGAAG 2488
QY 2480 AAGCTTGAATCTTGAATGTTTACTTATGTTGTCTGTCAATGCTGATCTGTGTGAC 2539
Db 2489 CTGTTTGGATCTTGGATGTTGCTTATGCTGTTTGAAGCAACAGAGATGCTGTGCC 2548
QY 2540 TTAATGAGGTGGGGAATCTCACAATATTAAGCAAAATTTCAATGCAAGAGGCGC---T 2596
Db 2549 TCATTTGAAGTGTGAGACCTCTGAACAATGTCTGACATTTCACTGAACGATGCAATG 2608
QY 2597 TGAAGGTGCACTGCTCAAGTTCACAGCACACACTATCATCATGTGCTCAAAAGCAAGA 2656

Db 2609 TGGCTGCTCAGACAGCCCTTCAACAAAGATGCCCTTGTGAATGGCTTAAAGATACAACT 2668
Oy 2657 AAGAGAAATATATATGATGAGCCATTGACCTGTTTACAGCTTATGCTGATGATG 2716
Db 2669 CTGGGATATACCTGGACCGACGATTTAGAAATTTACATCTGCTGCTGCTGCTG 2728
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Oy 3137 CACATCATGTGCTGCGACAAACAAATGATTTGATCTTCCACACAAAT 3186
Db 3143 CCGCTAGGGAAGCTGACTACTAAAGTAACTGATGAGCCACACAGTT 3192

RESULT 10
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ID AAL37431 standard, DNA; 4074 BP.
XX
AC AAL37431;
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3796.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01338.
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PR 31-JAN-2000; 2000US-0179065.
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PR 20-OCT-2000; 2000US-0241221.

KM gastrointestinal disorder; Crohn's disease; duodenal ulcer. ds.
XX Homo sapiens.
OS
XX
PN WO200155206-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01353.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.


```
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM,
XX WPI: 2001-45717/49.
XX
XX Isolated pancreatic cancer polypeptide for treating, preventing and/ or
PT prognosing disorders related to the pancreas including pancreatic
PT cancers and also for testing and detection e.g. diagnosis -
PS Disclosure: SEQ ID NO 608; 537pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an amino
CC acid sequence at least 90% identical to 188 amino acid sequences fully
CC defined in the specification and encoded by 188 cDNA clones fully
CC defined in the specification. The invention also relates to a fragment
CC having biological activity, a domain, an epitope, full length protein,
CC variant, allelic variant or a species homologue of the fully defined
CC sequence. The polynucleotide and polypeptide are useful for treating,
CC preventing and/or prognosing disorders related to the pancreas including
CC pancreatic cancer, pancreatitis, diabetes, endocrine disorders such as
CC acromegaly or hyperthyroidism, and gastrointestinal disorders such as
CC Crohn's disease and duodenal ulcers. The present sequence encodes a
CC pancreatic cancer-related polypeptide of the invention.
XX
XX Sequence 4074 BP; 1382 A; 640 C; 647 G; 1405 T; 0 other;
SQ
Query Match 13.2%; Score 452; DB 22; Length 4074;
Beet Local Similarity 98.6%; Pred. No. 4.1e-108;
Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
QY 2931 TGAGAGGTTTCAGAGATGTTTACAGGCTTATCTAGCTATTTCAGACATGCCATCT 2990
DB 659 TTATAGTTTCAGAGATGTTTACAGGCTTATCTAGCTATTTCAGACATGCCATCT 718
QY 2991 CTTCATTAATCTTTTCTCATATATGCTGGCTCTGGATGCCAGAACTTAACTTTTGA 3050
DB 719 CTTCATTAATCTTTTCTCATATATGCTGGCTCTGGATGCCAGAACTTAACTTTTGA 778
QY 3051 TGACATTCGATCATCTGGAAGACCTTACCTTAGTAAATTCGACAGAGCTTTTGA 3110
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QY 3111 GATTTTCATGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3170
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QY 3171 GATTTTCATGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3229
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QY 3230 CTCATCTCGACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 3289
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QY 3290 AGGAATTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 3348
DB 1019 AGGAATTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1078
QY 3349 ATATATATTAAATTAATGTAAGCAAGGATGATGATGATGATGATGATGATGATG 3408
DB 1079 ATATATATTAAATTAATGTAAGCAAGGATGATGATGATGATGATGATGATGATG 1138
QY 3409 AAAA 3412
DB 1139 AAAA 1142
RESULT 12
ABA07290
ID ABA07290 standard; DNA; 4074 BP.
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AC ABA07290;
XX
XX 14-JAN-2002 (first entry)
XX
XX Human pancreatic cancer related genomic DNA, SEQ ID NO: 609.
DE
XX
XX Human: cytostatic; antidiabetic; antiinflammatory; gastric; osteopathic;
KW antihormone; antitumor; thyroid-active; gene therapy; antisense therapy;
KW pancreatic cancer antigen inhibitor; pancreatic cancer; pancreatitis;
KW diabetes; endocrine disorder; acromegaly; hyperthyroidism;
XX gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200155206-A1.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01353.
PF
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XX 31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249249.
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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251030.

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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM,
XX WPI, 2001-45717/49.
XX
XX Isolated pancreatic cancer polypeptide for treating, preventing and/or
PT prognosing disorders related to the pancreas including pancreatic
PT cancers and also for testing and detection e.g. diagnosis -
XX
XX Disclosure; SEQ ID NO 609; 537pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an amino
CC acid sequence at least 90% identical to 188 amino acid sequences fully
CC defined in the specification and encoded by 188 cDNA clones fully
CC defined in the specification. The invention also relates to a fragment
CC having biological activity, a domain, an epitope, full length protein,
CC variant, allelic variant or a species homologue of the fully defined
CC sequence. The polynucleotide and polypeptide are useful for treating,
CC preventing and/or prognosing disorders related to the pancreas including
CC pancreatic cancer, pancreatitis, diabetes, endocrine disorders such as
CC acromegaly or hyperthyroidism, and gastrointestinal disorders such as
CC Crohn's disease and duodenal ulcers. The present sequence encodes a
CC pancreatic cancer-related polypeptide of the invention.
XX
XX Sequence 4074 BP, 1382 A, 641 C, 645 G, 1405 T, 1 other;
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DB 1138 AAAA 1141
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DT 05-NOV-2001 (first entry)
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DB Human digestive system antigen sequence SEQ ID NO: 3510.
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KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN MO200155314-A2.
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PD 02-AUG-2001.
XX
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 Db 1138 AAAA 1141
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 ID ABX60419 standard; cDNA; 4074 BP.
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 AC ABX60419;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE cDNA encoding novel human musculoskeletal system antigen #2763.
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 KW Gene; 66; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height;
 KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biorythm; cardiac rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.
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 OS Homo sapiens.
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 PN US2002147140-A1.
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 PR 08-DEC-2000; 2000US-251868P.
 PR 08-DEC-2000; 2000US-251869P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI: 2003-128199/12.
 XX
 PT Isolated nucleic acid molecules encoding musculoskeletal system
 associated polypeptides, useful for detecting disorders, e.g. cancer -
 XX
 PS Disclosure; SEQ ID NO 3796; 321pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule comprising a
 CC sequence encoding musculoskeletal system associated polypeptides useful
 CC for detecting disorders, e.g., cancer or cancer metastases, in animals
 CC or humans. The nucleic acid stimulates re-vascularisation of ischaemic
 CC tissues associated with conditions such as thrombosis, arteriosclerosis,
 CC and other cardiovascular conditions; treats wounds due to injuries,
 CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
 CC and limb regeneration; stimulates neuronal growth; can treat and prevent
 CC neuronal damage occurring in certain disorders or neurodegenerative
 CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
 CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
 CC used to enhance bone and periodontal regeneration and aid in tissue
 CC transports or bone grafts; prevents skin aging due to sunburn by
 CC stimulating keratinocyte growth; prevents hair loss, since FGF family
 CC members activate hair-forming cells and promotes melanocyte growth;
 CC stimulates growth and differentiation of hematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines; maintains
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues; induces tissue of mesodermal origin to differentiate in early
 CC embryos; increases or decreases the differentiation or proliferation of
 CC embryonic stem cells; besides, haematopoietic lineage, modulates
 CC mammalian characteristics, such as, body height, weight, hair colour, eye
 CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
 CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
 CC mammal's metal state or physical state by influencing biorythms;
 CC cardiac rhythms, depression, tendency for violence, tolerance for pain,
 CC reproductive capabilities, hormonal or endocrine levels, appetite,
 CC libido, memory, or stress; increases or decreases storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC or other nutritional components. This sequence encodes a novel human
 CC musculoskeletal system antigen.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.

XX Sequence 4074 BP; 1405 A; 645 C; 641 G; 1382 T; 1 other;

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Best Local Similarity 98.6%; Pred. No. 4,1e-108;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:09:02 ; Search time 8208.59 Seconds

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Minimum DB seq length: 0

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6	3407.2	99.9	3424	9	HSPH13K
7	3236.8	94.9	3240	6	AR048986
8	3236.8	94.9	3240	6	AR064287
9	3236.8	94.9	3240	6	AR164680
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11	3138.6	92.0	3498	6	A37232
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ALIGNMENTS

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VERSION AR048985.1 GI:6005024
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3412)
AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,
Otsu,M., Panayotou,G., Volinia,S. and Gout,I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5824492-A 32 20-OCT-1998;

Pred. No. is the number of results predicted by chance to have a

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 ORIGIN

Query Match 100.0% Score 3412; DB 6; Length 3412;
 Best Local Similarity 100.0%; Pred. No.0;
 Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 DEFINITION Sequence 32 from patent US 5946824.
 ACCESSION AR064286
 VERSION AR064286.1 GI:5993594
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unclassified.
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 Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
 Otsu, M., Panayotou, G., Volinia, S., and Gout, I.
 Polypeptides having kinase activity, their preparation and use
 Patent: US 5946824 A 32 08-DEC-1998;
 FEATURES
 source
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 Location/Qualifiers
 BASE COUNT 1129 a 616 c 706 g 961 t
 ORIGIN

Query Match 100.0%; Score 3412; DB 6; Length 3412;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Query Match	100.0%;	Score 3412;	DB 6;	Length 3412;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 3412;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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DB	1	ATGCTCCAGAACCATCATCATGAGTGAACCTGTGGGGCATCCCTTGATGCCCCCAAGATC	60		
QY	61	CTAGGGAAATTTTACTCTCCAAATGGAAATGATAGCATTTAGAAATGCTCCGAGAGCT	120		
DB	61	CTAGGGAAATTTTACTCTCCAAATGGAAATGATAGCATTTAGAAATGCTCCGAGAGCT	120		
QY	121	ACATTAGTACATATAAGCATGAATCTATTAAAGAGCAAAAAATACCTCTCCATCAA	180		
DB	121	ACATTAGTACATATAAGCATGAATCTATTAAAGAGCAAAAAATACCTCTCCATCAA	180		
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QY	241	GAATTTTGTGATGAACCAAGACGACTTTGTGATCTTGGCTTTTTCACCATTTTAAAA	300		
DB	241	GAATTTTGTGATGAACCAAGACGACTTTGTGATCTTGGCTTTTTCACCATTTTAAAA	300		
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DB	421	AGAAATATCTTTAATGTTTGTAAAGAGCTGTGATCTTTAGGATCTTAAATTCACCTCAT	480		
QY	481	AGTAGAGCAATGTATGTCTATCCGCAACATGTAGATCTTCCACAGAGCTGCGAAAGAC	540		
DB	481	AGTAGAGCAATGTATGTCTATCCGCAACATGTAGATCTTCCACAGAGCTGCGAAAGAC	540		
QY	541	ATATATAATAAATTTGATAGAGGCGCAATAATAGTGTGATTTGGGTAAATAGTTTCTCA	600		
DB	541	ATATATAATAAATTTGATAGAGGCGCAATAATAGTGTGATTTGGGTAAATAGTTTCTCA	600		
QY	601	AATAATGACAAAGCAAGTATCTCTGAAAAATCAAACATGACTGTGTCCAGAAACAACTA	660		
DB	601	AATAATGACAAAGCAAGTATCTCTGAAAAATCAAACATGACTGTGTCCAGAAACAACTA	660		
QY	661	ATTGCTGAGCAATCAGAAAAAAACCTGAAGTATGTGCTATCATCTGAACCAATTAAAA	720		
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QY	841	AGGATGCCCAATTTGAAAGATGATGGCTTAAAGAAAGCTTTATTTTCCACCTGCCAATGAGC	900		
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DB	901	TGTTTACAAATGCAATCTTATTTCCAGAGCAATTTTCCACAGCTACCACTATATGATGA	960		
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REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
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QY	721	CTGT	GTGTTTAGAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGATGAATAC	780
Db	733	CTGT	GTGTTTAGAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGATGAATAC	792
QY	781	TTCT	TAGAAAAATATCTCTGAGTCAGATTAAGTATATAAAGAGCTGATATAGTTGGG	840
Db	793	TTCT	TAGAAAAATATCTCTGAGTCAGATTAAGTATATAAAGAGCTGATATAGTTGGG	852
QY	841	AGGAT	GCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTATTTCTCAACTGCCAATGAC	900
Db	853	AGGAT	GCCCAATTTGAAGATGATGGCTAAAGAAAGCCTTATTTCTCAACTGCCAATGAC	912
QY	901	TGTTT	TACAATGCAATCTTATTTCCAGACGCAATTTCCACAGCTTACCACTATATGATGGA	960
Db	913	TGTTT	TACAATGCAATCTTATTTCCAGACGCAATTTCCACAGCTTACCACTATATGATGGA	972
QY	961	GAA	CACTTCAAAAATCCCTTTGGGTTATTAATAGAGACCTCAGAAATTAATTTCTTGT	1020
Db	973	GAA	CACTTCAAAAATCCCTTTGGGTTATTAATAGAGACCTCAGAAATTAATTTCTTGT	1032
QY	1021	GCA	ACTACGTGAATCTTAATATTTCSAGACATTTGACAAGATTTATGTTCCGAACAGGTATC	1080
Db	1033	GCA	ACTACGTGAATCTTAATATTTCSAGACATTTGACAAGATTTATGTTCCGAACAGGTATC	1092
QY	1081	TAC	ATGAGAGAACCCCTTATGTGACAAATGTGAACACTCAAAAGATACCTTGTTCAT	1140
Db	1093	TAC	ATGAGAGAGAACCCCTTATGTGACAAATGTGAACACTCAAAAGATACCTTGTTCAT	1152
QY	1141	CCG	AGGTGAGTGAATGAGCTGAATTAATGATATATACATCCCGATCTTCCCTCGTGTCT	1200
Db	1153	CCG	AGGTGAGTGAATGAGCTGAATTAATGATATATACATCTTCCCTCGTGTGTCT	1212
QY	1201	CGA	CTTGTCCCTTCCATTTGCTCTGTTAAAGCGCGAAAGGGTGTCTAAAGAGAACACTGT	1260
Db	1213	CGA	CTTGTCCCTTCCATTTGCTCTGTTAAAGCGCGAAAGGGTGTCTAAAGAGAACACTGT	1272
QY	1261	CCA	TTTGGCATGGGGAATATTAACCTTGTGTTATTAACAGACACTCTTAATCTTGGAAAA	1320
Db	1273	CCA	TTTGGCATGGGGAATATTAACCTTGTGTTATTAACAGACACTCTTAATCTTGGAAAA	1332

1321 ATGCGTTTGAACTTTGGCCAGTACTGATGTTAGAAATTTGCTGAACCTTATGGT 1380
1333 ATGGCTTTAACTTTGGCCAGTACTGATGTTAGAAATTTGCTGAACCTTATGGT 1392
1381 GTTACTGATCAAAATCCAAATAAAGAACTCCATGCTTAGAGTTGAGTTGACTGCTTC 1440
1393 GTTACTGATCAAAATCCAAATAAAGAACTCCATGCTTAGAGTTGAGTTGACTGCTTC 1452
1441 AGCAGTGTGTAAAGTTCCAGATATGTCAATGATTAAGAGCATGCCAATTTGCTGTA 1500
1453 AGCAGTGTGTAAAGTTCCAGATATGTCAATGATTAAGAGCATGCCAATTTGCTGTA 1512
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1513 TCCCGGAAGCAGGATTTAGCTATTTCCAGCAGGACTGATTAACGACTAGCTTAAGAC 1572
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1573 AATGAATTAAGGAAATGACAAAGAAAGCTCAAGCAATTTCTACGAGATCTCTC 1632
1621 TCTGAATCACTGAGCAGGAAAGATTTTCTATGAGTCAACAGACTATTTGCTACT 1680
1633 TCTGAATCACTGAGCAGGAAAGATTTTCTATGAGTCAACAGACTATTTGCTACT 1692
1681 ATCCCGAAATTTCAACCAATTTGCTTCTGTCTTTAAATGCAATTTCTAGAGTGAAT 1740
1693 ATCCCGAAATTTCAACCAATTTGCTTCTGTCTTTAAATGCAATTTCTAGAGTGAAT 1752
1741 GCCCAGATGATTTGCTGTAAAGATTTGGCTCCAAATCAACCTGAACAGGCTATGGA 1800
1753 GCCCAGATGATTTGCTGTAAAGATTTGGCTCCAAATCAACCTGAACAGGCTATGGA 1812
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1861 AATATTTTACGATGACAACTTTCTGATATTTAATTCAGTACTGATCAAGTCTTAA 1920
1873 AATATTTTACGATGACAACTTTCTGATATTTAATTCAGTACTGATCAAGTCTTAA 1932
1921 TATGAACAATTTTGAATTAAGTCTGATGATTTTCTAGAGAAACATTTGACTAT 1980
1933 TATGAACAATTTTGAATTAAGTCTGATGATTTTCTAGAGAAACATTTGACTAT 1992
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1993 CAAGAGATTTGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGACAAATTAACAGT 2052
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2353 TTGAATTTGGGAACCCAGACATCATGTCAGAGTTACTGTTTCAAGAACATGATCATC 2412
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2413 TTTAAAAATGGGATGATTTTACGGCAAGATATGCTAACCTTCAAAATTAATTCGATTA 2472
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2533 ATCGGTGACTGTGTGGGACTTATTAAGTGTGTGGCAAAATTTCTACACTTAATGCAAA 2592
2581 CAGTCAAAAGGCGGCTTGAAGGTCACCTGCACTTCAACAGCCACACACTACATCAGTGG 2640
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2641 CTCAAAGCAAGAACAAAGGAGAAATATATGTCAGGCAATTAACCTGTTTACAGTTCA 2700
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2761 ATCATGTGGAAGACATGACAACTGTTTCAATATAGTTTGGACACTTTTGGATCA 2820
2773 ATCATGTGGAAGACATGACAACTGTTTCAATATAGTTTGGACACTTTTGGATCA 2832
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2833 AAGAGAAATTTGTTATTAACGAGAACGTGGCCATTTGTTTACAGAGATTTTC 2892
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2953 CAGGAGATGTGTTACAAAGCTTATTTAGCTATTTGACAGCATGCCAATCTTCTAAAT 3012
3001 CTTTCTCAATGATGCTTTGGCTGGAATGTCAGAACTGATCTTTGATGACATTTGCA 3060
3013 CTTTCTCAATGATGCTTTGGCTGGAATGTCAGAACTGATCTTTGATGACATTTGCA 3072
3061 TACATTCGAAAGACCTTACCTTATGATTAACCTGAGCAAGGCTTTGGAGTATTTCA 3120
3073 TACATTCGAAAGACCTTACCTTATGATTAACCTGAGCAAGGCTTTGGAGTATTTCA 3132
3121 AAACAAATGATGATGACATCATGTCGTCGTCGACAAACAAATTTGATGATCTTCCAC 3180
3133 AAACAAATGATGATGACATCATGTCGTCGTCGACAAACAAATTTGATGATCTTCCAC 3192
3181 ACAATTAACAGCATGCTTGAACGTAAGTAACGTAAGTAACGTAAGTAACGTAAGTA 3240
3193 ACAATTAACAGCATGCTTGAACGTAAGTAACGTAAGTAACGTAAGTAACGTAAGTA 3252
3241 CACTACCTGCACTGTTAATTAATCTCTCAGCAGGCAAGACCGATTTGATAGAAATTCGAC 3300
3253 TTCACACTGCACTGTTAATTAATCTCTCAGCAGGCAAGACCGATTTGATAGAAATTCGAC 3312
3301 AATCAGTAACAGCATTTGATTAACGTAAGTAACGTAAGTAACGTAAGTAATTTAA 3360
3313 AATCAGTAACAGCATTTGATTAACGTAAGTAACGTAAGTAACGTAAGTAATTTAA 3372
3361 TAAATGAAGCAAGCAAGGCTTATGATGACCTTAACTAGTTCAATTTCAAA 3412
3373 TAAATGAAGCAAGCAAGGCTTATGATGACCTTAACTAGTTCAATTTCAAA 3424

RESULT 6
HSPH13K 3424 bp mRNA linear PRI 24-AUG-1995
LOCUS
DEFINITION H.sapiens mRNA for phosphatidylinositol 3-kinase.
ACCESSION Z25090

QY 1321 ATGGCTTTGAATCTTTGGCCAGTACCTCATGATTTAGAAATTTGCTGAACCCCTATTGGT 1380
DB 1333 ATGGCTTTGAATCTTTGGCCAGTACCTCATGATTTAGAAATTTGCTGAACCCCTATTGGT 1392
QY 1381 GTTACTGATCAAAATCCAAATAAGAAATCCATTCCTTAGAGTTGAGTTGACTGTGTC 1440
DB 1393 GTTACTGATCAAAATCCAAATAAGAAATCCATTCCTTAGAGTTGAGTTGACTGTGTC 1452
QY 1441 AGCAGTGTGTAAAGTTCCAGATATGTGATGATTAAGAGCATGCCAATTTGGTCTGTA 1500
DB 1453 AGCAGTGTGTAAAGTTCCAGATATGTGATGATTAAGAGCATGCCAATTTGGTCTGTA 1512
QY 1501 TCCCGAAGACAGGATTTAGCTATTCCTCAGCAGACGTAGTAACAGACTAGTAGAGAC 1560
DB 1513 TCCCGAAGACAGGATTTAGCTATTCCTCAGCAGACGTAGTAACAGACTAGTAGAGAC 1572
QY 1561 AATGAATTAAGGAAATGACAAAGAACGCTCAAGCAATTTCTACAGAGTCCCTCTC 1620
DB 1573 AATGAATTAAGGAAATGACAAAGAACGCTCAAGCAATTTCTACAGAGTCCCTCTC 1632
QY 1621 TCTGAATCACTGACGAGAGAAAGATTTCTATGAGATCACAGACACTATTGTCTACT 1680
DB 1633 TCTGAATCACTGACGAGAGAAAGATTTCTATGAGATCACAGACACTATTGTCTACT 1692
QY 1681 ATCCCGAAATTTCTACCCAAATTTGCTCTGTCTGTTAAATGGAATCTAGAGTGAAGTA 1740
DB 1693 ATCCCGAAATTTCTACCCAAATTTGCTCTGTCTGTTAAATGGAATCTAGAGTGAAGTA 1752
QY 1741 GCCCAGATGTATGCTTTGGTAAAGATTTGGCCCTCCCAATCAAACTGAACAGGATATGGA 1800
DB 1753 GCCCAGATGTATGCTTTGGTAAAGATTTGGCCCTCCCAATCAAACTGAACAGGATATGGA 1812
QY 1801 CTCTGAGCTGTAAATTAACCAAGTCTTATGATGTGAGATTTGCTGTGCTGGCTGGAA 1860
DB 1813 CTCTGAGCTGTAAATTAACCAAGTCTTATGATGTGAGATTTGCTGTGCTGGCTGGAA 1872
QY 1861 AAATATTTAAACAGATGACAAACCTTTCTCAGTATTTAATTCAGCTAGTACAGGCTCTTAAA 1920
DB 1873 AAATATTTAAACAGATGACAAACCTTTCTCAGTATTTAATTCAGCTAGTACAGGCTCTTAAA 1932
QY 1921 TATGAACAATATTTGGATTAATCTGCTTGTGAGATTTTACTGAGAAAGACATTTGACTAAT 1980
DB 1933 TATGAACAATATTTGGATTAATCTGCTTGTGAGATTTTACTGAGAAAGACATTTGACTAAT 1992
QY 1981 CAAGGATTTGGGCACTTTTCTTTTGGGCAATTTAAATTCGAGATGACAAATAAAGAGTT 2040
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DB 2113 CACCTGATTAAGCAAGTGCAGGCAATGGAAGAGCTCATTAATTAATTAATTAATTAATTAAT 2172
QY 2161 CAGGAGAGGAGATGAACACAAAGATGACAGATGATGATTTTGTAGAGAAATGAGG 2220
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QY 2281 CTAGGAAACCTGAGCTTTAAAGAGTGTGAATTAATGTCTTCTGCAAAAAGCCACTGTGG 2340
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DB 2353 TTGAATTTGGGAGAACCCAGACATCATGTGAGATTTACGTTTCAAGAACTAGATCATC 2412

QY 2401 TTTAAATTTGGGAGATTTTACGCCAAGATATGCTTAACAATTAATTTGATATG 2460
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QY 2461 GAAATATCTGGCAAAATCAAGGCTGTGATCTTGCAGAGTTTCCCTATGCTGTCTCA 2520
DB 2473 GAAATATCTGGCAAAATCAAGGCTGTGATCTTGCAGAGTTTCCCTATGCTGTCTCA 2532
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QY 2581 CAGTGCAAAAGGCGCTTGAAGGTGACAGTCTGCAATCAAGCACAACACTACATCATGTGG 2640
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QY 2641 CTCAAAAGACAAAGACAAAGGAGAAATATATATGATGAGCATTAAGCTGTGTTACAGCTTCA 2700
DB 2653 CTCAAAAGACAAAGACAAAGGAGAAATATATATGATGAGCATTAAGCTGTGTTACAGCTTCA 2712
QY 2701 TGTGCTGATACGTGTAGTACTTCAATTTTGGGAAATTTGAGATGCTCACAAATAGTAAC 2760
DB 2713 TGTGCTGATACGTGTAGTACTTCAATTTTGGGAAATTTGAGATGCTCACAAATAGTAAC 2772
QY 2761 ATCATGTGAAAGACGATGAGACAACTGTTTCAATATAGATTTTGAACACTTTTGGATCAC 2820
DB 2773 ATCATGTGAAAGACGATGAGACAACTGTTTCAATATAGATTTTGGATCAC 2832
QY 2821 AAGAAGAAATTTGGTATTAATGAAGAGACGTGTGCCAATTTGTTGAACACAGATTTTC 2880
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QY 2881 TTAATATGATTTAGTAAGAGAGCCCAAGAAATGACAAAGACAAAGAAATTTGAGAGTTT 2940
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QY 3001 CTTTCTCAATGATGCTTGGCTGTGGAATGCGCAAACTCAATCTTTGATGACATTTGCA 3072
DB 3013 CTTTCTCAATGATGCTTGGCTGTGGAATGCGCAAACTCAATCTTTGATGACATTTGCA 3084
QY 3061 TACATTCGAAAGACCCCTAGCTTATGATTAATACTGACAGAGGCTTTGGAGATTTTCAAT 3120
DB 3073 TACATTCGAAAGACCCCTAGCTTATGATTAATACTGACAGAGGCTTTGGAGATTTTCAAT 3132
QY 3121 AAACAAATGATGATGACATCATGTGTGGCTGTGACAAACAAATTTGATGATCTTCAC 3180
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QY 3181 ACAATTTAAACAGCATGCTTGAATCTGAAGAAAGTAACTGAGAAATTAAGAGCTCACCTGGA 3240
DB 3193 ACAATTTAAACAGCATGCTTGAATCTGAAGAAAGTAACTGAGAAATTAAGAGCTCACCTGGA 3252
QY 3241 CACTACACTGCACTGTTATTAATCTGACAGGCGCAAAACCGAATGCAATGAGATTTGAC 3300
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QY 3301 AATCCATGAACAGATTAATGATTTTACAGCAAGAAAGAAATTAATTAATTAATTAAT 3360
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QY 3361 TAAATTAAGCAAGAGGCTTTGATGACACTTAAATTAATTAATTAATTAATTAAT 3412
DB 3373 TAAATTAAGCAAGAGGCTTTGATGACACTTAAATTAATTAATTAATTAATTAAT 3424

RESULT 7
AR048986 3240 bp DNA linear PAT 29-SEP-1999
LOCUS AR048986 3240 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 34 from patent US 5824492.

ACCESSION AR048986
VERSION AR048986.1 GI:6005025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3240)
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
Otsu, M., Panayotou, G., Volinia, S., and Gout, I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5824492-A 34 20-OCT-1998;
FEATURES
Source location/Qualifiers
1..3240 /organism="unknown"
BASE COUNT 1057 a 582 c 682 g 919 t
ORIGIN
Query Match 94.9%; Score 3236.8; DB 6; Length 3240;
Beech Local Similarity 99.9%; Pred. No. 0;
Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 ATGCTCCAGACCATCATCAGTGAAGTGAAGTGGGCGATCCACTTGATGCCCCCAAGATC 60
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DB 361 ATCCGCAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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DB 421 AGAATATTTCTTAATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 AGTAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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DB 1381 GTTACTGATCAATCCAAATTAAGAAATCTCATGCTTGAAGTGGAGTTGACTGGTTC 1440
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QY 1681 ATCCCGAAATTTCTACCAATGCTGCTGCTGTTAATGAAATTTCTAGAGATGATGATGATGATGAT 1740
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QY 1741 GCCAGAT 1800
DB 1741 GCCAGAT 1800
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QY 1861 AATATTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920

Db 421 AGAAATATCTTAAAGTTGTAAGAAAGCTGTAGATCTTAGGATCTTAATTCACCTCAT 480
Qy 481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGATCTTACACAGAGCTGCCAAGCAC 540
Db 481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGATCTTACACAGAGCTGCCAAGCAC 540
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 AUTHORS Stidivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledger, L.M.,
 Oliffe, A. and Heimbrook, D.C.
 TITLE Cloning and mutagenesis of the p110 alpha subunit of human
 phosphoinositide 3'-hydroxylase
 JOURNAL Bioorg. Med. Chem. 5 (1), 65-74 (1997)
 MEDLINE 97196568
 PUBMED 9043658
 REFERENCE 2 (bases 1 to 3207)
 AUTHORS Stidivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledger, L.M.,
 Oliffe, A. and Heimbrook, D.C.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-1996) Cancer Research, Merck Research Labs,
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BASE COUNT
ORIGIN

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Query Match

Best Local Similarity 92.0%; Score 3138.6; DB 6; Length 3498;
Matches 3262; Conservative 0; Mismatches 144; Indels 7; Gaps 3;

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 REFERENCE 1 (Bases 1 to 3207)
 Hiles, I.D., Otsu, M., Volinia, S., Fry, M.J., Gout, I., Dhan, R., Panayotou, G., Ruiz-Larrea, F., Thompson, A.S., Totty, N.F., Hsuan, J.J., Courtneidge, S.A., Parker, P.J. and Waterfield, M.D. Phosphatidylinositol 3-kinase: structure and expression of the 110 kD catalytic subunit
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BASE COUNT

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ORIGIN

Query Match

Best Local Similarity 96.1%; Pred. No. 0;
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88.2%; Score 3008.6; DB 4; Length 3207;

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 VERSION A75936.1 GI:6088141
 KEYWORDS
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 AUTHORS Hiles, I.D. and Fry, M.J.
 TITLES POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE
 JOURNAL LUDWIG INST CANCER RES (GB); HILES IAN D (B)
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ACCESSION AR048987
VERSION AR048987.1 GI:6005026
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3207)
AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,
Oteu,M., Panayotou,G., Volinia,S. and Gout,I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5824492-A 35 20-OCT-1998;
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Qy	2461	GAAATATCTGGCAAAATCAAGGTCCTTGAATCTTGAATGTTACCTTAATGATGTCGTCA	2520
Db	2461	GAAATATCTGGCAAAATCAAGGTCCTTGAATCTTGAATGTTACCTTAATGATGTCGTCA	2520
Qy	2521	ATCGGTGACTGTGGGACCTTATTGAAGTGTGTGGAATTTCTGACACTAATTAAGCAATT	2580
Db	2521	ATCGGTGACTGTGGGACCTTATTGAAGTGTGTGGAATTTCTGACACTAATTAAGCAATT	2580
Qy	2581	CAGTGCAGAAAGCGGCTTGAAGGTGCACTGCAAGTCAACAGCCACACACTACATCAGTGG	2640
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Qy	2641	CTCAAAAGCAAGAACAAAGAGAAATTAATGATGCAAGCCATTGACCTGTTTACAGCTTCA	2700
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Db	2701	TGTCTGGATTAATGTGTGCACTTCATTTTGGGAATGGAAGTGTCACAATAGTAAT	2760
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Db	2761	ATCATGGTGAAGATGACACTGTTTCATATGATTTTGGACACTTTTGGATCAC	2820

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Db	3001	CTTTTTCATGATGCTGTGGCTCTGGAAATGCGACAACTCAATCTTTTGATGATTAATTTGCA	3060
QY	3061	TACATTCGAAAGACCTTAGCCTTAGATTTAAACTGACGACAGAGGCTTTGAGATATTTTCATG	3120
Db	3061	TACATTCGAAAGACCTTAGCCTTAGATTTAAACTGACGACAGAGGCTTTGAGATATTTTCATG	3120
QY	3121	AAACAAATGAATGATGACATCATCATGTGTGCTGTGACAAACAAAATGATTTGATCTTCCAC	3180
Db	3121	AAACAAATGAATGATGACACCATGATGTGTGCTGTGACAAACAAAATGATTTGATCTTCCAC	3180
QY	3181	ACAAATTAACGCGATGCTTTGAACTGCA 3207	
Db	3181	ACAAATTAAGCGATGCTTTGAACTGCA 3207	

RESULT 15			
AR064288			
LOCUS	AR064288	3207 bp	DNA
DEFINITION	Sequence 35 from patent US 5846824.	linear	PAT 29-SEP-1999

ACCESSION	AR064288	
VERSION	AR064288.1	GI:5993596
KEYWORDS		
SOURCE	Unknown.	

ORGANISM	unknown.
	Unclassified.

REFERENCE	1 (bases 1 to 3207)
AUTHORS	Hiles, I. D., Fry, M. J.

TITLE Otsu, M., Panayoutou, G., Volinn, S. and Gout, I.
Polypeptides having kinase activity, their preparation and use

JOURNAL	Patent: US 5846824-A 35 08-DEC-1998;
FEATURES	Location/Qualifiers
SOURCE	1 3207

Source	1. .320 /	/organism="unknown"
BASE COUNT	1028 a	581 c 680 t

ORIGIN

Query Match	88.2%	Score 3008.6	DB 6	Length 3207
Best Local Similarity	96.1%	Pred. No. 0		
Matches 3083; Conservative	0	Mismatches 124	Indels 0	Gaps 0

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D5 1 ATGCTTCAAGACCATCATCAGGTGAAGTGGGGCATCCACTTATGCCCCAAGAATC

61 CTAGTGGAATGTTTACTTACCAATGGAGATGATAGTGACTTAGAATGCCTCCGTAGAGCT

61 CTAGTAGATGTTTACTACCAAGGGATGATAGTACTTAGATGCGCTCCGTGAGGCT

121 ACATTAGTAACTATAAGCATGAACTATTTAAAGAGCAAGAAATACCCCTCCATCAA

Db 121 ACGTTAATAACGATTAAGCATGAACATTATTAAAGACAGAAAAATACCCCTCTCCATCAAA

181 CTTCTCAAGATGATCTTCTACATTTTCCTAAGTGTACCCAGAAGCAGAAAGGAA

181 CTTCTTCAAGATGAATCTTCTACATTTTCGTAAGTGTATACCCAGAAGACGAAAGGGA

241 GAA TTT TTT TGA TGA A C A G A C G A C T T T G T G A C C T T C G G T T T T T T C A A C C C G T T T T A A A A A A
 241 GAA T T T T T G A T G A A C A G A C G A C T T G T G A C T C G G T T T T T C A A C C A T T T T A A A A A A

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Db	361	ATCGGCATGCCAGTGTGCGAATTTGTATATGTTAAAGATCCAGAAAGTACAGAGACTTCCGA	420
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Db	481	AGTAGAGCAATGATATGTCATTTCTCCCAATGTAGAGATTTTCAACGAACTGCCAAAGCAC	540
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 DB 933 TAAAGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
 QY 1305 TCTAGATCTGGAATAATGCTTGTGATCTTGTGCTGCTGCTGCTGCTGCTGCTG 1364
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 QY 1365 GCTGAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1424
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 DB 1113 GGAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1172
 QY 1485 TGGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1544
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 DB 2133 GATTAATGCTTATGGAATAATCTGCGCAAAATCAAGGCTTTGATCTGCAATGTTACC 2192
 QY 2505 TTATGATGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2564
 DB 2193 TTATGATGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2252
 QY 2565 CACTATATGCAATTCAGTGTAAAGAGCTGAAAGGTGCACTGCACTTTAAACAGCA 2624
 DB 2253 CACTATATGCAATTCAGTGTAAAGAGCTGAAAGGTGCACTGCACTTTAAACAGCA 2312
 QY 2625 CACTCTCCATGCTGCTCAAGACAAAGAAAGGCGCAATATATATGATGCGCCATCA 2684
 DB 2313 CACTCTCCATGCTGCTCAAGACAAAGAAAGGCGCAATATATATGATGCGCCATCA 2372
 QY 2685 TTTGTTTACAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2744
 DB 2373 CTTGTTTACAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2432
 QY 2745 TGTCAACAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2804
 DB 2433 CCGGCACAACAGATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2492
 QY 2805 AACATTTTGTATCAACAAGAAATTTGCTTAAAGCAAGCGCTGCTGCTGCTGCTGCTG 2864
 DB 2493 AACATTTTGTATCAACAAGAAATTTGCTTAAAGCAAGCGCTGCTGCTGCTGCTGCTG 2552
 QY 2865 TTTGACACAAGATTTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2924
 DB 2553 GTTGAACAAGATTTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2612
 QY 2925 AGAATTTGAGAGTTTCAAGAGATGTTCAAGGCTTATCTAGATTTGCGCAGCATG 2984
 DB 2613 AGAATTTGAGAGTTTCAAGAGATGTTCAAGGCTTATCTAGATTTGCGCAGCATG 2672
 QY 2985 CAATCTCTTCAATATCTTTTCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3044
 DB 2673 CAATCTCTTCAATATCTTTTCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2732
 QY 3045 TTTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3104
 DB 2733 TTTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2792
 QY 3105 TTTGAGATTTTCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3164
 DB 2793 TTTGAGATTTTCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2852
 QY 3165 GATTTGATTTTCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3207
 DB 2853 GATTTGATTTTCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2895

RESULT 2
 BQ228953 872 bp mRNA linear EST 02-MAY-2002
 LOCUS BQ228953
 DEFINITION AGENCY: 7572613 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6044713
 5', mRNA sequence.

QY 1478 AAGAGATGCAATTGGTCTGTATCCCGTAGAGAGATTTAGTATTCCTCCATGCAGAGC 1537
 DB 607 AAGAGATGCAATTGGTCTGTATCCCGTAGAGAGATTTAGTATTCCTCCATGCAGAGC 666
 QY 1538 TGAGTACAGACTAGCTAGAGACAATGAAATTAAGAGAAATGATTAAGAAAGACCTCCAG 1597
 DB 667 TGAGTACAGACTAGCTAGAGACAATGAAATTAAGAGAAATGATTAAGAAAGACCTCCAG 726
 QY 1598 CATTTGTACAGAGATCTCTATCTGAAA--TCACTAGACA-AGAGAAAGATTTCTGT 1654
 DB 727 CATTTGTACAGAGATCTCTCTGAAAATCACTAGAGAGAGAGAAAGATTTCTAT 786
 QY 1655 GG-AGCCACAGACACTATT 1672
 DB 787 GGAAGTCACAGACCTATT 805
 RESULT 5
 BX437220 834 bp mRNA linear EST 15-MAY-2003
 LOCUS BX437220 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YF10
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BX437220
 VERSION BX437220.1 GI:30781556
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE Li, W.B., Gruber, C., Jessup, J. and Polayes, D.
 AUTHORS Li, W.B., Gruber, C., Jessup, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1992.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0CAP005DC05Q1&cluster=1992.f. Contact :
 Peng Liang Email : fliang@life.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0CAP005DC05Q1.
 Location/Qualifiers
 FEATURES
 source 1..834
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP005YF10"
 /issue_type="THYMUS"
 /clone_id="Homo sapiens THYMUS"
 /note="Vector: PCWVS/PORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWVS/PORT 6 vector. Library was not normalized."
 BASE COUNT 256 a 152 c 184 g 241 t 1 others
 ORIGIN
 Query Match 20.9%; Score 671.4; DB 13; Length 834;
 Best Local Similarity 94.8%; Pired. No. 1.8e-150; Indels 0; Gaps 0;
 Matches 693; Conservative 1; Mismatches 37;
 QY 1742 CTCAGATGATCTCTGTTAAAGATGGCTCCCAATCAAGCTGAACAGGCTATGAGC 1801
 DB 104 CACAGAGATGATCTCTGTTAAAGATGGCTCCCAATCAAGCTGAACAGGCTATGAGC 163
 QY 1802 TTCGAGCTCAATTAACCAAGATCTATGTTGTCAGAGTTTGTCTGTTGGTCTAGAAA 1861
 DB 164 TTCGAGCTCAATTAACCAAGATCTATGTTGTCAGAGTTTGTCTGTTGGTCTAGAAA 223

QY 1862 AATATTTAAGATGACAAACTTTCTCAGTACTTAATCAGTACTAGAGTACTAAAT 1921
 DB 224 AATATTTAAGATGACAAACTTTCTCAGTACTTAATCAGTACTAGAGTACTAAAT 283
 QY 1922 ATGACAGATTTGATTAACCTGCTTGAGATTTTAACTCAAAAAGCGTTAACTATC 1981
 DB 284 ATGACAGATTTGATTAACCTGCTTGAGATTTTAACTCAAAAAGCGTTAACTATC 343
 QY 1982 AAAGATCGGTCACTTTTCTTTGGCATTAAATTCGAGATGACATTAAGAGTTA 2041
 DB 344 AAAGATCGGTCACTTTTCTTTGGCATTAAATTCGAGATGACATTAAGAGTTA 403
 QY 2042 GTCAAGATTTGGCCCTGCTTTGGAGTCTTATTCGCGTCAATGAGATGATCTGAAC 2101
 DB 404 GTCAAGATTTGGCCCTGCTTTGGAGTCTTATTCGCGTCAATGAGATGATCTGAAC 463
 QY 2102 ACCTTAATAGGCAAGTGGATGAGGATGAGAAAGCTCAATTAAGTACTGACATTTCAAC 2161
 DB 464 ACCTTAATAGGCAAGTGGATGAGGATGAGAAAGCTCAATTAAGTACTGACATTTCAAC 523
 QY 2162 AAGAGAAAGATGAGTAAACAAACAAAGTACAGTGAAGTTTATGTTGAGCAATGAGC 2221
 DB 524 AAGAGAAAGATGAGTAAACAAACAAAGTACAGTGAAGTTTATGTTGAGCAATGAGC 583
 QY 2222 GACCAATTTCAATGAGATGCTCTCAGGAGTTTCTGCTCCTTAAACCTGCTCATCAGC 2281
 DB 584 GACCAATTTCAATGAGATGCTCTCAGGAGTTTCTGCTCCTTAAACCTGCTCATCAGC 643
 QY 2282 TGAGAAATTCAGGCTTGAAGATGTCGATTAATGTTCTTGTGCAAAAAGCCACTGTGT 2341
 DB 644 TAGAAACCTCAGGCTTGAAGATGTCGATTAATGTTCTTGTGCAAAAAGCCACTGTGT 703
 QY 2342 TGAATTTGGAGAACCCAGACATCATGTCAGATTAATGTTCTTGTGCAAAAAGCCACTGT 2401
 DB 704 TGAATTTGGAGAACCCAGACATCATGTCAGATTAATGTTCTTGTGCAAAAAGCCACTGT 763
 QY 2402 TTAATAATGGAGATTTACGGCAGATGATGCTTACCTTCAAGATTTATGCTATGAG 2461
 DB 764 TTAATAATGGAGATTTACGGCAGATGATGCTTACCTTCAAGATTTATGCTATGAG 823
 QY 2462 AAAATATCTGG 2472
 DB 824 AAAATATCTGG 834

RESULT 6
 BUI67122 883 bp mRNA linear EST 04-SEP-2002
 LOCUS AGENCOURT_7958965 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163390
 DEFINITION 5', mRNA sequence.
 ACCESSION BUI67122
 VERSION BUI67122.1 GI:22681087
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 plate: LLML3518 row: m column: 23
 High quality sequence stop: 555.
 Location/Qualifiers
 FEATURES

Source

1. .883
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6163390"
 /isue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."
 BASE COUNT 272 a 161 c 189 g 261 t
 ORIGIN

Query Match 20.3%; Score 669.2; DB 13; Length 883;
 Best Local Similarity 92.3%; Pred. No. 6.2e-150; Indels 2; Gaps 1;
 Matches 746; Conservative 0; Mismatches 58;

682 AAAAGTGAAGTATGTTGCTATCATCTGAACAATAAAGCTGTGTTTGAATATCAG 741
 1 ATAACTGGAAGTATGTTGCTATCATCTGAACAATAAAGCTGTGTTTGAATATCAG 60
 742 GCGAATATATTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 801
 61 GCGAAGTATATTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 120
 802 AGTCAGTATATGATATTAAGAGCTGATATGATGATGATGATGATGATGATGATGATGATG 861
 121 AGTCAGTATATGATATTAAGAGCTGATATGATGATGATGATGATGATGATGATGATGATG 180
 862 ATGGCTAAAGAAAGCTCTATATCTCACTGCAATGAGCTGTTTACATGCAATCATAT 921
 181 ATGGCTAAAGAAAGCTCTATATCTCACTGCAATGAGCTGTTTACATGCAATCATAT 240
 922 TCACAGCGCATCTCCACAGCTACGCCATATATGATGAGAAACATCTACAAATCCCTT 981
 241 TCACAGCGCATCTCCACAGCTACGCCATATATGATGAGAAACATCTACAAATCCCTT 300
 982 TGGGATTAAATATGTCAGCTCAGATTAATAATCTTTGTCAGCTCAGATTAATAAT 1041
 301 TGGGATTAAATATGTCAGCTCAGATTAATAATCTTTGTCAGCTCAGATTAATAAT 360
 1042 ATTCGACATTTGACAAAGATTTATGTCGAAACAGTATCTACCATGGAGAGAACCTT 1101
 361 ATTCGACATTTGACAAAGATTTATGTCGAAACAGTATCTACCATGGAGAGAACCTT 420
 1102 TGTGATATGTCAGCTCAGATTAATAATCTTTGTCAGCTCAGATTAATAAT 1161
 421 TGTGATATGTCAGCTCAGATTAATAATCTTTGTCAGCTCAGATTAATAAT 480
 1162 AATTAGATATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 1221
 481 AATTAGATATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 540
 1222 TGTGTTAAAGGCGGAAGGCTCTAAAGAGAAACATGTCATTTGGCTGGGAAATATA 1281
 541 TGTGTTAAAGGCGGAAGGCTCTAAAGAGAAACATGTCATTTGGCTGGGAAATATA 600
 1282 AACTGTTTGAATATACAGATTAATCTGATATCTGAAAAATGCTTTGAATCTTTGGCCA 1341
 601 AACTGTTTGAATATACAGATTAATCTGATATCTGAAAAATGCTTTGAATCTTTGGCCA 660
 1342 GTAACCTGAGATTAAGATTTGCTGAAGCC--TATGGTGTATTTGATCAAAATCCAA 1399
 661 GTAACCTGAGATTAAGATTTGCTGAAGCC--TATGGTGTATTTGATCAAAATCC 720
 1400 ATAAAGAACTCCATGTTAGAGTTGAGTTGACTGTTACAGCAGTGTGTAAG 1455
 721 AATTAAGAAAGAACTCCATGCTTGAAGTTGAGAGCTTTGAACTTGGGTTTCAAG 776

RESULT 7

CB723732
 LOCUS 854 bp mRNA linear EST 10-Apr-2003
 DEFINITION UI-M-FYO-cez-b-21-0-UI-r1 NIH BMAP_FYO Mus musculus CDNA clone
 IMAGE: 6844054 5', mRNA sequence.
 ACCESSION CB723732
 VERSION CB723732.1 GI:29780874
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 854)
 NIH-MGC <http://mgi.mc.nhl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapb-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers

FEATURES

source
 1. 854
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE: 6844054"
 /issue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5,pcp"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_id="NIH BMAP_FYO"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1995. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to RNA size fraction. Ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGGAGACAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

BASE COUNT 262 a 180 c 189 g 219 t 4 others
 ORIGIN

Query Match 20.3%; Score 651.4; DB 14; Length 854;
 Best Local Similarity 87.9%; Pred. No. 1.2e-145;
 Matches 742; Conservative 0; Mismatches 99; Indels 3; Gaps 3;

67 GAATGTTTACTCAAAATGGATGATGATGATGATGATGATGATGATGATGATGATGATG 125
 2 GAATGTTTACTCCCAATGGATGATGATGATGATGATGATGATGATGATGATGATGATG 61
 126 AATTACGATTAAGCATGAACTTTTAAAGAGCAAGAAATATCCCTTCATCAACTTCT 185
 62 CGTACCATCAAAACATGAACTTTTAAAGAGCAAGAAATATCCCTTCATCAACTTCT 121
 186 TCAAGATGAATGTTTCTTCACTTTGTAAGCTTCCCAAGAGCAAGAAATGAGGAAT 245
 122 GCAAGAGCAACTTCTTCACTTTGTAAGCTTCCCAAGAGCAAGAAATGAGGAAT 181
 246 TTTGATGAACAGACATTTGACCTTGGGCTTTTCAACCTTTTAAAGTAAT 305

Db 182 TTTTGATGAACAAGACGACTTTGTGACCTTCGGCTTTTTCACCTTTTAAAGTAT 241

Qy 306 TGACACCAATGAGCAACCCGTGAAGAAAAGATCCCTCATTCCGAATTTGTTTCTATCG 365

Db 242 TGAACCAAGTAGGCAACCGTGAAAGAAAAGATCCCTCATTCCGAATTTGTTTCTATCG 301

Qy 366 CATGCCAGTGTGATTCGATATGTTTAAAGATCCGAAGTACAGACTTCGAAAGAAA 425

Db 302 CATGCCAGTGTGATTCGATATGTTTAAAGATCCGAAGTACAGACTTCGAAAGAAA 361

Qy 426 TATTCATATGTTTGAAGAAAGCTGTGATCTTAGGGATCTTATTCACCTCATAGTAG 485

Db 362 CATTCGATATGTTTGAAGAAAGCTGTGACCTTCGGGATCTCAACTGCGCTCATAGTAG 421

Qy 486 AGCAATGATGTTTATTCCTCCAAATGTAAGTCTTCCAAACTGCGCAAGACATATA 545

Db 422 AGCAATGATGTTTATTCCTCCAAATGTAAGTCTTCCCAAGTCCCAAGACATATA 481

Qy 546 TAATTAATTTGATTAAGGCAATATATGATGTTGATTTGGTAAATAGTTTCTCCAAATA 605

Db 482 CAACAAGTTGATTAAGGCAATATATGATGTTTGGTAAATAGTTTCTCCAAATA 541

Qy 606 TGACAAACAGAAATATCTCTGAATAATCAACCATGACTGTGTCCCAAGCAAGTATTC 665

Db 542 CGACAAAGCAAGTACACTGTGAAGATCAATCATGACTGTGTCCAGAGCAAGTATTC 601

Qy 666 TGAAGCAATCGAAAAAATCTCGAATATGTTGATTCATCTGAACAATTAACCTCTG 725

Db 602 TGAAGCAATCGAAAAAATCTCGAATATGTTGATTCATCTGAACAATTAACCTCTG 661

Qy 726 TGTTTGATATATCGGCAAGTATATTTTAAAGTGTGTGATGATGATTAATCTTCT 785

Db 662 TGTCTTGAATATCGGCAAGTATATTTCTGAAGTGTGTGATGATGATTAATCTTCT 721

Qy 786 AGAAAAATATCTCTGATCAGTATATATGATTAAGAAAGCTGTATATGTTTGGAGAT 845

Db 722 GAAAAAGTACCTCTGATCAGTATATGATTAAGAAAGCTGTATATGTTTGGAGAT 781

Qy 846 GCCCAATTTGATGCTGATGCTTAAGAAAGCTCTATCTCAACGCGCAATGATGTTT 905

Db 782 GACC-ACCTGATGCTGATGCTTAAGAAAG-CTATATCTCTCAACGCGCAATGATGTTT 839

Qy 906 TACA 909

Db 840 CACA 843

RESULT 8
CB246283 809 bp mRNA linear EST 12-FEB-2003
DEFINITION UI-M-POO-cdv-f-18-0-UI-r1 NIH_BMAP_POO Mus musculus cDNA clone
IMAGE: 6834931 5', mRNA sequence.
ACCESSION CB246283
KEYWORDS CB246283.1 GI:28367927
SOURCE EST
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 809)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
FEATURES
source
1..809
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6834931"
/issue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP F00"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:781-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

BASE COUNT 248 a 173 c 179 g 206 t 3 others

ORIGIN
Query Match 20.3%; Score 650.6; DB 14; Length 809;
Best Local Similarity 88.3%; Pred. No. 1.8e-145;
Matches 715; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

Qy 177 TCAACTCTCAAGATGATCTTCTTACATTTTCGTAAAGTATACCAAGACAGAAAG 236

Db 1 TCACTCTCTGACAGCAAACTTTTACATTTTGTAAAGTATACCAAGACAGAAAG 60

Qy 237 GGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 296

Db 61 GGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 297 AAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 356

Db 121 AAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180

Qy 357 TGCTATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 416

Db 181 TGCTATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 240

Qy 417 CCGAAGAAATATTTCTCAATGTTTGAAGAAAGCTGTGATGATGATGATGATGATGAT 476

Db 241 TCGAAGAAATTTCTCAATGTTTGAAGAAAGCTGTGATGATGATGATGATGATGAT 300

Qy 477 TCAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536

Db 301 TCAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

Qy 537 GCAAT 596

Db 361 GCAAT 420

Qy 597 TCCAAAT 656

Db 421 TCCAAAT 480

Qy 657 AGTAATGCTGAAGCAATCAAGAAATTTTGAAGTATGATGATGATGATGATGATGAT 716

Db 481 AGTAATGCTGAAGCAATCAAGAAATTTTGAAGTATGATGATGATGATGATGATGAT 540

Qy 717 AAAAGCTGTGTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 776

Db 541 GAAACTCTGCTTACGATATGAGGCAAGTATATTTCTGAAAGTGTGTGCTGTGACGA 600

QY 777 ATACTCTTACGAAAAATATCTCTGAGTCACTATATAGTATATAGAAAGCTGTATATGCT 836

Db 601 ATACTCTTACGAAAAATATCTCTGAGTCACTATATAGTATATAGAAAGCTGTATATGCT 660

QY 837 TGGAGAGATGCCCATTTGATGCTGATGCTTAAAGAAAGCTCTATTTCTCACTGCGCAAT 896

Db 661 GGGGAGAGATGCCCATTTGATGCTGATGCTTAAAGAAAGCTCTATTTCTCACTGCGCGAT 719

QY 897 GAGCTGTTTACATGCGCATATTTCCAGAGCATCTCCAGCGCATATATAGAA 956

Db 720 TGTATGTTTACATGCGCATATTTCCAGAGCATCTCCAGCGCATATATAGAA 779

QY 957 TGGAGAAACATCTACAAATCCCTTTGG 984

Db 780 TGGAGAGACATCTACGAAATCTCTGGG 807

RESULT 9
CD349473 785 bp mRNA linear EST 29-MAY-2003
LOCUS UI-M-FY0-cfg-j-12-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
DEFINITION IMAGE: 6854605 5', mRNA sequence.
ACCESSION CD349473.1 GI:31140968
VERSION CD349473.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 785)
NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 785
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6854605"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX-Agc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. Ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Agc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chih, Ph.D.,
program coordinator."

BASE COUNT 238 a 169 c 172 g 203 t 3 others

ORIGIN

Query Match 19.4%; Score 622.8; DB 14; Length 785;
Best Local Similarity 88.3%; Pred. No. 8.9e-139;
Matches 686; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

QY 241 GAAATTTTGGATGAAACAGAGCATTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300

Db 1 GAAATTTTGGATGAAACAGAGCATTTGTGACCTTGGCTTTTCAACCTTTTAAAA 60

QY 301 GTAATTAACCACTAGGCAACCGCTGAAGAAATCTCTCAATGAGAAATTTGTTTGT 360

Db 61 GTTATTTGAAACCACTAGGCAACCGCTGAAGAAATCTCTCAATGAGAAATTTGTTTGT 120

QY 361 ATCGCATGCCATGCTGTGTAATTCGATATGTTTAAAGATCCAGAAAGTACAGACTTCGA 420

Db 121 ATTCGATGCCATGCTGTGTAATTCGATATGTTTAAAGATCCAGAAAGTACAGACTTCGA 180

QY 421 AGAATATTTCTCAATGTTGTGTAAGAAAGCTGTGATCTTAAGGATCTTAATCACTCAT 480

Db 181 AGAATATTTCTCAATGTTGTGTAAGAAAGCTGTGATCTTAAGGATCTTAATCACTCAT 240

QY 481 AGTAGAGCAATGATGTTTATCTCTCCAAATGTGAATCTTACCAAGACTGCGCAAGCAC 540

Db 241 AGCAGAGCAATGATGTTTATCTCTCCAAATGTGAATCTTACCAAGACTGCGCAAGCAC 300

QY 541 ATATATATATATATGATTAAGGCAATATATATGATGTTGAGTAAATATATGTTTCTCCA 600

Db 301 ATCTTACAAACAGTTAATTAAGGCAATATATATGATGTTGAGTAAATATATGTTTCTCCA 360

QY 601 AATATATGACAAACAGAAATATCTGAAATATCAACATGACTGTGCGCAAGCAAGTA 660

Db 361 AACAAAGACAGAGCAAGTACACTGGAAGATCAATCATGACTGTGCGCAAGCAAGTAC 420

QY 661 ATTGCTGAAGCATCGAGAAAAAACTCGAAGATGTTGCTATCATCTGAACAATGAAA 720

Db 421 ATTGCTGAAGCATCGAGAAAAAACTCGAAGATGTTGCTATCTGAGCAAGTAAA 480

QY 721 CTCTGCTTTTGAATATACAGGCAAGTATTTTAAAGTGTGTGATGATGATGATGATGAT 780

Db 481 CTCTGCTTTTGAATATACAGGCAAGTATTTTAAAGTGTGTGATGATGATGATGATGAT 540

QY 781 TTCTTGAAGAAATATCTCTGAGTCACTATTAATATTAAGAAAGCTGTATATGCTTGGG 840

Db 541 TTCTTGAAGAAATATCTCTGAGTCACTATTAATATTAAGAAAGCTGTATATGCTTGGG 600

QY 841 AGGATGCCCATTTGATGCTGATGCTTAAGAAAGCTCTTATTTCACTGCGCAATGAC 900

Db 601 AGGATG-CCAACTTGATGCTGATGCTTAAGAAAGCTCTTATTTCACTGCGCGATGAT 659

QY 901 TGTTTTCAATGCGCATATTTCCAGACCATCTCCAGCGCTTACGGCATATATGATGGA 960

Db 660 AGCTTACCATGCGCATATTTCCAGACCATCTCCAGCGCATCTCAAGCCATCAATGATGA 719

QY 961 GAAACATCTACAAATCCCTTTGGGTTTAAATAGTCACTGCAATTAATATTTCTT 1017

Db 720 GAGACATCTACGAAATCCCTCTGGGTCATTAATATGCGCTCAGATTAATATTTCTT 776

RESULT 10
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LOCUS UI-M-GH0-cel-r-01-0-UI-r1 NIH_BMAP_GH0 Mus musculus cDNA clone
DEFINITION IMAGE: 6841250 5', mRNA sequence.
ACCESSION CB520825.1 GI:29354180
VERSION CB520825.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 759)
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.utoa.edu/distribution/mouseell.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1..759
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6841250"
/tissue_type="whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pYX-Asc; Site: 1: Ecov 1; Site 2: Not 1; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT 232 a 161 c 168 g 197 t 1 others
ORIGIN

Query Match 19.2%; Score 614.2; DB 14; Length 759;
Best Local Similarity 88.8%; Pred. No. 1e-136;
Matches 675; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

1397 CAAATTAAGAACTCCATCTTTAGAGTTGAGTTGACGTTCAGCAGTGTGTAAGT 1456
1 CAAATTAAGAACTCCATCTTTAGAGTTGAGTTGACGTTCAGCAGTGTGTAAGT 60
1457 TTCGAGATATGTCAGGATTTGAAGAGCATGCCAATGCTCTATCCGTGAAGCAGAT 1516
61 TTCGAGACATGTCGTGATCGAAGAACATGCCAATGCTCTATCCGTGAAGCAGAT 120
1517 TTAGTATTTCCGATGAGAGCTGAGTACAGACTAGCTAGAGCAATGAATTAAGAGAA 1576
121 TCAGTTACTCCCATACAGAGCTGAGTACAGACTAGCTAGAGCAATGAATTAAGAGAA 180
1577 ATGATTAAGAAACAGCTCCGAGCAATTTGACAGAGATCTCTATTTGAAATCACTGAGC 1636
181 ATGACAAGAAACAGCTCCGAGCACTTTGACAGAGCCGAGCACTATTTGAAATCACTGAGC 240
1637 AAGAGAAAGATTTTCTGTGAGAGCAGACACTATTGTGTAATCTCCGAAATTTCTAC 1696
241 AAGAGAAAGATTTTCTGTGAGAGCAGACACTATTGTGTAATCTCCGAAATTTCTAC 300
1697 CCAATTTGCTTCTGTCTGTTAATGAACTCTAGAGATGAAGTCAAGTACTGCT 1756
301 CCAATTTGCTTCTGTCTGTTAATGAACTCTAGAGATGAAGTCAAGTACTGCT 360
1757 TGTAAAGATTTGGCTTCAATCAAGCTGAGAGCTATGAGCTTTGAGATTCGAAT 1816
361 TACTAAAGATTTGGCTTCAATCAAGCTGAGAGCTATGAGCTTTGAGATTCGAAT 420

QY 1817 ACCGAGATCTTATGTTGGAGGTTTGGCTTGGGCTTAGAGAAATATTTAACAGATG 1876
DB 421 ATCCAGATCTTATGTTGGAGGTTTGGCTTGGGCTTAGAGAAATATTTAACAGATG 480
QY 1877 ACAATCTTCTAGTACTAATTAATCAAGTACTAGTACTAATTAATTAAGAGATTTGG 1936
DB 481 ACAATCTTCTAGTACTAATTAATCAAGTACTAGTACTAATTAATTAAGAGATTTGG 540
QY 1937 ATACCTGCTGTGAGATTTTACTCAAAAAGCGTTAATCAATCAAGATTCGACACT 1996
DB 541 ATACCTGCTGTGAGATTTTACTCAAAAAGCGTTAATCAATCAAGATTCGACACT 600
QY 1997 TTTCTTTTGGCATTTAAATCTGAGATGCACATTAACAGTACTAGGCTTTGGCC 2056
DB 601 TTTCTTTTGGCATTTAAATCTGAGATGCACATTAACAGTACTAGGCTTTGGCC 660
QY 2057 TGTCTTTGAGTCTTATGCTGATGAGATGTATCTGAAGCACTTAATAGCAAG 2116
DB 661 TGTCTTTGAGTCTTATGCTGATGAGATGTATCTGAAGCACTTAATAGCAAG 719
QY 2117 TTGAGGCTATGAAAGCTCATTAATTAATTAATTAATTAATTAATTAATTAAT 2156
DB 720 TAGAGGCGATGAGAAAGCTCATTAATTAATTAATTAATTAATTAATTAATTAAT 759

RESULT 11
BG497751
LOCUS 753 bp mRNA linear EST 27-MAR-2001
DEFINITION 602543009F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4665482 5', mRNA sequence.
ACCESSION BG497751 GI:13459268
VERSION BG497751.1 GI:13459268
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 753)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: L10M1471 row: a column: 03
High quality sequence stop: 649.
Location/Qualifiers
1..753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4665482"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pNR-LIB (Clontech); Site: 1: S111 (ggcgcctggcgc); Site 2: S111 (ggcgcctatggcgc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGAGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

BASE COUNT 241 a 136 c 176 g 200 t

Library."

Query Match 19.1%; Score 612.2; DB 10; Length 753;
Best Local Similarity 90.9%; Pred. No. 3.1e-136;
Matches 666; Conservative 0; Mismatches 63; Indels 6; Gaps 3;

OR 2080 GCATGTGGATGTATCTGAAGCACCCTTAATAGGCAAGTTGAGCTATGAGAAAGCTATT 2139
1 GCATGTGGATGTATCTGAAGCACCCTTAATAGGCAAGTTGAGCTATGAGAAAGCTATT 60

OR 2140 AACTTGTCTGACATCTTCCAAACAGAGAAAGATGAAACAAACAAAGTTACAGATGAG 2199
61 AACTTGTCTGACATCTTCCAAACAGAGAAAGATGAAACAAACAAAGTTACAGATGAG 120

OR 2200 TTTTGTAGTGGAGAAATGGGCGACAGATTTTCAATGATGCTCTCCGAGGCTTCTCTCT 2259
121 TTTTGTAGTGGAGAAATGGGCGACAGATTTTCAATGATGCTCTCTCCGAGGCTTCTCTCT 180

OR 2260 CCTTAAACCCCTGCTCATCTGAGTGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCT 2319
181 CCTTAAACCCCTGCTCATCTGAGTGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCT 240

OR 2320 TCTGCAAAAAGGCCACTGTGGTGAATTTGGAGAACCCAGACATCATGTGAGATTAATCTC 2379
241 TCTGCAAAAAGGCCACTGTGGTGAATTTGGAGAACCCAGACATCATGTGAGATTAATCTC 300

OR 2380 TTTTCAAGACATGAGATCATCTTTAAATGGGGATGATTTACCGCAAGATATGCTTACC 2439
301 TTTTCAAGACATGAGATCATCTTTAAATGGGGATGATTTACCGCAAGATATGCTTACC 360

OR 2440 CTTCAGATTAATGCACTTATGAAATATCTGCAAAATCAAGCTTTGATCTTCGATG 2499
361 CTTCAGATTAATGCACTTATGAAATATCTGCAAAATCAAGCTTTGATCTTCGATG 420

OR 2500 TTACCTTATGATGTCTGTCAATGCTGATCTGTGTGGACTTATTCAGGTGTGAGAAAT 2559
421 TTACCTTATGATGTCTGTCAATGCTGATCTGTGTGGACTTATTCAGGTGTGAGAAAT 480

OR 2560 TCTCACACTAATAGCAGATTCAGTGTAAAGAGGCTGAAAGTGTGACTGCGCTTTAAC 2619
481 TCTCACACTAATAGCAGATTCAGTGTAAAGAGGCTGAAAGTGTGACTGCGCTTTAAC 540

OR 2620 AGCCACACACTCCATCATGAGTGGCTCAAGACAAAGAAAGGGGAAATATATGATGCGGCC 2679
541 AGCCACACACTCCATCATGAGTGGCTCAAGACAAAGAAAGGGGAAATATATGATGCGGCC 600

OR 2680 ATCGATTTGTTTACAGCATGATGTCTGATATTTGTTGCAACTTCATTT--TGGGAA 2737
601 ATCGATTTGTTTACAGCATGATGTCTGATATTTGTTGCAACTTCATTTGCGGGAAT 660

OR 2738 TTGGAATGCTGCATAG--TAATATCATGTTTAAAGATAGGACACTGTTTCAATA 2796
661 TTGGAATGCTGCATAG--TAATATCATGTTTAAAGATAGGACACTGTTTCAATA 720

OR 2797 GATTTTGACACTTTTGGATCAAGAGAAAA 2831
721 GATTTTG---ACATTTGATCAAGAGAAAA 752

RESULT 12
BM986382 833 bp mRNA linear EST 25-MAR-2002
LOCUS BM986382
DEFINITION EST311169 Rat gene index, normalized rat, norvegicus Rattus
subunit alpha, mRNA sequence.
ACCESSION BM986382
VERSION BM986382.1 GI:19705771
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 833)
AUTHORS Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G.,
Sultana, R., Tsai, J., White, J., Quakenbush, J., and Lee, N.H.
TITLE Generation of ESTs from a rat multiple tissue survey
JOURNAL Unpublished
COMMENT Other ESTs: EST745877 EST745567
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 reverse.

FEATURES
Location/Qualifiers
1..833
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="RG1AC69"
/tissue_type="mixed tissue"
/clone_lib="Rat gene index, normalized rat, norvegicus"
/note="Vector: pT73Pac; Site 1: EcoRI; Site 2: NotI;
Combination of untreated and NGF-treated P13 cell
libraries, and Benco Soares normalized libraries of ovary,
brain, kidney, liver, placenta, lung, embryo, skeletal
muscle, spleen, heart"

BASE COUNT 225 a 196 c 224 g 188 t

ORIGIN

Query Match 18.9%; Score 605; DB 12; Length 833;
Best Local Similarity 86.9%; Pred. No. 1.8e-134;
Matches 665; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

OR 2044 CAGAGTTGGGCTGCTTTGGAGTCTTATTTGCGGTGATGGAGATGATGAGAAC 2103
69 CAGAGTTGGGCTGCTGCTTTGGAGTCTTATTTGCGGTGATGGAGATGATGAGAAC 128

OR 2104 CTTAATAGCAAGTATGAGGCTATGAAAGCTGATTAATCTGATGATCTTCAACAA 2163
129 CTTAATAGCAAGTATGAGGCTATGAAAGCTGATTAATCTGATGATCTTCAACAA 188

OR 2164 GAGAAAGATTAACACAAAGATGACATGATTTTACTTGAACAAATGCGCGCA 2223
189 GAGAAAGATTAACACAAAGATGACATGATTTTACTTGAACAAATGCGCGCA 248

OR 2224 CCAGATTTGATGATGCTCTCCAGGCTTTCTGTCCTCTAAACCTGCTATCGAGCTG 2283
249 CCAGATTTGATGATGCTCTCCAGGCTTTCTGTCCTCTAAACCTGCTATCGAGCTG 308

OR 2284 GGAATCTGAGGCTTGAAGAGTGTCCGAATTAATCTTTCGAAAAGGCGACTGTGTTG 2343
309 GGAATCTGAGGCTTGAAGAGTGTCCGAATTAATCTTTCGAAAAGGCGACTGTGTTG 368

OR 2344 AATTGGGAAGCCGACATCATGTCAGAATTAATCTTTCGAAAAGGCGACTGTGTTG 2403
369 AATTGGGAAGCCGACATCATGTCAGAATTAATCTTTCGAAAAGGCGACTGTGTTG 428

OR 2404 AAAAATGGGAGATTTAGGCGCAAGATATGCTAACCTTCAGATTTTGGCATTTAGGAA 2463
429 AAAAATGGGAGATTTAGGCGCAAGATATGCTAACCTTCAGATTTTGGCATTTAGGAA 488

OR 2464 AATATCTGCAAAATCAAGATCTTGATCTTTCGAATGTTAATCTTATGATGATGCTGCAATC 2523
489 AATATCTGCAAAATCAAGATCTTGATCTTTCGAATGTTAATCTTATGATGATGCTGCAATC 548

OR 2524 GGTGATCTGTGTGGACTTATCGAGGTGTGAGAAATTTCAACACTTAATGCAAGATTGAG 2583
549 GGTGATCTGTGTGGACTTATCGAGGTGTGAGAAATTTCAACACTTAATGCAAGATTGAG 608

QY 2584 TGTAAAGAGGCTGAAAGGTGACATGACATTAAAGCCACACACTCCATCAGTGGCTC 2643
 DB 609 TGGAAAGAGGCTGAAAGGGGACCTGACATTCACAGCCACAGCTGATCAGTGGCTC 668
 QY 2644 AAGACACAGAACAGGGGAAATATATGATGCGCCCTGATTTGTTTAAAGCATATG 2703
 DB 669 AAGACACAGAACAGGGGCGAGATATATGACGACCCATTACCTGTTCTGCTGCTGC 728
 QY 2704 GCTGGATATGTTGTCACCTTCATTTTGGGAATTGAGATCGTCAATAGTAATATC 2763
 DB 729 GCTGGGACTGCGGGCACTTTATCTTGGGAATTGGAGCCGCGACACAGAAATC 788
 QY 2764 ATGTTAAGATGATGACACATGTTTCATATAGATTGGAAC 2808
 DB 789 ATGTGAAGATGACGACAGCTGTTTCATATAGATTGGAAC 833
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 LOCUS AUI29890 NT2RP2 Homo sapiens cDNA clone NT2RP206455 5', mRNA
 DEFINITION
 sequence.
 ACCESSION AUI29890
 VERSION AUI29890.1 GI:10990244
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 753)
 Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Isogai, T.
 HRI human cDNA project
 Unpublished
 JOURNAL Contact: Takao Isogai
 COMMENT Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RP206455"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_1ib="NT2RP2"
 /note="Vector: pME18FLJ; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"
 BASE COUNT 232 a 133 c 160 g 219 t 9 others
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 Query Match 18.7%; Score 599.2; DB 9; Length 753;
 Best Local Similarity 96.2%; Pred. No. 4.2e-133;
 Matches 654; Conservative 0; Mismatches 22; Indels 4; Gaps 4;
 QY 762 GTGTGATGTGATGATCTCTCTAGAAAATATCTCTGAGTCATATAGATATAG 821
 DB 1 GTGTGATGTGATGATCTCTCTAGAAAATATCTCTGAGTCATATAGATATAG 60
 QY 822 AAGCTTATATGCTTGGAGAGATGCCAATTGATGCTGATGCTTAAAGAAAGCTCTA 881
 DB 61 AAGCTTATATGCTTGGAGAGATGCCAATTGATGCTGATGCTTAAAGAAAGCTCTA 120
 QY 882 TTCTCAACTGCAATGAGACTGTTTCAATATGATCATATATTCAGACGATCTCAAGC 941

DB 121 TTCTCAACTGCAATGAGACTGTTTCAATATGATCATATATTCAGACGATCTCAAGC 180
 QY 942 TAGCCATATATGATGAGAAACATCTACAAATCCCTTGGGTTATTAATAGCACT 1001
 DB 181 TACACCATATATGATGAGAAACATCTACAAATCCCTTGGGTTATTAATAGCACT 240
 QY 1002 CAGAAATTAATCTTTTGGCAACCATGATGATGATTAATTTGACATTTGACAAAGAT 1061
 DB 241 CAGAAATTAATCTTTTGGCAACCATGATGATGATTAATTTGACATTTGACAAAGAT 300
 QY 1062 TTATGTTCCAAACGATATACCATGAGAGAGAACCTTATGATATATGTAACACTCA 1121
 DB 301 CTATGTTCCAAACGATATACCATGAGAGAGAACCTTATGATATATGTAACACTCA 360
 QY 1122 AAGAGTACCTGTTTCCAAATCCCAAGTGAATGAATGCTGGAATATAGATATATAC 1181
 DB 361 AAGAGTACCTGTTTCCAAATCCCAAGTGAATGAATGCTGGAATATAGATATATAC 420
 QY 1182 TGATCTTCTCGTCGTCGCTGACCTTGCTTCATTTGTTCTGTTAAAGCCGAAGG 1241
 DB 421 TGATCTTCTCGTCGTCGCTGACCTTGCTTCATTTGTTCTGTTAAAGCCGAAGG 480
 QY 1242 TGCTAAAGAGAACACTGTCATTTGCTGGGAGAAATATAACTGTTGATTACACAGA 1301
 DB 481 TGCTAAAGAGAACACTGTCATTTGCTGGGAGAAATATAACTGTTGATTACACAGA 540
 QY 1302 TACTTATGATCTGGAAGAAATGCTTTGATCTTTGGCCAGTACCTCATGAGACT-AGA 1360
 DB 541 CACTCTGATCTGGAAGAAATGCTTTGATCTTTGGCCAGTACCTCATGAGACT-AGA 600
 QY 1361 ATTTCGTCGACCT-ATTGCTGTTTACGATCAATCCAA-TAAGAAATCCATGTTT 1418
 DB 601 ATTTCGTCGACCT-ATTGCTGTTTACGATCAATCCAA-TAAGAAATCCATGTTT 660
 QY 1419 AGAG-TTGAGTTGACTGG 1437
 DB 661 AAGTTTGAGTTGACTGG 680

RESULT 14
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 LOCUS BG391265
 DEFINITION
 mRNA sequence.
 ACCESSION BG391265
 VERSION BG391265.1 GI:13284713
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 844)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
 http://image.llnl.gov
 Plate: ILNLI0460 row: P column: 01
 High quality sequence stop: 721.
 Location/Qualifiers
 1. 844
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 /db_xref="taxon:9606"
 /clone="IMAGE:4536816"

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/tissue_type="embryonal carcinoma, cell line"
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/notes="Organ: testis; Vector: PCMV-SPORE; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH_MGC Library."

BASE COUNT      286 a      149 c      177 g      232 t
ORIGIN

Query Match      18.7%; Score 599; DB 10; Length 844;
Best Local Similarity 95.8%; Pred. No. 5e-133;
Matches 658; Conservative 0; Mismatches 25; Indels 4; Gaps 4;

QY 445 GAAAGCTGTGATCTTAGGATCTTAATTCACCTAGTAGAGCAATGATGTTATCT 504
DB 1 GAAGCTGTGATCTTAGGATCTTAATTCACCTAGTAGAGCAATGATGTTATCT 60
QY 505 CCAATGTAGATCTTCCAGCAAGCTGCCAAGACATATATATTAATTGATTAAGG 564
DB 61 CCAATGTAGATCTTCCAGCAAGCTGCCAAGACATATATTAATTGATTAAGG 120
QY 565 CAAATATATGTTGGATTTGGTATAGTTTCTCAATATATGCAAGACAGATATCT 624
DB 121 CAAATATATGTTGGATTTGGTATAGTTTCTCAATATATGCAAGACAGATATCT 180
QY 625 CTGAAATCAACCATGATGCTGTGCCAGAACCAAGTAAATGCTGAAGCATGAGAAAA 684
DB 181 CTGAAATCAACCATGATGCTGTGCCAGAACCAAGTAAATGCTGAAGCATGAGAAAA 240
QY 685 ACTGGAAGTATGTTGCTATCATCTGAA CAACTAAACCTGTGTTTGAATATCAGGCG 744
DB 241 ACTGGAAGTATGTTGCTATCATCTGAA CAACTAAACCTGTGTTTGAATATCAGGCG 300
QY 745 AAGTATATTTTAAAGCTGTGGATGTGATGATGATATCTTCTGAAAAATATCCTCTGAGT 804
DB 301 AAGTATATTTTAAAGCTGTGGATGTGATGATGATGATATCTTCTGAAAAATATCCTCTGAGT 360
QY 805 CAGTATATGATATATTAAGAGCTGATATGCTTGGAGAGATGCGCAATTTGATGCTGATG 864
DB 361 CAGTATATGATATATTAAGAGCTGATATGCTTGGAGAGATGCGCAATTTGATGCTGATG 420
QY 865 GCTAAAGAAAGCCTTATCTTCAACTGCCAATGAGCTGTTTACATGCCATCATATTC 924
DB 421 G-TAAAGAAAGCCTTATCTTCAACTGCCAATGAGCTGTTTACATGCCATCATATTC 479
QY 925 AGAGCGCATCTCCACAGCTACGCCATATATGATGAGAGAAACATATCAAAAATCCCTTGG 984
DB 480 AGAGCGCATCTCCACAGCTACGCCATATATGATGAGAGAAACATATCAAAAATCCCTTGG 538
QY 985 GTTATATATGTGACCTCAGAAATTAATCTTGTGCCAACCCTATGATGATGTAATAT 1044
DB 539 GTTATATATGTGACCTCAGAAATTAATCTTGTGCCAACCCTATGATGATGTAATAT 597
QY 1045 CGAGACATTCAGACAGATTATGTTGCAACAGGATCTACCAATGAGAGAGAACCTTATGT 1104
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QY 1105 GATTAATGTGAACACTCAAGAGTACT 1131
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RESULT 15
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LOCUS         CD351100
DEFINITION   U1-M-FY0-c-fc-b-19-0-U1.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6852116 5', mRNA sequence.
ACCESSION    CD351100
VERSION      CD351100.1 GI:31142675
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Murinae; Mus.
REFERENCE     NIH-MGC http://mgc.nci.nih.gov/
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE         Unpublished
JOURNAL       Contact: Robert Straubeberg, Ph.D.
COMMENT       Email: cgaabs-remail.nih.gov
               Tissue Procurement: Dr. Jim Lin, University of Iowa
               CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
               CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
               DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
               Clone Distribution: Distribution information can be found at
               http://genome.uiowa.edu/distribution/mousefl.html
               This clone was contributed by the Brain Molecular Anatomy Project
               (BMAP)
Seq primer: pyx-5.
FEATURES
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        Site 2: Not I; The library was constructed according
        to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
        1996. Denatured RNA was size fractionated on a 1% agarose
        gel. First strand cDNA synthesis was primed with oligo-dT
        primer containing a Not I site. Double strand cDNA was
        size selected according to mRNA size fraction, ligated
        with EcoR I adaptor, digested with NotI and then cloned
        directionally into pyx-Aac vector. The library tag
        sequence located between the Not I site and the polyA tail
        is AGGAGAGCAG. This library was created for the University
        of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
        Developing Mouse Nervous System, supported by National
        Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
        program coordinator."
BASE COUNT    217 a      140 c      159 g      179 t      1 others
ORIGIN

Query Match      18.0%; Score 578.2; DB 14; Length 696;
Best Local Similarity 89.4%; Pred. No. 4.7e-128;
Matches 622; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
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Qy 2597 TGAAGGTGCACTGCACTTAACAGCCACACTCCATCAGGTGCTCAAAAGCAAGACA 2656
Db 2947 TGCGTGTGAGCAGCGCTTCAACAAAGATGCCCTTGAAGCTGCTTAAGAAATACAACT 3006
Qy 2657 AGGGGGAATATATGATGCGGCCATCATTTGTTTAAACGATCATGTGCTGATATGTTG 2716
Db 3007 CTGGGGAATGACCTGAGCCGAGCAATGAGAAATTTAATGCTGTGCTGTGCTACAGTGTG 3066
Qy 2717 TTTGACCTTCATTTTGGGAATTTGAGATGCTCACAATAGTAATATCATGTTTAAAGATG 2776
Db 3067 TAGCTTTATATGCTCTTGGATGTGTATGACAGACATAGTACAAATCATGTCTCAAAAAA 3126
Qy 2777 ATGACAACCTGTTTCATATAGATTTTGAACACTTTTGGATCACAAGAAAGAAATTTG 2836
Db 3127 CTGGCAGCTCTTCCAACTGACCTTGGACATATTTCTTGAATAATCTTAAGTTTG 3186
Qy 2837 GTTATTAACGAGAGCGGTGCGTTTGTGTTGAACAAGATTTCTTAAATAGTGAATTGATA 2896
Db 3187 GCATTAAGAGGAGCGAGTGTCTTTTATCTTACTATGATTTGATCATGATCATTCGAAC 3246

QY 2897 AAGAGCCCAAGAAATGCAAAAGCAAGAAATTTGAGAGTTTCAAGAGATGCTTTACA 2956
DB 3247 AAGG-----AAAACAGAAATACAGAAAAGTTTGGCCGGTTCCCGACAGTTGTAGG 3300
QY 2957 AGGCTATCTAGCATATTCGGAGCATGCCATCTCTTATTAATCTTTTCTCATGTATGC 3016
DB 3301 ATGCATATCTGATTTTTCAGACGGCATGGAAATCTTTCATCACTCTTTTGGCGTATGT 3360
QY 3017 TTGGCTCTGGAATGCGAATCTGCAATCTTTTGTATGATTTGATACATTCGAAAGACC 3076
DB 3361 TGACGTAGGGCTTCCTGAACTCATCATCATCAAGATATACGATATCTTAAGGACTCTC 3420
QY 3077 TACCTTACATAAAGTACGACAAAGAGGCTTTGAGTATTTTCATGAAACAAATGATATG 3136
DB 3421 TTGCATTTAGGGAAGAGTGAAGAAAGACACTCAACAGTTTAAAGAAAATTGATGAGG 3480
QY 3137 CACAC 3141
DB 3481 CGCTC 3485

RESULT 3

US-09-960-352-2439
Sequence 2439, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathiasagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960.352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2439
LENGTH: 412
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 11-LIB3058-019-Q1-K1-C11
US-09-960-352-2439

Query Match 12.7%; Score 408.8; DB 10; Length 412;
Best Local Similarity 99.5%; Pred. No. 1.5e-97;
Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 CTAGAAATTTGCTGAACCTTATGTTGTTACTGATCAATCAATAAAGAACTCCA 1413
DB 1 CTAGAAATTTGCTGAACCTTATGTTGTTACTGATCAATCAATAAAGAACTCCA 60
QY 1414 TGTTTGAGTTGGAGTTTGACTGCTTCAGAGTGTGTAAGTTTCCAGTATGTCAAGT 1473
DB 61 TGTTTGAGTTGGAGTTTGACTGCTTCAGAGTGTGTAAGTTTCCAGTATGTCAAGT 120
QY 1474 ATTGAAGACATGCCAATTGTTGTATCCCGTGAAGACAGATTTAGTTATCCATGCA 1533
DB 121 ATTGAAGACATGCCAATTGTTGTATCCCGTGAAGACAGATTTAGTTATCCATGCA 180
QY 1534 GGACTGATGAACAGACTAGCTAGAGCAATGAATTAAGAGAAAATGATAAGAAACAGCTC 1593
DB 181 GGACTGATGAACAGACTAGCTAGAGCAATGAATTAAGAGAAAATGATAAGAAACAGCTC 240
QY 1594 CGAGCAATTTGTAACAGAGATCCTATATGAAATCACTGAGCAAGAAAGATTTTTCG 1653
DB 241 CGAGCAATTTGTAACAGAGATCCTATATGAAATCACTGAGCAAGAAAGATTTTTCG 300
QY 1654 TGGAGCCACAGACACTATTTGTGTAATATCCCGAAATTTCTACCAATTTGCTTGTCT 1713
DB 301 TGGAGCCACAGACACTATTTGTGTAATATCCCGAAATTTCTACCAATTTGCTTGTCT 360
QY 1714 GTTAAATGGAATCTTAGAGATGAAGTCTCAAGTACTGCTTGTAAAG 1765

DB 361 GTTAAATGGAATCTTAGAGATGAAGTCTCAAGTACTGCTTGTAAAG 412

RESULT 4

US-10-162-160-2
Sequence 2, Application US/10162160
Publication No. US20030099627A1
GENERAL INFORMATION:
APPLICANT: Van Hasebroeck, Bart
APPLICANT: Materfield, Michael D.
TITLE OF INVENTION: No. US20030099627A1e1 Lipid Kinase
FILE REFERENCE: 2332-1-002
CURRENT APPLICATION NUMBER: US/10/162.160
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/194.640
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: 9611460.8
PRIOR FILING DATE: 1996-06-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 3387
TYPE: DNA
ORGANISM: Homo sapiens
US-10-162-160-2

Query Match 10.5%; Score 336.2; DB 14; Length 3387;
Best Local Similarity 53.5%; Pred. No. 9.7e-78;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

QY 1682 TCCCCCAAAATTCACCAAAATGCTTCTGTGTGTAATGAACCTAGAGATGAGTAG 1741
DB 1625 TCCCGAGGCGCTAGCCCGGCTCTCTGTGTATCACAAGTGAACAAAGATGAGATGTG 1684
QY 1742 CTCAGATGATGCTGCTTGTGTAAGATGCTTCAATCAAGCTGAACAGCTATGAGC 1801
DB 1685 CCCAGATGCTTACCTGCTGTGTCTCTGCGCGGAGCTGCCCGTCTGAGGCGCTGAGC 1744
QY 1802 TTCTGAGCTGCAATTTCCAGATCTTATGTTGAGAGTTTGTGTGTGCTTGAAGA 1861
DB 1745 TGTGATACCTTCAAGCTTCCCGGATTCGACGTAGGCTCTTCCGATCAATGCTCGTGG 1804
QY 1862 AATATTAAACAGATGCAAAATTTCTCAGTACTTAATCAGTAGTACAGGTACTAAAT 1921
DB 1805 AAC--TGACGACAGATGAGCTCTTCCAGTACTGCTGACAGCTGTGCAAGTCTTAAGT 1861
QY 1922 ATGAACAGTATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAGGTTAACTAATC 1981
DB 1862 ACAGATCTTACCTGAGCTGCAAGCTGACCAAAATTCCTGTGGAACGGGCTGGCCAGC 1921
QY 1982 AAAGATGCTCACTTTTCTTTTGGCATTTAATCTGATGCAATTAAGCAAGTTA 2041
DB 1922 GCAAGATCGCCACTTCTTCTGACCTCCGCTCCAGATGCAAGTGCCTGCTG 1981
QY 2042 GTGAGAGTTTGGGCTTTTGGAGTCTTATTTGCCGTGCAATGAGTATCTGAAGC 2101
DB 1982 CCTGCGCTTCGCTCATCTGAGGCTTACTGCGGGGCAAGCAACCAACCACTAAGG 2041
QY 2102 ACCTTAATAGGCAAGTTGAGGCTATGAAAGCTCAATTAATCTGACTGACATTTCAAC 2161
DB 2042 TGTGATGAAGCAGGGGGAAGCACTGAGCAAACTGAAGGCTCTGAATGATCTGTCAAGC 2101
QY 2162 AAGAGAAAGATGAACACAAAAGGTACAGATGAAGTTTATGTTAGCAATTTGGCG 2221
DB 2102 TGAAGCTCTCAGAAAGCCCAAGCCCAAGCAAGAGCTGATGCACTTGTCAATGCGGC 2161
QY 2222 GACCAAGATTCATGATGCTCTCCAGGCTTTCTGCTCTTAACCTGTCTCATACAG 2281
DB 2162 AAGAGGCTTCACTTAAGGCTCTTCCCACTGACGTCCCACTGCAAGCCCAAGCCCTGC 2221
QY 2282 TGGAAATCTCAGGCTTGAAGAGTGTGCAATATGCTTCTGCAAAAAGGCCACTGTGCT 2341
DB 2222 TGGCTGAAGTGTGCTGAGCAGTGCACCTTATGAGACTCCAAATGAAGGCCCTGTGGA 2281

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OY 2342 TGAATTGGGAGAACCCAGCATCATCTCGAATTAATCTTTTCAGAACAAATGATCATCT 2401
DB 2282 TCATGTACAGCAACGAGAG-----GCAGGACGCGCGGACCGCTGGGATCATCT 2332
OY 2402 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCTTCAGATTAATTCGATTATG 2461
DB 2333 TTAAAGAACGGGATGACCTCCGACAGACATGCTGACCTCGACAGATGATCAGACTCATG 2392
OY 2462 AAAATATCTGGCAAAATCAAGGCTTGATCTTGAAATGTTAATCTTATGATGATCTGCA 2521
DB 2393 ACCTCTGTGAGACGAGAGGGCTGGAAGCTGAGATGACCCCTATGCTGCTCCCA 2452
OY 2522 TCGGTACCTGTGGGACTTATGAGGTGTGAGAAATTCCTACATATAACAGATTC 2581
DB 2453 CCGGGGACCCGACAGGCTCATGAGTGTGATCTCCGTGACACACATGCGCAATCC 2512
OY 2582 A---GTGTAAAGAGGCTGAAAGGTGACCTGACGTTTAAACGCAACACACTCCATCAGT 2638
DB 2513 AACTCAACAAAGACATGACAGCCACAGCCGCTTCACACAGGATGCTGCTCACT 2572
OY 2639 GGCTCAAGACAAAGAACAGGCGGAAATATATGATGCGGCCATGATTTGTTTACAGAT 2698
DB 2573 GGCTGAAGTCCAGAACCCGGGGAGGCGCTGATGACGATGAGAGATTCACTCT 2632
OY 2699 CAGTGTGATGATTTGTTGCTTCCACTTCAATTTGGGAATTTGAGATGCTGACAAATGTA 2758
DB 2633 CCGTGTGCTGATTTGTTGCTTCCACTTCAATTTGGGAATTTGAGATGCTGACAAATGTA 2758
OY 2759 ATATCATGTTAAAGATGATGAGCAACGTTTCAATATGATTTTGAACACTTTTGGATC 2818
DB 2693 ACATCATGATCCGAGAGAGTGGCAGCTGTTCCATTTGATTTTGGCATTCTCGGGA 2752
OY 2819 ACAAGAAAGAAAAATTTGGTTATAAACGAGCGCGTGTGTTTGTGACAAAGATT 2878
DB 2753 ATTTCAAGACCAAGTTTGAATCAACCGGAGCGTGTCCCATTTCACTCTACCTACGACT 2812
OY 2879 TCTTAATAGTATTAAGTAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGT 2938
DB 2813 TTGTCAATGATTAATGACAGG-----GAAAGACTAATTAATGAGAAATTTGAACGT 2866
OY 2939 TTCAGGAAATGTTTACAGGCTTATAGCTATTCGCGACAGCATCCATCTCTTCAATTA 2998
DB 2867 TCCGGGGTACTGTGTAAGGCTTACACCATCTCGGCGCCAGGGGCTCTCTCTCC 2926
OY 2999 ATCTTTCTCATATGATGCTTGTGCTGTGAATGCAAGAACTGCAATCTTTTGAATATG 3058
DB 2927 ACCTCTTGGCCCTGATGGCGGGGAGGCTGCTGAGCTGACGTCTCCAAAGACATCC 2986
OY 3059 CATACATTCGAAGACCTAGCTTTAGATTAATGAGCAAGAGGCTTTGAGTAATTTCA 3118
DB 2987 ACTATCTCAAGGACTCCCTGGGACCTGGGAAACAGAGGAGGACTGAAGCACTTCC 3046
OY 3119 TGAACAAATGAAATGTCACACATGCTGTCGACCAAAATGATTTGATCTTCC 3178
DB 3047 GAGTGAAGTTTAAAGAACCTTCCTGTAGAGCTGGAACCAAGTGAAGTGGCTGGCC 3106
OY 3179 ACA 3181
DB 3107 ACA 3109

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RESULT 5
US-10-337-192-1
; Sequence 1, Application US/10337192
; Publication No. US20030195211A1
; GENERAL INFORMATION:
; APPLICANT: SABOHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 2786/39033
; CURRENT APPLICATION NUMBER: US/10/337,192
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/199,655

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; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
; US-10-337-192-1

Query Match 10.5%; Score 336.2; DB 12; Length 5220;
Best Local Similarity 53.5%; Pred. No. 1,3e-77;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

OY 1682 TCCCGAAATTTCTACCAAAATTTGCTTGTGTTAAATGGAATCTTGAAGATGATAG 1741
DB 1820 TCCCGAGGCGCTAGCCGCTGCTGTGTGTACCAAGTGAACAAAGATGAGATGTG 1879
OY 1742 CTCAGATGTACTGCTGTAAAGATTGGCTTCAATCAAGCTGAACAGCTATGAGC 1801
DB 1880 CCGAGATGCTTACCTGCTGTGTGTCTCTGCGCGGAGCTGCCGCTGAGCGCTGAGC 1939
OY 1802 TTCTGACAGCAATTAACCAAGATCTATGTTGAGGTTTGTCTTCGTTGTTGAA 1861
DB 1940 TGTGACCTTCACTTCCCGATTTGACAGCTAGGCTCTTGGCATCAAGTCCCTGCGGA 1999
OY 1862 AATATTTAAAGATGACAACTTCTCAGTACCTAATTCAGTACTAGATGATGAT 1921
DB 2000 AAC---TGACGACGATGAGCTGTTCCAGTACTGCTGAGCTGTGTGAGTGTCTCAAGT 2056
OY 1922 ATGAACGATATTGGATTAACCTGCTGTGAGATTTTACTCAAAAAAGCTTAACTATC 1981
DB 2057 ACGAGTCTTACCTGAGCTGAGAGTACCAATTTCTGTGACCGGGCTGCGCAAC 2116
OY 1982 AAGAGATCGTCACTTTTCTTTTGGCATTTAAATCTGAGTGCACAAATTAACAGTTA 2041
DB 2117 GCAAGATCGGCACTTCTTTTCTGCGACCTCCGCTCGAGATGACAGTCCGCTGCTG 2176
OY 2042 GTGAGAGTTTGGCTGCTTTTGGAGTCTATTGCGGTGATGAGGATGATCTGAAGC 2101
DB 2177 CCGTCCGCTGCGCTCACTCTGAGGCTTACTGAGGCGGACAGCACCAACATGAAG 2236
OY 2102 ACCTTAATAGCAGTGAAGGCTATGAAAGCTCATTAATCTGACTGACATTTCAAC 2161
DB 2237 TGTGATGAACAGGGGGAACACTGAGCAATGAAGGCTGATGATCTGTCAAGC 2296
OY 2162 AAGAGAAAGATGAACACAAAGGTAAGATGAATTTTATGTTGAGCAATGCGGC 2221
DB 2297 TGAAGTTCAGAAAGACCCCAAGGCCCAAGACAGAGCTATGACATTTGTGATGCGC 2356
OY 2222 GACGAGATTTTATGATGATCTTCCAGGCTTTCTGCTCTCTAAACCTCTCATCAGC 2281
DB 2357 AAGAGGCTTACCTTAAGGCTCTTCTCCACCTGCACTCCCACTGACCCAGACCTGCG 2416
OY 2282 TGGAAATCTCAGGCTTGAAGGTGCAATTAATGATCTTTGCAAAAGGCACTGTGCT 2341
DB 2417 TGGCTGAAGTGTGCTGAGAGGACCTTATGAGATCTCCAAAGATGAAGCCCTGTGGA 2476
OY 2342 TGAATTTGGAGAACCCAGACATCATGTCAAAATTTCTTTCAAGAAATGAGATCATCT 2401
DB 2477 TCATGTACAGCAACGAGAG-----GCAGGACGCGCGGAGCGCTGGGATCATCT 2527
OY 2402 TTTAAAAATGGGATGATTTACGCAAGATATGCTAACCTTCAATTAATTCGATTAATG 2461
DB 2528 TTAAAGAACGGGATGACCTCCGACAGACATGCTGACCTGCAAGATGATCCAGCTCATG 2587
OY 2462 AAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTTAACTTAATGATGATCTGCA 2521
DB 2588 ACCTCTGTGAGAGCAGAGGGGCTGAGCTGAGAGATGACCCCTATGCTGCTCTCCCA 2647

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OY 2522 TCGGTGACTGTGTGGACTTATGAGGTGTGAGAAATTCCTCACTATATATGACAGATTG 2581
DB 2648 CCGGGGACCGCACAGGCTTCATTTAGGTGTACTCCGTTGACAGACATGCCAACATCC 2707
OY 2582 A---GTGTAAGAGGCGCTGAAAGGTGCATGTGAGTTTACACGACACTGCATCAGT 2638
DB 2708 AACTCAACAAGACCAACATGGCAGCCACAGCCCTTCAACAGAGATGCCCTCTCAACT 2767
OY 2639 GGCTCAAGACCAAGAACAGGGGGAAATATATGATGCGGCTCATCTTTGTTACAGAT 2698
DB 2768 GGCTGAAGTCCAGAACCCGGGGAGGCCCTGATGAGGCAATTAGAGATTCACTCT 2827
OY 2699 CATGTCTGATATTTGTGTGCCACTTCACTTTGGGAATGGAGATGTCACAAATAGTA 2758
DB 2828 CCGTGTCTGATTTGTGTGGCCACATATGTGCTGGGCAATGGCGATGGGCAAGGAGCA 2887
OY 2759 ATATCATGTGTTAAGATGATGCACTGTTTATATGATTTTGGACACTTTTGGATC 2818
DB 2888 AACTCATGATCCGAGAGAGTGGCAGCTGTTCCATGATTTTGGCCACTTTCTGGGGA 2947
OY 2819 ACAAGAGAGAAAAATTTGGTTATTAACGAGAGCGCGTCCGTTGTTGACACAGATT 2878
DB 2948 ATTCAAGACCAAGTTTGGATATACCGGAGGCTGTCCATTCACTCACTATGACT 3007
OY 2879 TCTTAATAGTATTAAGTAAGAGCCCAAGATGCAAAAGACAGAAATTTGAGAGT 2938
DB 3008 TGTCCATGTGATTCAGCAGGG-----GAAAGCTAATAATGTAAGAAATTTGAAGGT 3061
OY 2939 TTCAGAGATGTGTTCACAGGCTTATCTAGTATTTGGCAGCATGCCAATCTTTATTA 2998
DB 3062 TCCGGGGCTACTGTGAAAGGGCTTACACCATCTGGGGGCGCCAGGCTTCTCTCTCC 3121
OY 2999 ATCTTTCTCAATGATGCTTGGCTGTGATGCGCAGACATGCAATCTTTGATGATTTG 3058
DB 3122 ACTCTTTCCTGATGCGGGGCGGAGGCTGCTTACGCTCTCCAAAGACATCC 3181
OY 3059 CATACATTCGAAAGACCTTAGCTTTAGATTAACCTGAGCAAGGCTTTGGAATTTGA 3118
DB 3182 ACTATCTCAAGACCTCCCTGGCAGCTGGGGAACAGAGGAGGAGTCACTGAAGCACTTCC 3241
OY 3119 TGAACCAATGATATGACACACATGTGGCTGCAACAAATATGATTTGATCTTCC 3178
DB 3242 GAGTGAAGTTTAAAGAGCCCTCCGTGAGAGCTGGAACCAAAAGTAACTGGCTGGCC 3301
OY 3179 ACA 3181
DB 3302 ACA 3304

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RESULT 6
US-10-027-591-1
; Sequence 1, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADDU, Chanchai et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/149,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p10delta complete cDNA
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (196)...(3327)
US-10-027-591-1
Query Match 10.5%; Score 336.2; DB 13; Length 5220;
Best Local Similarity 53.5%; Pred. No. 1,3e-77;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;
OY 1682 TCCCGAAATTTACCCAAATGCTTCTGCTTTAAATGGAACCTTAGAGTGAAGTATG 1741
DB 1820 TCCCGAGGCGGTAGCCCGGCTGCTCTGTCTACCAAGTGAACCAAGATGAGATGTG 1879
OY 1742 CTCAGATGATGCTTGTGTAAGATTAAGATTTGCTTCAATCAAGCTGAACAGGCTATGAGC 1801
DB 1880 CCGAGATGCTTCACTGCTGTGTCTCTGCGCGGAGCTGCCCTGCTGAGCCCTGAGC 1939
OY 1802 TTCTGACTGCAATTAACCAAGATCTATGCTTGAGAGTTTGTGCTGCTGCTTAA 1861
DB 1940 TGTATGACTTCAAGCTTCCCGATGGCAGTGAAGCTCTTCCCATCAAGTGGCTGCGA 1999
OY 1862 AATATTAAACAGATGCAAACTTCTCACTACTTAATGAGTGAAGTGAAGTGAAGT 1921
DB 2000 AAC---TGACGAGCGATGAGCTGTCTGATGATCTGTGAGCTGTGAGTGTCTCAAGT 2056
OY 1922 ATGAACAGTATTTGATTAACCTGCTTGTGAGATTTTAACTCAAAAAGGCTTAATAATC 1981
DB 2057 AGGAGTCTTACCTGAGCTGCGAGCTGACCAATTCCTGCTGAGACCGGCTGCGCAAC 2116
OY 1982 AAGGATCGGTACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGTTA 2041
DB 2117 GCAGATCGGCCCATCTTCTTCTGCACTCCGCTCCGAGATGACGCGCTGCTG 2176
OY 2042 GTGAGGTTTGGCTGCTTGTGAGTCTTATGCTGCTGAGTGTGAGTGTATGTAAC 2101
DB 2177 CCTGCGCTTCCGCTCATCTCTGAGGCTTACTGAGGCGGACCCACCAATGAAAG 2236
OY 2102 ACCTTAATAGGCAAGTTGAGGCTATGAGAAACCTCAATTACTGACTGATTTCTCAAC 2161
DB 2237 TGTGATGAGAGAGGAGGAGACCTGAGCAATCTGAGGCTTGAATGATCTGCTACAC 2296
OY 2162 AAGAGAGAGATGAACACAAAGGTACAGATGAAGTTTATGAGCAATGCGGC 2221
DB 2297 TGAGCTCTCAAGAACCCCAAGCCCAAGACCAAGAGGTATGACCTGTGATGCGGC 2356
OY 2222 GACCAATTTTCAATGATGCTCTCCAGGCTTCTGCTCTTAAACCTGCTCATAGC 2281
DB 2357 AGGAGGCTTACCTAAGGCGCTCTCCACCTGCACTGACCTGACCTGACCACTGAC 2416
OY 2282 TGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTTCTGCAAAAAGGCACTGTG 2341
DB 2417 TGGCTGAAGTCTGCTGAGAGCTGACCTTATGATGATCTCCAAAGTGAAGCCCTGTG 2476
OY 2342 TGAATTTGGAGAACCCAGACATCATGTCAAAATTAATCTTTTCAAGCAATGATCATCT 2401
DB 2477 TCATGTACAGCAACGAGAG-----GAGGAGGCGGGGCGAGCGTGGCATCATCT 2527
OY 2402 TTAATAATGGGATATTTAGCGCAAGATGTCTTAACCTTCAAGTTATTTGCAATTAAG 2461
DB 2528 TTAACAAAGGGATGACCTCCGCGAGCAATGCTTACCTGAGATGATTCAGCTCATG 2587
OY 2462 AAAATATCTGCGCAAAATCAAGGCTTGAATCTTCAATGATTAATGATGATGCTGTCAA 2521
DB 2588 AGCTCTGTGAGAGAGAGAGGAGGCTGAGCTGAGAGATTAACCTCTATGCTGCTGCCA 2647
OY 2522 TCGGTGACTGTGTGACTTATGAGGTGTGAGAAATTTTCACTAATATGACAGATTG 2581
DB 2648 CCGGGGACCGCACAGGCTCTCATATGAGTGTGATCCGTTCAAGACCAATGCGCAATCC 2707
OY 2582 A---GTGTAAGAGGCGCTGAAAGGTGCATGTGAGTTTACACGACACTGCATCAGT 2638
DB 2708 AACTCAACAAGACCAACATGGCAGCCACAGCCCTTCAACAGAGATGCCCTGCTCAACT 2767
OY 2639 GGCTCAAGACCAAGAACAGGGGGAAATATATGATGCGGCATGATTTGTTACAGAT 2698

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Db      2768  GGCCTAAAGTCCAAAGAACCCGGGAGGCGCTTGATGAGCCATTGAGAGTTCAACCTCT 2827
QY      2699  CATGTCGTGATATGTTGTTGACCTTCATTTTGGAAATGGAATGCTCAACAATAGTA 2758
Db      2828  CCTGTCGTGCTATGTTGTTGCGCAACATATGCTGGGCAATGCGCACAGCGACA 2887
QY      2759  ATATCATGCTTAAAGATGATGACCAACTGTTTATATATTTTGGACACTTTTGGATC 2818
Db      2888  ACATCATGATCCGAGAGATGGGCACTGTTCCACTATATTTTGGCACTTTTGGGGA 2947
QY      2819  ACAAGAAAGAAAAATTTGGTTTAAAGAGAGCGGCTTGTGTTGACACAGAT 2878
Db      2948  ATTTCAAGACCAAGTTTGAATCACCGAGCGTGTCCATTCATTCCTCACTATAGCT 3007
QY      2879  TCTTAATAGTATTAGTAAAGAGAGCCCAAGATGCAACAAAGAGAAATTTGAGAGT 2938
Db      3008  TTGTCATGATGATTCAGCAGGG-----GAAAGCTAATATATGAGAAATTTGAACGGT 3061
QY      2939  TTCAGAGATGTTTACAGGCTTATCTAGCTATTCGGCAGCATGCCAATCTCTCATTA 2998
Db      3062  TCCGGGGCTACTGTGAAGAGGCTACACCATCCGCGCGCCACGCGCTTCTCTCTCC 3121
QY      2999  ATCTTTTCTCAATGATGCTTGGCTCTGGAAATGCCAGAACTGCAATCTTTGATGATATG 3058
Db      3122  ACCTCTTTGCTGATGCTGGGCGGAGCGCTGCTGAGCTGAGCTGCTCCAAAGACATCC 3181
QY      3059  CATCATTCGAAAGACCTTGAATTAATTAACCTGACAGAGAGGCTTTGGAGTATTTCA 3118
Db      3182  AGTATCTCAAGAGCTCCCTGCGCACTGGGGAACAGAGAGAGGAGGCACTGAAAGCACTTCC 3241
QY      3119  TGAACCAATGATGATGACACCATGCTGCTGACACAAACAAATGATGATGATCTTCC 3178
Db      3242  GAGTGAAGTTTAAAGAAAGCCCTCGTGAAGCTGGAACCAAGTGAATGCTGGCCC 3301
QY      3179  ACA 3181
Db      3302  ACA 3304

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RESULT 7

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US-10-101-235A-3
; Sequence 3, Application US/10101235A
; Publication No. US2003018269A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyanangla V.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-235A-3

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Query Match          9.0%; Score 288.8; DB 12; Length 3342;
Best Local Similarity 54.0%; Pred. No. 3.4e-65;
Matches 757; Conservative 0; Mismatches 615; Indels 30; Gaps 7;

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QY      1793  CTATGAGCTTTGAGCTGCAATTAACCAATCCATATGTTGAGGTTTGGCTGCTGCT 1852
Db      1877  CATGCGAGCTCCGAGCTGCACTTCTCAAGATGAATGTAAGAGCCATTGCACTTCA 1936
QY      1853  GCTTGAATAATTTTAAAGATGACAAAGCTTCTCAGTACTTAATTCAGCTAGTACAG 1912
Db      1937  AACTGAGAGAGATGATGTTCTGCACTTAACCTTCTCAATTTGGTCCAG 1993

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QY      1913  TACTAAATATGAAACGATATTGGATTAACCTGCTTGAGATTTTACTCAAAAAGCGT 1972
Db      1994  CTGTGAATTTTGAACCATATCATTATAGCGCTTGGCAAGTTTCTGTGGAAGCTGCTT 2053
QY      1973  TAACTAATCAAGATGCTGCTACTTTTCTTTTGGCATTTAAATCTGAGAT--GCACA 2029
Db      2054  TAAGAAACAAAGAAATTTGCTCACTTTTGTGTTGGTTCTTGAAGATGAGATGCCAGT 2113
QY      2030  ATAAACAGTTAGTCAAGAGTTTGGCTTTTGGAGTCCATATGCTGATCCGTGCAATGGGA 2089
Db      2114  CCAAGACATATCAGCAGAGGTTGCTGTGATTTCTGAAGCCATATCTGAGGGGCTGGGA 2173
QY      2090  TGTATCTGAGACCTTATATAGCAAGTTGAGGCTATGGAAGGCTAATTAATTGACTG 2149
Db      2174  CAGCCATGCTGACAGCTTTTACCACCAAGCTCAAGTATGAGATGTTACAAAAGTCA 2233
QY      2150  ACATTTCTCAAGAGAGAAAGATGAACACAAAGGTACAGATGAAGTTTATGTTG 2209
Db      2234  CCTTGATATTAATGCTCTCTGCTGAAAGATATGAGTCAAGTCCCAAGTTATTTCA 2293
QY      2210  AGCAATGCGGCGACCAATTTATGATGCT-----CTCAGGCTTCTGTCTC 2260
Db      2294  AACTTAAACAAAAGCTTGAACCTGCAAGATTTCTCACTCCCGCAAGCTTTAGAGTTC 2353
QY      2261  CTCTAAACCTGCTCATACGCTGGAAATCTCAGGCTTGAAGTGTGCAATATGCTT 2320
Db      2354  CATATATCTGTGACTGAAAGAGAGCGCTGGCAATTAATAATTAATGTAATGGCT 2413
QY      2321  CTGCAAAAAGGCGCACTGTGGTTGATTTGGAGAACCCAGCATCATGTCAGATTACTCT 2380
Db      2414  CCAAGAAAACCACTATGCTTGAATTAATATGTCAGTCTTA--CAGCCCTATCAA 2470
QY      2381  TTCAGAACATGATGATCATCTTTAAATGAGGATGATTTAGGCAAGATATGCTAACCC 2440
Db      2471  ATGAACAAATTTGAATATCTTTAAACATGATGATGATCTGCGCCAAAGACATCTTATT 2530
QY      2441  TTCAGATTTATTCGATTAATGAAATATCTGCGCAAAATCAAGGCTTGAATGT 2500
Db      2531  TACAGATTTCAAGATATGATGAGCTATTTTGGAGACTGATCTTTGATCTATGCTCC 2590
QY      2501  TACCTTATGATGCTGTCAATGCTGACTGTGTGGACTTATGAGGTGAGAAAT 2560
Db      2591  TGCATATGCTTGAATTTCACTGTGACAAATAGSAGATGAGATTTGTGAAGACG 2650
QY      2561  CTCACACTATATCAGATTCAGTGAAGAGAGGCTTGAAGGCTGACAGTTTAA 2620
Db      2651  CCAGCAGATTTGCCAAATTCAGCAAGACAGTGGGCAACACGAG--CATTTAAAG 2707
QY      2621  GCCACACCTGCATCAGTGGCTCAAAAGACAGAAAC---AGGGGGAATATATGATGCGG 2677
Db      2708  ATGAAGTCTGAATCACAGCTCAAGAAAGAAATCCCTACTGAAGAAAGTTTCAAGCAG 2767
QY      2678  CCATGATTTGTTTACAGATCATGTGCTGATATTTGTGTGCACTTCAATTTGGAA 2737
Db      2768  CAGTGAAGAGTTGTTTATTTCTGTGAGGCTACTGTGTGCAACTTTGTTGGAA 2827
QY      2738  TTGAGATGCTCAAAATGATATATCATGTTTAAAGATGAGCAACTGTTTCAATATG 2797
Db      2828  TAGGGAGACAGACAAATGACATATATGATCACCGAGCAAGAACTATTTCAATATG 2887
QY      2798  ATTTGAGACCTTTTGGATCAACAAGAAAGAAATTTGGTTATTAAGAGCGCTGTC 2857
Db      2888  ACTCGGGGACATTTCTTGGAAATTCAAAGTTTCTGTGGCAATTAATAAGAGAGAGTCC 2947
QY      2858  CGTTTCTTTGACACAAGATTTCTTAATAGTATTAAGAGAGCCCAAGATGACAA 2917
Db      2948  CATTTGTCTAACCTCTGCTCTCTTTGTAT-----GGGAATCTGGAAGAGAA 3001
QY      2918  AGACAGAGAAATTTGAGAGTTTCAAGAGATGTTTAAAGGCTTATCTAGCTATTCGGC 2977
Db      3002  CAAGCCCACTTCCAGAAATTTCAAGGACATGTTGTTAAGGCTTATCTAGCCCTTGTGC 3061

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QY 2978 AGGATGGCAATCTTTCATATAATCTTTCATATGATGCTGGCTCGAATGCCAGAAC 3037
 DB 3062 ATACACAAACCTACTGATATATCTGTTCTCCAGATGCTGATGACGAGATGCCAGT 3121
 QY 3038 TGCATCTTTGATGATATGATGATACATTCGAAAGACCCCTAGCTTGTATTAACGTAGC 3097
 DB 3122 TAACAGCAAGAGACATGATGATATATTCGGGATGCCCTTCACAGTGGGAAAAATGAGG 3181
 QY 3098 AAGAGGCTTGGAGTATTTTCATGAAACMAATGATGATGACACATGCTGCTGACAA 3157
 DB 3182 AGGATGCTAAAGATATTTCTGATCAGATCGAAGTTTGACAGAACAAAGATGAGCTG 3241
 QY 3158 CAAAAATGATGATGATCTTCCA 3179
 DB 3242 TGCAGTTAATGTGTTCTTACA 3263

RESULT 8
 US-09-764-877-3796/c
 Sequence 3796, Application US/09764877
 Patent No. US20020147140A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PC005
 CURRENT APPLICATION NUMBER: US/09/764,877
 CURRENT FILING DATE: 2001-01-17
 Prior application data removed - refer to PALM or file wrapper
 NUMBER OF SEQ. ID NOS: 4031
 SOFTWARE: PatentIn Ver. 2.0
 SEQ. ID NO 3796
 LENGTH: 4074
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (1934)
 OTHER INFORMATION: n equals a,c,g, or c
 US-09-764-877-3796

Query Match 8.2%; Score 262.6; DB 10; Length 4074;
 Best Local Similarity 96.8%; Pred. No. 3,4e-58;
 Matches 268; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2931 TGAGAGTTTCAGAGATGTTTACAAAGGCTTATCTAGCTATTCGGAGACGCCAATCT 2990
 DB 3417 TTATAGTTTCAGAGATGTTTACAAAGGCTTATCTAGCTATTCGGAGACGCCAATCT 3358
 QY 2991 CTTCATTAATCTTTCTCATGATGCTTGGCTCGAATGCGAAGCTGCAATCTTTGA 3050
 DB 3357 CTTCATTAATCTTTCTCATGATGCTTGGCTCGAATGCGAAGCTGCAATCTTTGA 3298
 QY 3051 TGATATTCATGATGCTTGGAGAGCCCTAGCTTATGATTAACCTGAGCAAGGCTTTGA 3110
 DB 3297 TGCAATTCGATATGATGCTTGGAGAGCCCTAGCTTATGATTAACCTGAGCAAGGCTTTGA 3238
 QY 3111 GATATTCATGAACCAATGATGATGACACCATGCTGCTGAGCAACAAATGGAATTG 3170
 DB 3237 GATATTCATGAACCAATGATGATGACACCATGCTGCTGAGCAACAAATGGAATTG 3178
 QY 3171 GATCTTCACACATTAAGCAGCATCTTGAACCTGA 3207
 DB 3177 GATCTTCACACATTAAGCAGCATCTTGAACCTGA 3141

RESULT 9
 US-10-092-219-1
 Sequence 1, Application US/10092219
 Publication No. US20020115114A1
 GENERAL INFORMATION:
 APPLICANT: Domin, Jan
 TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
 FILE REFERENCE: 1064HG/50947

CURRENT APPLICATION NUMBER: US/10/092,219
 CURRENT FILING DATE: 2002-03-07
 PRIOR APPLICATION NUMBER: PCT/GB98/00244
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/355,160
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 9701652.1
 PRIOR FILING DATE: 1997-01-28
 NUMBER OF SEQ. ID NOS: 11
 SOFTWARE: PatentIn version 3.1
 SEQ. ID NO 1
 LENGTH: 5061
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(5058)
 OTHER INFORMATION:
 US-10-092-219-1

Query Match 6.8%; Score 218.4; DB 13; Length 5061;
 Best Local Similarity 49.2%; Pred. No. 1,9e-46;
 Matches 799; Conservative 0; Mismatches 786; Indels 39; Gaps 7;

QY 1577 ATGATTAAGAACAGCTCCGAGCAATTTGTACACAGATCCTCTATCTGAATCACTGAGC 1636
 DB 2609 ATATTAAGGAACCTCTTGATATTTCTTAAAGACATCACTTGACCTTTGAAG 2668
 QY 1637 AAGAGAAATTTTCTGTGAGGACACAGACATATTGTGAATATCCCGAAATCTAC 1696
 DB 2669 AAGATTAAGCTTTTATGAGGAGAAACGTTATATGCTCAACACCCAAATGCTTC 2728
 QY 1697 CCAATTTGCTCTGCTGTGTTAATGGAATCTAGATGATGATGATGATGATGATGATGAT 1756
 DB 2729 CTAAATATTTAGCAAGCCGCCCAACTGAAATGGGTAATCTTGCAAACTTACTCAT 2788
 QY 1757 TGGTAAAGATTGAGCTCCCAATCAAGCTGAAACAGGCTATGAGCTTCTGCACTGCAATT 1816
 DB 2789 TGCTTACAGAGGCGCTGATGTACCCCACTAATTCATTTGAACTTCTGATTTCAAAAT 2848
 QY 1817 ACCCAGATCTATGCTTGAAGTTTGTGCTTGTGCTGCTTGAAGAAATATTTAAGATG 1876
 DB 2849 TTGCTGATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2905
 QY 1877 ACAAACTTTCTAGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1936
 DB 2906 ATGAGCTAACAGATCTTCTTCAAGTTTGTCAAGCTTTGAAATATGAAATTTACTTGA 2965
 QY 1937 ATAACTGCTTGTGATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1996
 DB 2966 ATAGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 3025
 QY 1997 TTTCTTTTGGCAATTTAACTTGAATGACAAATAAACAGTTAGTCAGAGTTTGGCC 2056
 DB 3026 ATTTATATGCTTGTCAAAAGATGCTTCAATGATGATGATGATGATGATGATGATGATGATG 3085
 QY 2057 TCGTTTGGAGTCATATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2116
 DB 3086 ATGTTTGG-----GTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3137
 QY 2117 TTGAGGCTTGTGAAAGCTCAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 2176
 DB 3138 TCTAAACAGAGAACTTTGACGCTTTTGAAGAGATGATGATGATGATGATGATGATGATGATG 3197
 QY 2177 AAACAAAGGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
 DB 3198 TAGTGATCAGCAGCAGAGTGTCTCCAAAGAA- GATGAGAGAGATGATGATGATGATGATG 3256
 QY 2237 ATGCTCTCCAGGCTTTCTGTCTCTTAAACCTGCTCTCATAGCTGGGAAATCTCAGGC 2296
 DB 3257 TTCAGAAAAATTAATGCGCTCTCTCAAGCCCAAGCTAGTGGCAAAAGATTAATA 3316
 QY 2297 TTGAAGATGCTGATTAATGCTTCTGCAAAAGCCACTGTGTTGAATGGAGAAC 2356


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QY 2277 TCAGCTGGGAAATCTCAGGCTTGAAAGGTGCGAATTAATGCTTCTGCAAAAAGGCCACT 2336
Db 2936 GTGCGTAAAGAAATGATGCGGATGCATGTTCAATTTTCAATCATATGCGCTTGCCATT 2995
QY 2337 GTGGTGAATTTGGAGAAACCCAGCATCATGTCAGAAATTAATCTTTGAGAAACATGAGAT 2396
Db 2996 GAAGATCACTT-----TCATCAATGCTAAATCCAAATGG3CAAAAATATACAGTGT 3043
QY 2397 CATCTTTAAATATGGGATGATTTACGGCAAGATATGCTAAACCTTCAGATTATTCGCAT 2456
Db 3044 TATTTTAAAGCCGCGCAAGATCTTCGCGAAGATATGCTTCTTGCAATTAATTCAGAT 3103
QY 2457 TATGAAAATATATGCGAAATCAAGGCTTGATCTTCAATGTTTACCTTATGAGATGCT 2516
Db 3104 GATGSAACAAAGTGTGCTTCAAGAGGCTTCGATATCAATATGATTCATTATGATGCTCT 3163
QY 2517 GTCAATCGGTGACGTGTGGGACTTATCGAGGTGTGAGAAATTTTCAACTATATATGCA 2576
Db 3164 AGCCACAGAAAGGCTCAAGGATTCATAGAGATGTGCTGATGCTTAAACGCTTGCCAA 3223
QY 2577 GATTAGATTAAGAGAGGCTGAAAGGTGCACTGCACTTTAAACGCCACACTCCATCA 2636
Db 3224 GATTCATCTGCACTCTGCGCTGATAGAACCTCTGAAAGAAACCATCA--AGAAATG 3280
QY 2637 GTGGCTCAAGACAAAGCAAGAGGGGAAATATATGATGCGGCATTCGATTTGTTACAG 2696
Db 3281 GTTCAGTCAACACACACTTAAAGAAATATAGAAAGGCTTGAGAACTTTT 3340
QY 2697 ATATATGCTGATATTTGTTGTCACCTTCAATTTTGGAAATGGAGATGTCACAAATAG 2756
Db 3341 CTCTTGCTGCGGTGCTGTGTGTGATTCATCTTGGGAGTGTATACCGAATATATGA 3400
QY 2757 TAATATCATGTTAAAGATGATGACAACTGTTTCAATATGATTTTGGACATTTTGA 2816
Db 3401 CAATATCATCTGCAAAAGTCAAGCCACATGTTTCAATATGATTTGGAATTTCTTG 3460
QY 2817 TCACAAAGAAATAATTTGGTTATTAACGAGAGCGGCTGCTTTGTTGACACAGA 2876
Db 3461 TCAGCGCAAAACATTTGGCGGTATTAAGAGAGCGGCTTTCATTTTACTTCAGA 3520
QY 2877 TTTCTTATATGATATATTAAGAGAGCCCAAGAAATGCAAAAGCAAGAAATTTGAGAG 2936
Db 3521 GATGAGTACTTATTAACGAGAGGTG-----GGAAAAACACAGCATTTTCAAGA 3571
QY 2937 GTTTCAGAGATGTTTACAGGCTTATAGCTATTCGCGCAGATGCCAATCTTTCAT 2996
Db 3572 CTTCGTGGAACCTGCTGCGAGAGCTTAACAACATTTGAGGAAGCACAGCACTGCTCCT 3631
QY 2997 AATCTTTTCTCAATGATGCTTGGCTCTGGAATGCGCAACTGCAATCTTTGATGATAT 3056
Db 3632 GAGCCTTCTTAAGAAATATGATGCTGATGCGGCTTCCGAGCTAGGGGGAATTAAGACCT 3691
QY 3057 TGCATATCAATTCGAAAGACCTTACCTTTAGATTAACCTGAGCAAGGCTTTGAGATATTT 3116
Db 3692 GAATATCGTACAGACATCTCCGCGCAAGACACAGACTGGAAGCCCAAGATCATTT 3751
QY 3117 CATGAACCAATGAA 3131
Db 3752 TACCAAGAAATATAA 3766

```

RESULT 11

US-10-101-235A-5

Sequence 5, Application US/10101235A

Publication No. US20030182669A1

GENERAL INFORMATION:

APPLICANT: Rockman, Howard A.

APPLICANT: Naga Prasad, Sathyamangla V.

APPLICANT: Laporte, Stephanie A.

APPLICANT: Barak, Larry S.

APPLICANT: Caron, Marc G.

TITLE OF INVENTION: Phosphoinositide 3-kinase Mediated inhibition of GPCRs

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; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-101-235A-5

```

Query Match 5.2%; Score 167; DB 12; Length 3237;

Best Local Similarity 52.7%; Pred. No. 5.9e-33;

Matches 510; Conservative 0; Mismatches 433; Indels 24; Gaps 6;

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QY 1793 CTATGAGCTTCTGAGCTGCAATTAACCAATCCATGCTTATGCAAGTTTGTCTGCT 1852
Db 1877 CAATGACGCTCGAGCTGCACTTCTCAGATAAATGTAAGAGCCATTGCAAGTTTCA 1936
QY 1853 GCTTAGAAATATTTAACAGATGACAACTTCTCAGTACTTAATTCAGCTAGTACAGG 1912
Db 1937 AACTGAGAG--GCTTGAGAGAGAGATGATTTCTGATTAATCTTCAATTTGTCAGG 1993
QY 1913 TACTAAATATGAAAGATTTTGAATTAACCTGCTGTGAGATTTTACTCAAAAAGCGT 1972
Db 1994 CTGTGAATTTGAACCATACATGATAGCGCCTTCCAGATTTCTGCTGAAGCGTGT 2053
QY 1973 TAATCAATCAAAAGATCGGTCATTTTCTTTTGGCATTTAAATCTGAGAT--GCACA 2029
Db 2054 TAAGAAACAAAMAAATTTGGTCACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2113
QY 2030 ATAAACAGTTAGTACAGAGTTTGGCTGCTTGTGAGTCTTATGCGGCTGATGAGGA 2089
Db 2114 CCAGACATATCAGCAGAGGTTGCTGTATTTCTGAAGCTTATCTGAAGGCTGTGCGCA 2173
QY 2090 TGTATGAGACACCTTAATAGGCAAGTTGAGGCTATGAAAAAGTCATTAACCTGACTG 2149
Db 2174 CAGCAGATGCGACGACCTTAAACCAAGTCCAGATTAAGATGTTTCAAAAAGTCA 2233
QY 2150 ACATTTCTCAACAGAGAAAGAGATGAAACACAAAAGTACAGATGAAATTTTGTGTTG 2209
Db 2234 CCCTTATATTAATATGCTCTCTGCTGAAAGATGACGTCAGTCCCAAGTATTTTAC 2293
QY 2210 AGCAATGCGGCGACAGATTTTCATGATGCT-----CTCCAGGCTTCTGCTC 2260
Db 2294 AACTTAAACAAAGCTTTGAAACCTTCAGATTTCTCAACTCCCGCAAGCTTTAGGCTTC 2353
QY 2261 CTCTAAACCTGCTCATCAGCTGGAATCTCAGGCTTGAAGATGTCGATATATGCTTT 2320
Db 2354 CATATGATCTGAGCTGAAAGCAGAGCGCTGCAATTAAGAAATGTAAGTATGCGCT 2413
QY 2321 CTGCAAAAAGGCGACCTGTGTTGAATTTGGAGAACCCAGACATCATGTCAGAAATTA 2380
Db 2414 CCAGGAAAAAACCATATGCTTGAATTAATGTCGATCTCA--CAGCCCTATCA 2470
QY 2381 TTGAGAACATGATGATCATCTTTAAATAGGGAGTATTTAGGCAAGATATGCTAACCC 2440
Db 2471 ATGAACCAATTTGAATTAATTTTAAACATGATGATATCTGCGCAAGACATGCTTATTT 2530
QY 2441 TTCAGATTATTCGATTAAGAAATATCTGCAAAATCAAGGCTTGTGAATCTTGAATGT 2500
Db 2531 TACAGATTTCAAGAAATCATGAGATTAATTTGGAGACTGAATCTTTGATTAATGCTCC 2590
QY 2501 TACCTTAAGAGATGCTGTAATGCTGCTGTGTGAGCTTATGAGGTGTGAGAAATTT 2560
Db 2591 TGCATATGATGCTGATTAACCTGCGCAAAAATAGAAATGATGAGATTTGTAAGAGAG 2650
QY 2561 CTCACACTATATGAGATTCAGATTCAGTGAAGAGGCTGAAAGGTGACGAGTTTAAACA 2620
Db 2651 CCAGCAATTTGCAAAATTTGCAAGAGCAGTGTGGCAACGGGA---GCAATTTAAAG 2707
QY 2621 GCCACACTTCATCAGTGTCTCAAGACAGAAC---AAGGGGAAATATATGATGCGG 2677

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Db 2708 ATGAAGTCTGAACTACTGCTCAAGAAAAATCCCTACTGAAGAAAGTTTCAGGAG 2767
Oy 2678 CCATGATTTGTTTACACGATTCATGCTGGAATATGTTGTCACCTTCATTGGA 2737
Db 2768 CAGTGGAGAAATTTGTTATTTCTGTCGACGCTACTGTGGAACTTTGTTGAA 2827
Oy 2738 TTGGAGA 2744
Db 2828 TAGGCGA 2834

RESULT 12
US-09-814-353-21472
; Sequence 21472, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21472
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1018, 1019, 1020
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21472

Query Match 5.2%; Score 165.4; DB 12; Length 1020;
Best Local Similarity 88.6%; Pred. No. 7.4e-33;
Matches 203; Conservative 0; Mismatches 21; Indels 5; Gaps 2;

Oy 2933 AGAGGTTTCAGAGATGTTCTTCAAGGCTTATCTAGCTATTTGGAGAGATGGCAATCT 2992
Db 666 ATAGGTTTCAGAGATGTTCTTCAAGGCTTATCTAGCTATTTGGAGAGATGGCAATCT 725
Oy 2993 TCATAAATCTTTCT-CATGATGCTGCTCTGGAATCCGAACTGCAATCTTTTGT 3051
Db 726 TCATAAATCTTTCTTCCAGAGATGCTGGGTTCTGGAATCCGAACTGCAATCTTTGAT 785
Oy 3052 GATATTCATACATTCGAAAGACCCCTAGCTTAGATTAATACTGAGCAAGGCTTTGGAG 3111
Db 786 GACATTCGATACATTCGAAAGACCCCTAGCTTAGAT----CTGAGAGAGAGGCTTTGAAG 841
Oy 3112 TATTTTCAGAAACAAATGATGATGACACCATGATGCTGACACAA 3160
Db 842 TATTCATGAAACCAATGATGATGACACCATGATGAGGAGGCTGGCCACCA 890

RESULT 13
US-10-027-632-213996
; Sequence 213996, Application US/10027632

; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213996
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213996

Query Match 5.0%; Score 159.8; DB 12; Length 1248;
Best Local Similarity 86.7%; Pred. No. 2.6e-31;
Matches 176; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Oy 1987 ATCGTCACCTTTCTTTTGGCATTTAAATCTGAGATGCAATTAACAGTTAGTCAG 2046
Db 751 ATTTTCTAATTTGATGATCTTTAGATCTGAGATGCAATTAACAGTTAGTCAG 810
Oy 2047 AGCTTGGCTGCTTTTGGAGTCTTATGCGGATGCGGATGATCTGAGCAGCTT 2106
Db 811 AGTTTGGCTGCTTTTGGAGTCTTATGCTGATGCGGATGATCTGAGCAGCTT 870
Oy 2107 AATAGCAAGTTGAGGCTATGAAAGCTCATTAATTGACTGACATTTCTCAACAGAG 2166
Db 871 AATAGCAAGTTGAGGCTATGAAAGCTCATTAATTGACTGACATTTCTCAACAGAG 930
Oy 2167 AAGAAGATGAACACAAAGGT 2189
Db 931 AAGAAGATGAACACAAAGTT 953

RESULT 14
US-10-027-632-213996
; Sequence 213996, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 213996
LENGTH: 1248
TYPE: DNA
ORGANISM: Human
US-10-027-632-213996

Query Match 5.0%; Score 159.8; DB 13; Length 1248;
Best Local Similarity 86.7%; Pred. No. 2.5e-31;
Matches 176; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1987 ATCGTCACCTTTCTTTGGCATTTAAATCTGAGTGCACATTAACAGTTAGTCAG 2046
DB 751 ATTTTCTAATTTTGATGATTTCTTTAGATCTGAGATGCACATTAACACTTAGCCAG 810
QY 2047 AGGTTGGCCTGCTTTTGGAGTCTTATGGCCGTCATGGGATGTATCTGAAGCACCTT 2106
DB 811 AGGTTGGCCTGCTTTTGGAGTCTTATGGCCGTCATGGGATGTATTTGAAGCACCTG 870
QY 2107 AATAGGCAAGTGTAGGCTATGAAAGCTGATTACTGACATCTTCAACAAAGAG 2166
DB 871 AATAGGCAAGTGTAGGCAATGAAAGCTGATTACTGACATCTTCAACAAAGAG 930
QY 2167 AAGAAGATGAACACAAAAGT 2189
DB 931 AAGAAGATGAACACAAAAGT 953

RESULT 15
US-09-878-178-229
Sequence 229, Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 229
LENGTH: 167
TYPE: DNA
ORGANISM: Homo sapien
US-09-878-178-229

Query Match 4.6%; Score 147.2; DB 10; Length 167;
Best Local Similarity 98.0%; Pred. No. 1.5e-28;
Matches 149; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1358 AAGATTGCTGAACCTATATGTTACTGATCAATCAATTAAGAACTCCATGTT 1417
DB 16 AAGATTGCTGAACCTATATGTTACTGATCAATCAATTAAGAACTCCATGCT 75
QY 1418 TAGAGTTGAGTTGACTGTTGACGAGTGTGTTAAAGTTCCAGATATGTCAGTATTG 1477
DB 76 TAGAGTTGAGTTGACTGTTGACGAGTGTGTTAAAGTTCCAGATATGTCAGTATTG 135
QY 1478 AAGAAGATGCCAATTTGCTGTATCCCGTGA 1509
DB 136 AAGAAGATGCCAATTTGCTGTATCCCGAAGAA 167

Search completed: November 7, 2003, 13:39:18
Job time : 670.362 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:38:38 ; Search time 145.839 Seconds
(without alignments)
9706.030 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207
Sequence: 1 ATGCTTCAAGACCATCATC.....AGCAGATGCTTGAACCTGA 3207

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/prodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUTUS_COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3207	100.0	3207	1	US-08-162-081B-35
2	3207	100.0	3207	2	US-08-780-872-35
3	3207	100.0	3207	3	US-09-085-957-35
4	3011.8	93.9	3240	1	US-08-162-081B-34
5	3011.8	93.9	3240	2	US-08-780-872-34
6	3011.8	93.9	3240	3	US-09-085-957-34
7	3008.6	93.8	3412	1	US-08-162-081B-32
8	3008.6	93.8	3412	2	US-08-780-872-32
9	3008.6	93.8	3412	3	US-09-085-957-32
10	448.2	14.0	3213	3	US-09-392-350-1
11	336.2	10.5	3387	4	US-09-194-640A-2
12	336.2	10.5	3387	3	US-09-357-070-1
13	336.2	10.5	5220	2	US-08-777-405A-1
14	336.2	10.5	5220	2	US-08-977-871A-1
15	336.2	10.5	5220	2	US-09-225-951-1
16	336.2	10.5	5220	4	US-08-941-341-1
17	288.8	9.0	5162	2	US-08-916-917-13
18	288.8	9.0	5162	3	US-08-916-917-13
19	285	8.9	4134	2	US-08-817-090B-1
20	285	8.9	4137	2	US-08-817-090B-3
21	277.6	8.7	3808	2	US-08-916-917-3
22	277.6	8.7	3808	2	US-08-972-631-3
23	277.6	8.7	3808	2	US-08-972-629-3
24	277.6	8.7	3808	2	US-08-972-630-3
25	277.6	8.7	3808	2	US-08-672-211-3
26	277.6	8.7	3808	2	US-08-672-211-3
27	224.8	7.0	5285	2	US-08-609-049A-29

28	224.8	7.0	5285	3	US-09-170-996-29	Sequence 29, Appl
29	218.4	6.8	5061	4	US-09-355-160D-1	Sequence 1, Appl
30	146.4	4.6	3504	3	US-08-857-076-47	Sequence 47, Appl
31	111.8	3.5	6831	2	US-08-609-049A-27	Sequence 27, Appl
32	111.8	3.5	6831	3	US-09-170-996-27	Sequence 27, Appl
33	108.6	3.4	393	1	US-08-162-081B-40	Sequence 40, Appl
34	108.6	3.4	393	2	US-08-780-872-40	Sequence 40, Appl
35	108.6	3.4	393	3	US-09-085-957-40	Sequence 40, Appl
36	85.4	2.7	357	4	US-09-765-298A-13	Sequence 13, Appl
37	68.6	2.1	204	4	US-09-016-434-245	Sequence 245, App
38	66	2.1	222	4	US-09-016-434-525	Sequence 525, App
39	62.2	1.9	3063	4	US-09-620-312D-474	Sequence 474, App
40	62.2	1.9	3252	3	US-09-118-442-1	Sequence 1, Appl
41	62.2	1.9	3252	3	US-09-677-064-1	Sequence 1, Appl
42	48	1.5	381	1	US-08-162-081B-38	Sequence 38, Appl
43	48	1.5	381	2	US-08-780-872-38	Sequence 38, Appl
44	48	1.5	381	3	US-09-085-957-38	Sequence 38, Appl
45	45.2	1.4	277	4	US-09-313-294A-6757	Sequence 6757, Ap

ALIGNMENTS

RESULT 1
US-08-162-081B-35
Sequence 35, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hites, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Panayotov, George; Volinla,
APPLICANT: Stepan, Gou, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OR INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162, 081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
LUD 5256
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-35

Query Match 100.0%, Score 3207, DB 1, Length 3207,
Best Local Similarity 100.0%, Pred. No. 0,
Matches 3207, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

OY		1	ATGCTTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCTCACTTAATGCCCCCAAAGAATC	60
Db		1	ATGCCTTCGAAGACCATCATCAGGTGAACCTGTGGGGCATCTCACTTAATGCCCCCAAAGAATC	60
OY		61	CTGTAGAAATGTTTACTTACCAATGGGAGATAGTGACCTTTAGAAATGCGTCCGTAGGCT	120
Db		61	CTAGTAGAAATGTTTACTTACCAATGGGAGATAGTGACCTTTAGAAATGCGTCCGTAGGCT	120
OY		121	ACGTTAATAAGATTAAGACATGACTATTAAAAGAACAAAGAAAAATCCCTCTCATCAA	180
Db		121	ACGTTAATAAGATTAAGATGAATTAATTAAGAAACAAGAAAAATACCTCTCATCAA	180
OY		181	CTTCTTCAGATGAATCTTTACATTTTCTGAAGTTCACCAAGAACCAAGAGGAA	240
Db		181	CTTCTTCAGATGAATCTTTACATTTTCTGAAGTTCACCAAGAACCAAGAGGAA	240
OY		241	GAATTTTTGTATGTAAGAAACAAGCACTTGTGACCTTCGGCTTTTGAACCTTTTAAAA	300
Db		241	GAATTTTTGTATGTAAGAAACAAGCACTTGTGACCTTTCGGCTTTTGAACCTTTTAAAA	300
OY		301	GTAATTGAAACAGTAGGCAACCCGTGAAGAAAGATCCTCAATCAGAAAAATGGTTTGGT	360
Db		301	GTAATTGAAACAGTAGGCAACCCGTGAAGAAAGATCCTCAATGAGAAAAATGGTTTGGT	360
OY		361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCAAAGATACAGACCTTCGGA	420
Db		361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCAAAGATACAGACCTTCGGA	420
OY		421	AGAAATATTCCTCAATGTTTGTAAAGAAAGCTGTGATCTTGAAGGATCTTAATTCACCTCAT	480
Db		421	AGAAATATTCCTCAATGTTTGTAAAGAAAGCTGTGATCTTGAAGGATCTTAATTCACCTCAT	480
OY		481	AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAAATCTTCACAGAACTGCCAAAGCAC	540
Db		481	AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAAATCTTCACAGAACTGCCAAAGCAC	540
OY		541	ATAATATTAATTAATGATGAATAAGGGCAATAATTAATGTGTGATTTGGGTAATAGTTTCCCA	600
Db		541	ATAATATTAATTAATGATGAATAAGGGCAATAATTAATGTGTGATTTGGGTAATAGTTTCCCA	600
OY		601	AATAATGACAAACAGAAATPACTCTGAATAATCAACATGACTGTGTCCAGAACAAAGTA	660
Db		601	AATAATGACAAACAGAAATPACTCTGAATAATCAACATGACTGTGTCCAGAACAAAGTA	660
OY		661	ATTGTGGAAGCAATCAGMAAAAAAACTCGAAGTATGTTGCTATCATCTGAAACAATPAAA	720
Db		661	ATTGTGGAAGCAATCAGMAAAAAAACTCGAAGTATGTTGCTATCATCTGAAACAATPAAA	720
OY		721	CTCTGTGTTTGAATATACAGGGCAAGTATTTTAAAGGTGTGAGTGAATAC	780
Db		721	CTCTGTGTTTGAATATACAGGGCAAGTATTTTAAAGGTGTGAGTGAATAC	780
OY		781	TTCCTTGAAGAAAAATATCCTCTGAGTCAGTATTAAGTATTAAGAAGCTGTATTAATGCTTGGG	840
Db		781	TTCCTTGAAGAAAAATATCCTCTGAGTCAGTATTAAGTATTAAGAAGCTGTATTAATGCTTGGG	840
OY		841	AGGATGCCCAATTTTGAATGCTGATGCTTAAGAAAGACCTTATTTCTCAACTGCCAATGAC	900
Db		841	AGGATGCCCAATTTTGAATGCTGATGCTTAAGAAAGACCTTATTTCTCAACTGCCAATGAC	900
OY		901	TGTTTTCATGATGCATCATATTCACAGCCATCTCCAGAGTACGCCATATATGATGGA	960
Db		901	TGTTTTCATGATGCATCATATTCACAGCCATCTCCAGAGTACGCCATATATGATGGA	960
OY		961	GAAACATCTACAAATATCCCTTTGGGTTATTAATAGTGCATCAGAAATAAAATCTTTGGT	1020
Db		961	GAAACATCTACAAATATCCCTTTGGGTTATTAATAGTGCATCAGAAATAAAATCTTTGGT	1020
OY		1021	GCAACCTATGTGAATGTAAATATTTGAGACATTTGACAGATTTATGTTTGAACAGGTATC	1080
Db		1021	GCAACCTATGTGAATGTAAATATTTGAGACATTTGACAGATTTATGTTTGAACAGGTATC	1080
OY		1081	TACCATGAGAGAAACCCCTTATGTGTATATGTGAACAACCTCAAGAGTACCTTGTCCAAAT	1140

Db	1081	TACCATGAGAGAAACCCCTTATGTATATGAAACCTCAAAAGATACCTTGTCCAAAT	1140
Qy	1141	CCGAGGTGAAATGAATGGCTGAATTAACGATATATACATTCCTCGATCTTCTGTGCTGCT	1200
Db	1141	CCGAGGTGAAATGAATGGCTGAATTAACGATATATACATTCCTCGATCTTCTGTGCTGCT	1200
Qy	1201	CGACTTTGGCTTTCCATTTGTTCTGTAAAGCCGAAAGGGTGTAAAGAGAAACACTGT	1260
Db	1201	CGACTTTGGCTTTCCATTTGTTCTGTAAAGCCGAAAGGGTGTAAAGAGAAACACTGT	1260
Qy	1261	CCATTGGCCCTGGGAAATATAAACCCTTGTTGATTTACACGATACCTGTATCTCGAAAAA	1320
Db	1261	CCATTGGCCCTGGGAAATATAAACCCTTGTTGATTTACACGATACCTGTATCTCGAAAAA	1320
Qy	1321	ATGGCTTGAATCTTTGGCCAGACACTCATGACATGAAAGATTTGGTGAACCTATTTGGT	1380
Db	1321	ATGGCTTGAATCTTTGGCCAGACACTCATGACATGAAAGATTTGGTGAACCTATTTGGT	1380
Qy	1381	GTTACTGATCAAAATCCAAATTAAGAAACCTCATGTTTAAAGTTGAGTTTGACTGGTTTC	1440
Db	1381	GTTACTGATCAAAATCCAAATTAAGAAACCTCATGTTTAAAGTTGAGTTTGACTGGTTTC	1440
Qy	1441	AGCAGTGTGTAAGTTTCCAGATATGTCAAGTATTAAGAGAGATGCCAATTGGTCTGTA	1500
Db	1441	AGCAGTGTGTAAGTTTCCAGATATGTCAAGTATTAAGAGAGATGCCAATTGGTCTGTA	1500
Qy	1501	TCCCGGTGAAGAGATTAGTTTATTCCTCATGACAGACTGAGTAACAGACTAGCTAGACAC	1560
Db	1501	TCCCGGTGAAGAGATTAGTTTATTCCTCATGACAGACTGAGTAACAGACTAGCTAGACAC	1560
Qy	1561	AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACAGCAATTCCTCTA	1620
Db	1561	AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACAGCAATTCCTCTA	1620
Qy	1621	TCTGAATCACTGACGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTTGTGTAAT	1680
Db	1621	TCTGAATCACTGACGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTTGTGTAAT	1680
Qy	1681	ATCCCGGAAATTTACCCCAATTTGCTCTGTGTTAAATGAACTGTAGAGATGAAGTA	1740
Db	1681	ATCCCGGAAATTTACCCCAATTTGCTCTGTGTTAAATGAACTGTAGAGATGAAGTA	1740
Qy	1741	GCTCAGATGTACTGCTTGTGTAAGAAAGATTTGGCTTCCAATCAAGCCTGAACAGGCTATGGAG	1800
Db	1741	GCTCAGATGTACTGCTTGTGTAAGAAAGATTTGGCTTCCAATCAAGCCTGAACAGGCTATGGAG	1800
Qy	1801	CTTTGGAAGTGAATTAACCGAGATTCCTATGTTTGAAGGTTTGGTGTGGTGTGTAAGAA	1860
Db	1801	CTTTGGAAGTGAATTAACCGAGATTCCTATGTTTGAAGGTTTGGTGTGGTGTGTAAGAA	1860
Qy	1861	AAATATTTAAGAGATGACAAACTTCTCAGTACCTAAATTCAGTATGACAGTACTAAAA	1920
Db	1861	AAATATTTAAGAGATGACAAACTTCTCAGTACCTAAATTCAGTATGACAGTACTAAAA	1920
Qy	1921	TATGAACAGTATTTGAGTAACTGCTGTGAGATTTTATCTCAAAAAAGCCTTAACTAAT	1980
Db	1921	TATGAACAGTATTTGAGTAACTGCTGTGAGATTTTATCTCAAAAAAGCCTTAACTAAT	1980
Qy	1981	CAAAAGATGCTGACTTTTCTTTTGGCATTTAAATCTGAGAGGCAATTAATAACAGTT	2040
Db	1981	CAAAAGATGCTGACTTTTCTTTTGGCATTTAAATCTGAGAGGCAATTAATAACAGTT	2040
Qy	2041	AGTCAAGGTTTGGCTGCTTTTGGAGTCCATTTGCGGTGATGAGGATGTATCTGAAG	2100
Db	2041	AGTCAAGGTTTGGCTGCTTTTGGAGTCCATTTGCGGTGATGAGGATGTATCTGAAG	2100
Qy	2101	CACCTTAATAGGCAATGAGCTATGAAAAAGCTCATTAATTAAGTACATGCAATTCCTCAAA	2160
Db	2101	CACCTTAATAGGCAATGAGCTATGAAAAAGCTCATTAATTAAGTACATGCAATTCCTCAAA	2160
Qy	2161	CAGAGAGAGAGATGAACCAAAAGGTACAGATGAAGTTTATGTTGAGCAATGGGG	2220
Db	2161	CAGAGAGAGAGATGAACCAAAAGGTACAGATGAAGTTTATGTTGAGCAATGGGG	2220

2161 CAAGAGAAAGAGATGAAACACAAAAGCTACAGATGAAGTTTGTAGTGACAAATGCGG 2220
2221 CGACCAATTTTCATGATGCTCTCCAGGGGCTTTCTGCTCTCTAAACCTGCTCATCAG 2280
2222 CGACCAATTTTCATGATGCTCTCCAGGGGCTTTCTGCTCTCTAAACCTGCTCATCAG 2280
2281 CTGGGAAATCTCAGGCTTGAAAGGTGCTCAATTAATGCTTTCTGCAAAAAGGCACTGTGG 2340
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2341 TTGAATTTGGAGAACCCAGACATCATGTAGAAATTTCTTTTCAAAAATGATGATC 2400
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2461 GAAAATATCTGGCAAAATCAAGGCTTTGATCTTCAATGTTACCTTAATGATGCTGCA 2520
2461 GAAAATATCTGGCAAAATCAAGGCTTTGATCTTCAATGTTACCTTAATGATGCTGCA 2520
2521 ATCGGTGACTGTGGGACTTATCGAGGTGTGAGAAATTTCTCACTAATATGAGATT 2580
2521 ATCGGTGACTGTGGGACTTATCGAGGTGTGAGAAATTTCTCACTAATATGAGATT 2580
2581 CAGGTGAAAGAGAGGCTGAAAGGTGATGAGTTTAAAGCCACATCTCATGATGAG 2640
2581 CAGGTGAAAGAGAGGCTGAAAGGTGATGAGTTTAAAGCCACATCTCATGATGAG 2640
2581 CAGGTGAAAGAGAGGCTGAAAGGTGATGAGTTTAAAGCCACATCTCATGATGAG 2640
2581 CAGGTGAAAGAGAGGCTGAAAGGTGATGAGTTTAAAGCCACATCTCATGATGAG 2640
2641 CTCAAAAGACAAAGCAAGGGGAAATATATGATGCGGCAATGATTTGTTTACAGATCA 2700
2641 CTCAAAAGACAAAGCAAGGGGAAATATATGATGCGGCAATGATTTGTTTACAGATCA 2700
2701 TGTGCTGATATGTTGTGCTCACTTCAATTTTGGGAATTTGGAGATTTGATTAAT 2760
2701 TGTGCTGATATGTTGTGCTCACTTCAATTTTGGGAATTTGGAGATTTGATTAAT 2760
2761 ATCATGTTTAAAGATGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATCAG 2820
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2821 AAGAAAGAAAAATTTGGTTATTAAGAGAGCGGCTCCGTTGTTTGAACAAGATTTT 2880
2821 AAGAAAGAAAAATTTGGTTATTAAGAGAGCGGCTCCGTTGTTTGAACAAGATTTT 2880
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2941 CAGAGATGTTTAAAGGCTTATCTAGGCTATTCGCGAGATGCCAATCTTCAATTAAT 3000
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2941 CAGAGATGTTTAAAGGCTTATCTAGGCTATTCGCGAGATGCCAATCTTCAATTAAT 3000
3001 CTTTCTCAATGATGCTTGTGCTTGTGAATGCCAATCTTCAATCTTTTGAATTAATGCA 3060
3001 CTTTCTCAATGATGCTTGTGCTTGTGAATGCCAATCTTCAATCTTTTGAATTAATGCA 3060
3061 TACATTTGAAAGACCTTACCTTTAATTAATGAGCAAGAGGCTTTGAGATTTTCAATG 3120
3061 TACATTTGAAAGACCTTACCTTTAATTAATGAGCAAGAGGCTTTGAGATTTTCAATG 3120
3121 AAACAAATGATGATGACACCATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
3121 AAACAAATGATGATGACACCATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
3181 ACAATTAAGCAGATGCTTTGAATGCA 3207
3181 ACAATTAAGCAGATGCTTTGAATGCA 3207

RESULT 2
US-08-780-872-35

Sequence 35, Application US/08780872
Patent No. 5846824
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Olen, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-780-872-35
Query Match 100.0%; Score 3207; DB 2; Length 3207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3207; Mismatches 0; Indels 0; Gaps 0;
1 ATGCCTCCAAAGCCATCATCAGTGAATCTGGGGCATCCATTGATGCCCAAGATC 60
1 ATGCCTCCAAAGCCATCATCAGTGAATCTGGGGCATCCATTGATGCCCAAGATC 60
61 CTAGTAGAATGTTTACTACCAATGGATGATGATGATGATGATGATGATGATGATGATGATG 120
61 CTAGTAGAATGTTTACTACCAATGGATGATGATGATGATGATGATGATGATGATGATGATG 120
121 ACGTTAATTAACGATTAAGCATTAATTAATTAAGCAAGAAATATCCCTCTCATCA 180
121 ACGTTAATTAACGATTAAGCATTAATTAATTAAGCAAGAAATATCCCTCTCATCA 180
181 CTTCTCAAGATGATCTTTTCAATTTTGTAGTGTATCCCAAGAAAGGAGAA 240
181 CTTCTCAAGATGATCTTTTCAATTTTGTAGTGTATCCCAAGAAAGGAGAA 240
241 GAATTTTGTAGTAAGCAAGAGCACTTTGTGACCTTTTCAACCCCTTTTAA 300
241 GAATTTTGTAGTAAGCAAGAGCACTTTGTGACCTTTTCAACCCCTTTTAA 300
301 GTAATTGAACGATGAGCAACCGTGAAGAAAGATCTCAATCGAATAATGCTTTGCT 360
301 GTAATTGAACGATGAGCAACCGTGAAGAAAGATCTCAATCGAATAATGCTTTGCT 360

QY 361 ATCGGATCCAGTGTGTAATTCGATATGCTTAAAGATCCAGAAAGTACAGGACTTCCGA 420
 DB 361 ATCGGATCCAGTGTGTAATTCGATATGCTTAAAGATCCAGAAAGTACAGGACTTCCGA 420
 QY 421 AGAAATATCTCAATTTGTTGTAAGAAGCTGTGATCTTAGGATCTTAATTCACCTCAT 480
 DB 421 AGAAATATCTCAATTTGTTGTAAGAAGCTGTGATCTTAGGATCTTAATTCACCTCAT 480
 QY 481 AGTAGAGCAATGATGTTTATCTCCAAATGTAAGATCTTACACAGAACTGCCAAAGCAC 540
 DB 481 AGTAGAGCAATGATGTTTATCTCCAAATGTAAGATCTTACACAGAACTGCCAAAGCAC 540
 QY 541 ATATATATTAATTTGGATTAAGGCAAAATAATAGTGTGATTTTGGTAATAGTTCTCCA 600
 DB 541 ATATATATTAATTTGGATTAAGGCAAAATAATAGTGTGATTTTGGTAATAGTTCTCCA 600
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 QY 781 TTCTCAAAAAATTCCTCTGAGTCAAGTATGATATTAAGAACTGTATATGCTGGG 840
 DB 781 TTCTCAAAAAATTCCTCTGAGTCAAGTATGATATTAAGAACTGTATATGCTGGG 840
 QY 841 AGAGTCCCAATTTGATGCTGATGCTTAAGAAAGCTCTATTTCTCAATGCTCAATGAC 900
 DB 841 AGAGTCCCAATTTGATGCTGATGCTTAAGAAAGCTCTATTTCTCAATGCTCAATGAC 900
 QY 901 TGTTTTACAAATGCTATATTTCCAGAGCATCTCCAGAGTACCCCATATATGATGGA 960
 DB 901 TGTTTTACAAATGCTATATTTCCAGAGCATCTCCAGAGTACCCCATATATGATGGA 960
 QY 961 GAAACATCTACAAAATCCCTTTGGGTTAATAATAGTCACTCAGATTAATAATCTTTGT 1020
 DB 961 GAAACATCTACAAAATCCCTTTGGGTTAATAATAGTCACTCAGATTAATAATCTTTGT 1020
 QY 1021 GCACCTATGTAATGTAATATTCGAGACATTCGAAAGATTTATGTTGGAACAGATAC 1080
 DB 1021 GCACCTATGTAATGTAATATTCGAGACATTCGAAAGATTTATGTTGGAACAGATAC 1080
 QY 1081 TACCATGAGAGAAACCTTATGCTATATGTAAGTGAACACTCAAGAAATACCTTTGTCAT 1140
 DB 1081 TACCATGAGAGAAACCTTATGCTATATGTAAGTGAACACTCAAGAAATACCTTTGTCAT 1140
 QY 1141 CCCAGTGAATGAATGCTGTAATTCGATATGATTAATGATCTTCTGCTGCTGCT 1200
 DB 1141 CCCAGTGAATGAATGCTGTAATTCGATATGATTAATGATCTTCTGCTGCTGCTGCT 1200
 QY 1201 CGACTTGGCTTCCATTTGCTGTTAAAGGCCGAAAGGCTTAAGAGAACTGT 1260
 DB 1201 CGACTTGGCTTCCATTTGCTGTTAAAGGCCGAAAGGCTTAAGAGAACTGT 1260
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 DB 1261 CCATGAGCTGGGAAATATAACTTGTGTTGATTAACAGATATCTCTAGATCTGGAAA 1320
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QY 1441 AGCAGTGTGTAATTTCCAGATATGTCAGATGTAAGAGCATGCCAATGCTGTGA 1500
 DB 1441 AGCAGTGTGTAATTTCCAGATATGTCAGATGTAAGAGCATGCCAATGCTGTGA 1500
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 DB 1621 TCTGAATACAGAGAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTACT 1680
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 DB 1681 ATCCCGAAATCTACCCAAATGCTTGTGTGTTAAATGAACTGTAGATGAAGTA 1740
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 DB 1741 GCTCAGATGATCTGCTGTTAAAGATTTGCTCCAAATGAGCTGGAAGGCTATGAG 1800
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 DB 1801 CTCTGAGCTGCAATTAACCAAGATCCTATGATTCGAGGTTTGTGCTGCTTGA 1860
 QY 1861 AAATATTTAAGATGACAAATTTCTCAGTACTAATTCAGTACTAGTACTAATA 1920
 DB 1861 AAATATTTAAGATGACAAATTTCTCAGTACTAATTCAGTACTAGTACTAATA 1920
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 DB 1921 TATGAACATGATTTGATTAACCTGCTTGTGATTTTACTCAAAAAGGCTTAAT 1980
 QY 1981 CAAAGATCGGTCACTTTTCTTTGCAATTTAAATCTGAGATGCAATTAACAGTT 2040
 DB 1981 CAAAGATCGGTCACTTTTCTTTGCAATTTAAATCTGAGATGCAATTAACAGTT 2040
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 DB 2041 AGTGAAGTTTGGCTGCTTTTGGAGTCTATGTCGCTGATGCTGATGCTGATGCTGATG 2100
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 DB 2101 CACCTTAATGAGCAATTTGAGGCTATGGAAGAACTCTAATCTGACTGATCTGATA 2160
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 DB 2161 CAAGAGAAAGATGTAAGCAAAAGGTAAGATGAAGTTTATGTTAGCAAAATGCGG 2220
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 DB 2221 GCACGAGATTTCAATGATGCTCTCCAGGCTTTCTGTCTCTTAACCTGCTCATAG 2280
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 QY 2401 TTTAAATATGGGATGATTTTAAAGCAATATGCTTAACCTTCAGATTTTGCATATG 2460
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Db 2581 CAGTGTAAAGAGGCTGAAAGGTGACATGAGTTAAAGCCACACACTCCATGAGTGG 2640
Qy 2641 CTCGAAAGACAAAGCAAGGGGGAATATATATGATGCGGCCATCGATTGTTACAGATCA 2700
Db 2641 CTCGAAAGACAAAGCAAGGGGGAATATATGATGCGGCCATCGATTGTTACAGATCA 2700
Qy 2701 TGTGCGGATATGTTGCTTCCACCTTCACTTTTGGGAATGGAGATGTCACATAGTAAT 2760
Db 2701 TGTGCGGATATGTTGCTTCCACCTTCACTTTTGGGAATGGAGATGTCACATAGTAAT 2760
Qy 2761 ATCATGTTAAAGATGATGGAACAAGTTCATATATGATTTTGGACACTTTTGGATGC 2820
Db 2761 ATCATGTTAAAGATGATGGAACAAGTTCATATATGATTTTGGACACTTTTGGATGC 2820
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Db 2821 AAGAAAGAAAAATTTGGTTATATAAGAGAGCGCGCTGCTTTGTTTGACACAGATTTC 2880
Qy 2881 TTAATAGTATAGTAAAGAGACCCCAAGATGCAAAAGACAAAGAAATTGAGAGTTT 2940
Db 2881 TTAATAGTATAGTAAAGAGACCCCAAGATGCAAAAGACAAAGAAATTGAGAGTTT 2940
Qy 2941 CAGAGATGTGTTTACAGGCTTATCTAGTATTTGGGCGAGCAATCTCTCAATAAT 3000
Db 2941 CAGAGATGTGTTTACAGGCTTATCTAGTATTTGGGCGAGCAATCTCTCAATAAT 3000
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Db 3121 AAACAAATGATGATGACACCATGCTGGCGAGCAAAAGAAATGATATGATCTTCCAC 3180
Qy 3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207
Db 3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207

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RESULT 3
US-09-085-957-35
Sequence 35, Application US/09085957
Patent No. 6274327

GENERAL INFORMATION:

APPLICANT: Hilee, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Balai, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Panayocou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
TITLE OF INVENTION: THEIR PREPARATION AND USE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-35

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Query Match 100.0%; Score 3207; DB 3; Length 3207;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CTAGTAGAATGTTTACTACCAATGGAATGATAGTGAATCTTGAAGATGCTCCGTGAGGCT 120
Qy 121 ACGTTAATTAAGATTAAGATGAACTATTTAAAGAGCAAAATACCTCTCCATCA 180
Db 121 ACGTTAATTAAGATTAAGATGAACTATTTAAAGAGCAAAATACCTCTCCATCA 180
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DB 1621 TCTGAATTAAGAGAAAGATTTCTGTCAGGCTGAGTAAAGAGCTAGAGATCTCTA 1680
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DB 1921 TATGAACAGATTTGATTAACCTGCTGAGATTTTACTCAAAAAGCTTAACTAAT 1980
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DB 2401 TTTAAATGAGGAGATTTTACGCAAGATATGCTTAACTCTGCAATTAATGCTGATG 2460
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DB 2521 ATCGTGAATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTAT 2580
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DB 2581 CAGTAAAGAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTT 2640
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DB 2641 CTCAAGAGCAAGACAAAGGAGGATATATGATGAGGCTTAAAGGCTTAAAGGCTT 2700
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DB 2701 TGTGCTGATATTTGTTGCTGCTCACTTCTGATTTGAGATTTGAGATCTGATCAAT 2760
OY 2761 ATCATGTTAAAGATGAGCAAACTGTTTCAATATGATTTTGAACATTTTGAATC 2820
DB 2761 ATCATGTTAAAGATGAGCAAACTGTTTCAATATGATTTTGAACATTTTGAATC 2820
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 Db 3181 ACAATTAAGCAGATGCTTGAACCTGA 3207

RESULT 4

US-08-162-081B-34

Sequence 34, Application US/08162081B
 Patent No. 582492

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 APPLICANT: Biles, Waterfield, Michael Derek; Parker, Peter
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
 APPLICANT: Stefano, Gout, Ivan Tarasovitch
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162, 081B
 FILING DATE: February 7, 1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.

REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-162-081B-34

Query Match 93.9%; Score 3011.8; DB 1; Length 3240;
 Best Local Similarity 96.2%; Pred. No. 0;
 Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGCCCTCAAGACCATCATCAGGTGAACCTGCGGGGATCCACTTGAATGCCCAAGAAATC 60
 Db 1 ATGCCCTCAAGACCATCATCAGGTGAACCTGCGGGGATCCACTTGAATGCCCAAGAAATC 60
 QY 61 CTAGTGAAATGTTTACTACCAATGGAGATAGTAACTTTGAAATGCTCCGTGAGGCT 120
 Db 61 CTAGTGAAATGTTTACTACCAATGGAGATAGTAACTTTGAAATGCTCCGTGAGGCT 120
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 Db 121 ACGTTAATACGATTAAGCATGAACCTATTAAAGAGCAAGAAATACCTCTCCATGCA 180
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 Db 361 ATCGGATGCGCATGCTGTGAATTCGATATGTTAAAGATCCGAAGTACAGAGACTTCGA 420
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 QY 541 ATATATTAATTAATTTGATTAAGGCGCAATTAATAGTGTGATTTGGGTATTAATCTTCCA 600
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 Db 721 CTCTGTGTTTGAATATCAGGCAAGTATATTTTAAAGTGTGATGATGAATATC 780
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 Db 841 AGGATGCCCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
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 QY 961 GAAACATCTCAAAATCCCTTTGGGTTTAAATGTGATCAGATTAATAAATCTTTGT 1020
 Db 961 GAAACATCTCAAAATCCCTTTGGGTTTAAATGTGATCAGATTAATAAATCTTTGT 1020
 QY 1021 GCAACCTATGTGAATGTAAATTTTCAGACATTCGAAGATTTATGTTCCAAAGGTATC 1080

Db	1021	GCAACCTATGTGAATGATAAATATTCGAGACATTCGACAAATTTAGTTTGGAAACAGGTATC	1080
Qy	1081	TACCATGAGAGAAACCTTATGTGTATTAATGTGAACACTCCAAAGAGTACCTTGTTCCAAAT	1140
Db	1081	TACCATGAGAGAAACCTTATGTGTATTAATGTGAACACTCCAAAGAGTACCTTGTTCCAAAT	1140
Qy	1141	CCCAAGTGAATGAATGAGTGAATTAACGATATATACATTTCTGATCTTCTGTGCTGCT	1200
Db	1141	CCCAAGTGAATGAATGAGTGAATTAATGATATATATACATTTCTGATCTTCTGTGCTGCT	1200
Qy	1201	CGACTTTGCTTTCCATTTGTTCTGTTAAAGCCGGAAGAGGCTAAAGGAGAACTGT	1260
Db	1201	CGACTTTGCTTTCCATTTGCTGTTAAAGCCGGAAGAGGCTAAAGGAGAACTGT	1260
Qy	1261	CCATTGCGCTGGGGAATATTAACCTTGTTGATTAACAAGATCTAGTATCTGGAAA	1320
Db	1261	CCATTGCGATGGGGAATATTAACCTTGTTGATTAACAAGATCTAGTATCTGGAAA	1320
Qy	1321	ATGGCTTTGATCTTTGGCCAGTACCTCATGACCTAGAAATTTGCTGAACCTTATTTGT	1380
Db	1321	ATGGCTTTGATCTTTGGCCAGTACCTCATGATTTAGAAATTTGCTGAACCTTATTTGT	1380
Qy	1381	GTTACTGATCAAAATCCAAATTAAGAAACCTCCATGTTAGAGTTGGAGTTGACTGTTTC	1440
Db	1381	GTTACTGATCAAAATCCAAATTAAGAAACCTCCATGTTAGAGTTGGAGTTGACTGTTTC	1440
Qy	1441	AGCAGTGTGTTAAAGTTTCCAGATATGTCAAGTGAATGAGACATGCCAATTTGTTCTGTA	1500
Db	1441	AGCAGTGTGTTAAAGTTTCCAGATATGTCAAGTGAATGAGACATGCCAATTTGTTCTGTA	1500
Qy	1501	TCCCGTGAACAGAGATTAGTTATTTCCCATGACAGACTGAGTAACAACCTGATGAGAGAC	1560
Db	1501	TCCCGAAGAGAGATTAGTTATTTCCCATGACAGACTGAGTAACAAGCTGATGAGAGAC	1560
Qy	1561	AATGAATTAAGAGAAATGATTAAGAAGAGTCCGAGCAATTTGTACACGATCTCTTA	1620
Db	1561	AATGAATTAAGAGAAATGACAAAGAAAGCTCAAGCAATTTCTACACGAGATCTCTTC	1620
Qy	1621	TCTGAATCACTGACAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTATACT	1680
Db	1621	TCTGAATCACTGACAGAGAAAGATTTCTATGAGTACAGACACTATTTGTATACT	1680
Qy	1681	ATCCCGGAATTTCTAACCCAAATTGCTTCTGTCTGTTAAATGGAACCTAGATGAAGTA	1740
Db	1681	ATCCCGGAATTTCTAACCCAAATTTGCTTCTGTCTGTTAAATGGAATTTCTAGATGAAGTA	1740
Qy	1741	GCTCGAGTACTGCTGTGGTAAAGATTTGGCTCCCATCAATCAACCTGAAACAGGCTATGAG	1800
Db	1741	GCCCGAGTATGCTGTGGTAAAGATTTGGCTCCCATCAATCAACCTGAAACAGGCTATGAG	1800
Qy	1801	CTTCTGCACTGCAATTAACCCAGATCTATAGTTGAGGTTTGGTGTGTGGTCTTAGAA	1860
Db	1801	CTTCTGCACTGTAATTAACCCAGATCTTATAGTTGAGGTTTGGTGTGTGGTCTTAGAA	1860
Qy	1861	AAATATTTAACAAGTACAAACCTTTCTCAGTATTTAAATTCAGCTAGTACAGTCTTAA	1920
Db	1861	AAATATTTAACAAGTACAAACCTTTCTCAGTATTTAAATTCAGCTAGTACAGTCTTAA	1920
Qy	1921	TATGAACAGATTTGATTAACCTGCTGTGAGATTTTCTCAAAAAAGCTTAACTAAT	1980
Db	1921	TATGAACAAATTTTGGATTAACCTGCTTGTGAGATTTTCTGAAGAAAGCAATGACTAAT	1980
Qy	1981	CAAGGATCGGTCACTTTTCTTTTGGCAATTAATCTGAGATGCAATTAAGACGT	2040
Db	1981	CAAGGATTTGGCACTTTTCTTTTGGCAATTAATCTGAGATGCAATTAAGACGTT	2040
Qy	2041	AGTCAAGGTTTGGCTGCTTTTGGATCCGATTTGCGTGCATGTCGATGATGATCTGAG	2100
Db	2041	AGGCAAGGTTTGGCTGCTTTTGGATCTCATTTGCTGATGATGATGATGATGATGATG	2100
Qy	2101	CACCTTAATGAGCAATGAGGCTATGAGAAAGCTCATTAATCTGACTGACTTCTCAA	2160

D	2101	CACCTGATATGCAAGATCGAGCGCAATGGAANAAGCTATTAACTTAACGACATTCCTCAAA	2160
Q	2161	CAAGGAGAAGAGATGATAACACAAAGGTACAGATGAAGTTTAACTTGAGCAAAATGCGG	2220
D	2161	CAGGAGAGAAAGATGTAACACAAAGGTACAGATGAAGTTTAACTTGAGCAAAATGAGG	2220
Q	2221	CGACCAGATTTCATGATGCTCTCCAGGGCTTCCTGCTCCCTCTAAACCTCGTCAATCAG	2280
D	2221	CGACCAGATTTCATGATGCTCTCCAGGGCTTCCTGCTCCCTCTAAACCTCGTCAATCAA	2280
Q	2281	CTGGGAAATCTCAGGCTTGAAAGTGCAGATTATGTCCTCTGCAAAAAGGCCACTGTGG	2340
D	2281	CTAGGAAACCTCAGGCTTTAAAGTGTCCAAATTATGTCCTCTGCAAAAAGGCCACTGTGG	2340
Q	2341	TTGAATTGGAGAACCCAGACATCATGTCAAGATTACTCTTTCAAGAACAAATGATCATC	2400
D	2341	TTGAATTGGAGAACCCAGACATCATGTCAAGATTACTCTTTCAAGAACAAATGATCATC	2400
Q	2401	TTTAAATATGGGAGTATTTACGGCAAGATATGCTAACCCCTCAGATTATTCGCATTATG	2460
D	2401	TTTAAATATGGGAGTATTTACGGCAAGATATGCTAACCCCTCAGATTATTCGCATTATG	2460
Q	2461	GAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTTTAACTTATGATGTCTGCA	2520
D	2461	GAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTTTAACTTATGATGTCTGCA	2520
Q	2521	ATCGGTACTGTGTGGACTTATCGAGTGTGTGAAAAATTCCTACACTATAATGACAGTT	2580
D	2521	ATCGGTACTGTGTGGACTTATCGAGTGTGTGAAAAATTCCTACACTATAATGACAGTT	2580
Q	2581	CAGTGTAAAGAGAGCCCTGAAAGGTGCACCTGATTAACAGCCACACACTCCATCAGTGG	2640
D	2581	CAGTGTAAAGAGAGCCCTGAAAGGTGCACCTGATTAACAGCCACACACTCCATCAGTGG	2640
Q	2641	CTCAAGACACAGAACAGGGGAAATATATGATCGGCGCATCGATTGTTTACACATCA	2700
D	2641	CTCAAGACACAGAACAGGGGAAATATATGATCGGCGCATCGATTGTTTACACATCA	2700
Q	2701	TGTGCTGATATATGTTGTCACCTCTCATTTTGGAAATGGAGATTCGTACAAATGTGAT	2760
D	2701	TGTGCTGATATATGTTGTCACCTCTCATTTTGGAAATGGAGATTCGTACAAATGTGAT	2760
Q	2761	ATCATGTTAAAGATGATGACACACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2820
D	2761	ATCATGTTAAAGATGATGACACACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2820
Q	2821	AAGAGAAAAAATTTGTTATTAACGAGAGCGGTGCGCTTGTGTTGACACAAGATTTC	2880
D	2821	AAGAGAAAAAATTTGTTATTAACGAGAGCGGTGCGCTTGTGTTGACACAAGATTTC	2880
Q	2881	TTAATATGATTAATAGTAAGAGAGCCCAAGAAATGCACAAAGACAAAGAAATTTGAGAGTTT	2940
D	2881	TTAATATGATTAATAGTAAGAGAGCCCAAGAAATGCACAAAGACAAAGAAATTTGAGAGTTT	2940
Q	2941	CAGGAGATGTGTACAGGCTTATCTAGCTATTTGGCAGACATGCCAATCTTTCATTAAT	3000
D	2941	CAGGAGATGTGTGTACAGGCTTATCTAGCTATTTGGCAGACATGCCAATCTTTCATTAAT	3000
Q	3001	CTTTTCTCATGATGCTTGCGCTCTGGAAATGCCAAGCTGCAATCTTTTATGATTAATGCA	3060
D	3001	CTTTTCTCATGATGCTTGCGCTCTGGAAATGCCAAGCTGCAATCTTTTATGATTAATGCA	3060
Q	3061	TACATTGGAAGACCTTAGCTTAAATAGAGTGAAGAGGCTTTGGAGATATTTCATG	3120
D	3061	TACATTGGAAGACCTTAGCTTAAATAGAGTGAAGAGGCTTTGGAGATATTTCATG	3120
Q	3121	AACCAATGAATGATGACACCATGTGTGCTGCAACAAAAAAATGATGGATCTTCCAC	3180
D	3121	AACCAATGAATGATGACACCATGTGTGCTGCAACAAAAAAATGATGGATCTTCCAC	3180
Q	3181	ACAATTAAAGCAGCATGCTTTGAACTGA 3207	
D	3181	ACAATTAAAGCAGCATGCTTTGAACTGA 3207	

RESULT 5
US-08-780-872-34
Sequence 34, Application US/08780872
Patent No. 5846824
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Oesu, Masayuki; Panayotou, George; Volintu,
APPLICANT: Stefano; Gout, Ivan Tarasovich
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-780-872-34

Query Match 93.9%; Score 3011.8; DB 2; Length 3240;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 1 ATGCTCCAGACATCATCAGTGAAGTGTGGGATCCATCTGATGCCCCAAGAATC 60
DB 1 ATGCTCCAGACATCATCAGTGAAGTGTGGGATCCATCTGATGCCCCAAGAATC 60
QY 61 CTAGTGAAGTGTCTACCAAAATGGAGATGATGACTTTAGAAATGCTTCGGTAGGCT 120
DB 61 CTAGTGAAGTGTCTACCAAAATGGAGATGATGACTTTAGAAATGCTTCGGTAGGCT 120
QY 121 AGCTTAATAAGATAAGATGATGATTAATAAGAAAGAAATACCTCTCCATCAA 180
DB 121 ACATTAGTACTATAAGATGATGATTAATAAGAAAGAAATACCTCTCCATCAA 180
QY 181 CTTCTCAAGATGATCTTCTTACATTTTCTAGTGTATACCAAGAAAGAGAGGAA 240
DB 181 CTTCTCAAGATGATCTTCTTACATTTTCTAGTGTATACCAAGAAAGAGAGGAA 240
QY 241 GAATTTTGTAGTGAACAAGACGACTTTGTGACTTCGGCTTTTCAACCTTTTAA 300
DB 241 GAATTTTGTAGTGAACAAGACGACTTTGTGACTTCGGCTTTTCAACCTTTTAA 300

QY 301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAAGAAATGGTTGGCT 360
DB 301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAAGAAATGGTTGGCT 360
QY 361 ATCGGCATCCAGTGTGTAATTCGATATGTTAAAGATCCAGAAAGTACAGACCTTCCGA 420
DB 361 ATCGGCATCCAGTGTGTAATTCGATATGTTAAAGATCCAGAAAGTACAGACCTTCCGA 420
QY 421 AAAAAATTTCTAAAGTGTGTAAGAAAGTGTGATCTTAGGATCTTAATTCACCTCAT 480
DB 421 AAAAAATTTCTAAAGTGTGTAAGAAAGTGTGATCTTAGGATCTTAATTCACCTCAT 480
QY 481 AGTAGAGCAATGATGTTATCTCCTCAAAATGTAATCTTCAACCAAGTCCCAAGCAC 540
DB 481 AGTAGAGCAATGATGTTATCTCCTCAACCAAGTCCCAAGTCCCAAGCAC 540
QY 541 ATATATTAATTAATGATTAAGAGGCAATTAATAGTGTGATTTGGGTATAGTTCTCCA 600
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DB 601 AATTAATGACAAACAGAGTATCTGAAATCAACATGACTGTGTCCAGAACAGTA 660
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DB 661 ATTGCTGAAGCAATGAGGAAAAAACTCGAAGTATGTTCTTCACTGGAACACTTAAA 720
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DB 721 CTCTGTGTTTGAATATACAGGCAAGTATATTTTAAAGTGTGATGATGATATAC 780
QY 781 TTCTTGAAGAAATATCTCTGAGTCAATTAATTAAGAAAGTGTGATATGCTTGGG 840
DB 781 TTCTTGAAGAAATATCTCTGAGTCAATTAATTAAGAAAGTGTGATATGCTTGGG 840
QY 841 AGGATGCCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 841 AGGATGCCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 TGTTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 901 TGTTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 961 GAAACATCTACAAATTCCTTGGGTATTAATTAAGACATCAGAAATTAATTCCTTGT 1020
DB 961 GAAACATCTACAAATTCCTTGGGTATTAATTAAGACATCAGAAATTAATTCCTTGT 1020
QY 1021 GCAACCTATGTAATGTAATTAATTCGAGACATGTAATTAATTAATTAATTAATTAAT 1080
DB 1021 GCAACCTATGTAATGTAATTAATTCGAGACATGTAATTAATTAATTAATTAATTAAT 1080
QY 1081 TACCATGAGAGGAAACCTTATGATATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 TACCATGAGAGGAAACCTTATGATATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CCCAGGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 CCCAGGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 CGACTTTGCTTTTCAATTTGCTGTTAAAGCCGAAAGGATGCTTAAAGAGAAACATCT 1260
DB 1201 CGACTTTGCTTTTCAATTTGCTGTTAAAGCCGAAAGGATGCTTAAAGAGAAACATCT 1260
QY 1261 CCATTGGGCTGGGAAATATAAATGTTGATTAACAGATCTTATGATGATGATGATGAT 1320
DB 1261 CCATTGGGCTGGGAAATATAAATGTTGATTAACAGATCTTATGATGATGATGATGAT 1320
QY 1321 ATGCTTTGAATCTTTTGGCAGTACCTCATGAGTACGAAAGTGTGTAACCTTATGGT 1380
DB 1321 ATGCTTTGAATCTTTTGGCAGTACCTCATGAGTACGAAAGTGTGTAACCTTATGGT 1380

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
Prior APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-34

Query Match 93.9%; Score 3011.8; DB 3; Length 3240;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGCTCCAGAGCCATCATCAGGTGAAGTGGGGCATCCACTTGATGCCCCAGAAATC 60
DB 1 ATGCTCCAGAGCCATCATCAGGTGAAGTGGGGCATCCACTTGATGCCCCAGAAATC 60
QY 61 CTAGTAGAATGTTTACTACCAAAATGGGATGATGACTTTAGAAATGCTCCGTAGAGT 120
DB 61 CTAGTAGAATGTTTACTACCAAAATGGGATGATGACTTTAGAAATGCTCCGTAGAGT 120
QY 121 AGCTTAATACGATTAAGGATGACTTTTAAAGAGCAAGAAATACCTCTTCATCAA 180
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QY 181 CTCTCTCAAGATGAAATCTTCTAATTTCTGTAAGTGTACCCAGAAAGCAAGAGGAA 240
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DB 241 GAATTTTGTAGTAAGCAAGAGCACTTTGTGACTTGGCTTTTCAACCTTTTAAAA 300
QY 301 GTAATTGAAACGATGAGCAACCGTGAAGAAATGCTCAATCGAAATTTGTTTCT 360
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QY 361 ATCGGCAATGCAATGTAATGTAATGTTAAAGATCCGAAAGTACAGAACTTCCGA 420
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DB 601 AATATGACAAACAGAGTATATCTGAAAAATCAACCATGACTGTGTGCGAGAACAGTA 660
QY 661 ATTGCTGAAGCAATCAGAAAAAACTCGAAGTATGTTCTATCATCTGAACAATTA 720
DB 661 ATTGCTGAAGCAATCAGAAAAAACTCGAAGTATGTTCTATCATCTGAACAATTA 720
QY 721 CTCTGTGTTTGAATATCAGGGCAAGTATTTTAAAGTGTGGAATGTAATGATAC 780
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QY 841 AGAGTCCCAATTTGATGCTGATGCTTAAAGAAAGCTTATCTCAACCTGCAATGAC 900
DB 841 AGAGTCCCAATTTGATGCTGATGCTTAAAGAAAGCTTATCTCAACCTGCAATGAC 900
QY 901 TGTATTACAAATGCCATCATATTCAGACGATCTCCAGAGCTACGCCATATATGATGA 960
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QY 1081 TACGATGAGAGAGAACCTTATATGATATATGAAACACTCAAGAGTACCTTTGCAAT 1140
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DB 1201 GCACTTTCCTTTCCATTTGTTGTTTAAAGGCGGAAAGGCTGTAAGAGAAACACTGT 1260
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DB 1261 CCATTGCGCTGGGAAATATTAACCTGTTGATTAACAGATATCTAGTATCTGGA 1320
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Db 1681 ATCCCGAATATTCACCAATTCCTCTCTGTAAATGAAATTCAGAGTA 1740
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 Qy 1801 CTTCTGAGCTGCAATTTACAGATCTTATGTTGAGGTTTGTCTGTTGCTTA 1860
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 Qy 1861 AAATATTTAAGATGACAACTTTCTCACTTAATGAGCTGTACAGGTA 1920
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 Qy 1921 TATGAACTATTTGATTAACCTGCTTGTGAGATTTTACTCAAAAAGCTTA 1980
 Db 1921 TATGAACTATTTGATTAACCTGCTTGTGAGATTTTACTCAAAAAGCTTA 1980
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 Db 1981 CAAAGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2040
 Qy 2041 AGTCAGAGTTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
 Db 2041 AGTCAGAGTTTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
 Qy 2101 CACCTTAATAGGCAAGTTGAGCTTATGGAAGCTCATTAAGTGAAGTCTCA 2160
 Db 2101 CACCTTAATAGGCAAGTTGAGCTTATGGAAGCTCATTAAGTGAAGTCTCA 2160
 Qy 2161 CAAAGAGAAAGATGAACAACAAGATGATGAAGTGAAGTGAAGTGAAGTGA 2220
 Db 2161 CAAAGAGAAAGATGAACAACAAGATGATGAAGTGAAGTGAAGTGAAGTGA 2220
 Qy 2221 CGACCAATTTTCAATGATCTCTCAGAGGCTTCTCTCTCTCTCTCTCTCTCT 2280
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 Qy 2281 CTGGAAATCTCAGGCTTGAAGAGTGTGAAATTAATGCTTCTGCAAAAAGCC 2340
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 Qy 2401 TTTAAATTTGGAGATTTTACGGCAAGATGCTTACCTTCAATTTATGCA 2460
 Db 2401 TTTAAATTTGGAGATTTTACGGCAAGATGCTTACCTTCAATTTATGCA 2460
 Qy 2461 GAAATATCTGCAAAATCAAGGCTTGAATCTTGAATTTACTTATGCTGTA 2520
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 Qy 2521 ATGCTGATCTGCTGGAGCTTATGAGTGTGAGAAATTTCTCACTATATG 2580
 Db 2521 ATGCTGATCTGCTGGAGCTTATGAGTGTGAGAAATTTCTCACTATATG 2580
 Qy 2581 CAGTGTAAAGAGGAGCTTGAAGGTCATCTGCACTTAAAGCCACATCTC 2640
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 Qy 2641 CTCAAAAGCAAGAACAAAGGGAATATATGATGCAAGCCATGCTGTTAC 2700
 Db 2641 CTCAAAAGCAAGAACAAAGGGAATATATGATGCAAGCCATGCTGTTAC 2700
 Qy 2701 TGTGCTGATTTGTGTTGCACTTATTTGGAATTTGGAATTTGGAATTTG 2760
 Db 2701 TGTGCTGATTTGTGTTGCACTTATTTGGAATTTGGAATTTGGAATTTG 2760
 Qy 2761 ATCATGTTAAGATGAGCAACTGTTTATATGATTTTGAACCTTTTGAT 2820

Db 2761 ATCATGTTAAGATGAGCAACTGTTTATATGATTTTGAACCTTTTGAT 2820
 Qy 2821 AAGAGAAAAATTTGTTTAAACGAGAGCGGCTGTTGTTTGAACAAAGATT 2880
 Db 2821 AAGAGAAAAATTTGTTTAAACGAGAGCGGCTGTTGTTTGAACAAAGATT 2880
 Qy 2881 TTAATAGTATTTAAGAGGCCCAAGATGCAAAAGCAAGAGATTTGAGGTT 2940
 Db 2881 TTAATAGTATTTAAGAGGCCCAAGATGCAAAAGCAAGAGATTTGAGGTT 2940
 Qy 2941 CAGAGATGTTTCAAGGCTTATCTAGCTATTTGCGAGCATGCCAATCTT 3000
 Db 2941 CAGAGATGTTTCAAGGCTTATCTAGCTATTTGCGAGCATGCCAATCTT 3000
 Qy 3001 CTTTCTCAATGATGCTTGGCTGTAATGCAAGCAAGCAATCTTTGATG 3060
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RESULT 7
 US-08-162-081B-32
 Sequence 32, Application US/08162081B
 Patent No. 5824492
 GENERAL INFORMATION:
 APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
 APPLICANT: Stefano, Gout, Ivan Tarasovitch
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,081B
 FILING DATE: February 7, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 688-3884
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3412 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
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LOCATION: 1..3204
OTHER INFORMATION: /standard_name= "CDS"
US-08-162-081B-32

Query Match 93.8%; Score 3008.6; DB 1; Length 3412;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 32, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinla,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 638-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name="CDS"
; US-08-780-872-32

Query Match 93.8%; Score 3008.6; DB 2; Length 3412;
Best local similarity 96.1%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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Qy      2641 CTCAAAAGCAAGAACAAAGGGGAAATATATATGATGCGGCCATCGATTTGTTTACA 2700
Db      2641 CTCAAAAGCAAGAACAAAGGGGAAATATATATGATGCGGCCATCGATTTGTTTACA 2700
Qy      2701 TGTCGTGATATTTGTTGCCACTTCAATTTTGGGAATTTGAGATGTCACATATGAT 2760
Db      2701 TGTCGTGATATTTGTTGCCACTTCAATTTTGGGAATTTGAGATGTCACATATGAT 2760
Qy      2761 ATCATGTTAAAGATGATGCAACCTGTTCAATATATATGATTTTGGACATTTTGGATAC 2820
Db      2761 ATCATGTTAAAGATGATGCAACCTGTTCAATATATATGATTTTGGACATTTTGGATAC 2820
Qy      2821 AAGAAGAAAAATTTGGTTATTAACGAGAGGCGCTGCCGTTGTTTACACAAAGATTTC 2880
Db      2821 AAGAAGAAAAATTTGGTTATTAACGAGAGGCGCTGCCGTTGTTTACACAAAGATTTC 2880
Qy      2881 TTTAATAGTATTAGTAAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Db      2881 TTTAATAGTATTAGTAAAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Qy      2941 CAGAGATGTTTAAAGGCTTATAGTATTTGGGAGCATGCCATCTGTTCAAT 3000
Db      2941 CAGAGATGTTTAAAGGCTTATAGTATTTGGGAGCATGCCATCTGTTCAAT 3000
Qy      3001 CTTTCTCATGATGCTTGGCTCTGGAATGCCAGAACTAATCTTTTGAATGATGCA 3060
Db      3001 CTTTCTCATGATGCTTGGCTCTGGAATGCCAGAACTAATCTTTTGAATGATGCA 3060
Qy      3061 TACATTGCAAAAGCCCTTACCTTATAGTAAACTGAGCAAGAGGCTTTGAGATTTCATG 3120
Db      3061 TACATTGCAAAAGCCCTTACCTTATAGTAAACTGAGCAAGAGGCTTTGAGATTTCATG 3120
Qy      3121 AAACAAATGATGATGACACATGCTGAGCAACAAATGATGATGATGCTTCCAC 3180
Db      3121 AAACAAATGATGATGACACATGCTGAGCAACAAATGATGATGATGATGCTTCCAC 3180
Qy      3181 ACAATTAAAGCAGATGCTTTGAACTGA 3207
Db      3181 ACAATTAAAGCAGATGCTTTGAACTGA 3207

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RESULT 9
US-09-085-957-32
Sequence 32, Application US/09085957
Parent No. 6274327

GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritun
APPLICANT: Bala, Waterfield, Michael Derek, Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki, Panayotou, George, Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch

```

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085.957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"

US-09-085-957-32

Query Match 93.8%; Score 3008.6; DB 3; Length 3412;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy      1 ATGCTCCAGAGACCATCATCAGTGAAGTGGGCAATCCACTTGATGCCCCCAAGATC 60
Db      1 ATGCTCCAGAGACCATCATCAGTGAAGTGGGCAATCCACTTGATGCCCCCAAGATC 60
Qy      61 CTACTAGATGTTTACTACCAATGAGATGATGATCTTTAGATGCTTCGGAGGCT 120
Db      61 CTACTAGATGTTTACTACCAATGAGATGATGATCTTTAGATGCTTCGGAGGCT 120
Qy      121 ACGTTAATAGAAAGAGATGAACTATTTAAAGAAAGAAATACCTCCATCAAA 180
Db      121 ACGTTAATAGAAAGAGATGAACTATTTAAAGAAAGAAATACCTCCATCAAA 180
Qy      181 CTTCTCAAGATGATCTTCTTACATTTTGTAGGTGTAACCAAGAGCAAGAGGAA 240
Db      181 CTTCTCAAGATGATCTTCTTACATTTTGTAGGTGTAACCAAGAGCAAGAGGAA 240
Qy      241 GAAATTTTGTATGAAACAGACCTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300
Db      241 GAAATTTTGTATGAAACAGACCTTGTGATCTTGGCTTTTCAACCTTTTAAAA 300
Qy      301 GTAATTGAAACAGAGCAACCGTGAAGAAAGATCCTCAATGAGAAATTTGGTTGCT 360
Db      301 GTAATTGAAACAGAGCAACCGTGAAGAAAGATCCTCAATGAGAAATTTGGTTGCT 360

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QY 361 ATGGCATGCGAGTGTGTGAATTCGATATGTTAAAGATCCAGATGACGAGACTTCCGA 420
DB 361 ATGGCATGCGAGTGTGTGAATTCGATATGTTAAAGATCCGTAAGTACGAGACTTCCGA 420
QY 421 AGAATATTTCTCATGTTTGTAAAGAGCTGTGATGTTAGGAGTCTTAATTCACCTCAT 480
DB 421 AGAATATTTCTCATGTTTGTAAAGAGCTGTGATGTTAGGAGTCTTAATTCACCTCAT 480
QY 481 AGTAGAGCAATGTATGTTTATCTCCMAATGTAGAAATCTTCACCGAAGTCCCAAGCAC 540
DB 481 AGTAGAGCAATGTATGTTTATCTCCMAATGTAGAAATCTTCACCGAAGTCCCAAGCAC 540
QY 541 ATTATATATTAATTTGATTAAGGCAAAATATATGTGTGATTTTGAGTAAATGTTTCTCA 600
DB 541 ATTATATATTAATTTGATTAAGGCAAAATATATGTGTGATTTTGAGTAAATGTTTCTCA 600
QY 601 AATAATGACAAACAGAGTACTCTGAAATATCAACCATGACGTGTGCGCAAGATGA 660
DB 601 AATAATGACAAACAGAGTACTCTGAAATATCAACCATGACGTGTGCGCAAGATGA 660
QY 661 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTCTATCATCTGAACTAAATAA 720
DB 661 ATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTGTATCATCTGAACTAAATAA 720
QY 721 CTCTGTGTTTAAATATCTAGGCGCAAGTATTTTAAAGTGTGTGATGTAATAC 780
DB 721 CTCTGTGTTTAAATATCTAGGCGCAAGTATTTTAAAGTGTGTGATGTAATAC 780
QY 781 TTCTTGAATAAAATATCTCTGAGTCAAGTAAATATTAAGTCTGTATTAATGCTTGGG 840
DB 781 TTCTTGAATAAAATATCTCTGAGTCAAGTAAATATTAAGTCTGTATTAATGCTTGGG 840
QY 841 AGGATGCCCAATTTGATGCTGATGCTTAAAGAAAGCTCTATCTCACTGCCAATGAG 900
DB 841 AGGATGCCCAATTTGAAAGATGATGCTTAAAGAAAGCTTATTTCTCACTGCCAATGAG 900
QY 901 TGTTTTAAATGCGATATCTCAACGCACTCCACAGCTAGCCCATATATGAATGA 960
DB 901 TGTTTTAAATGCGATATCTCAACGCACTCCACAGCTAGCCCATATATGAATGA 960
QY 961 GAAACATCTAACAAATTCCTTTGGGTATTAATAATGTCACCTGAGTAAATAATCTTTGT 1020
DB 961 GAAACATCTAACAAATTCCTTTGGGTATTAATAATGTCACCTGAGTAAATAATCTTTGT 1020
QY 1021 GCAACCTATGTAATTAATATTTGAGACATTTGACAAAGTAAATGTTGGAACAGGTATC 1080
DB 1021 GCAACCTATGTAATTAATATTTGAGACATTTGACAAAGTAAATGTTGGAACAGGTATC 1080
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DB 1081 TACCATGAGAGAAACCTTATGTGATTAATGTGAACACTCAAGAGTACCTTGTCCAAAT 1140
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DB 1141 CCAGGTGGAATGAATGCTGTAATTAACATATTAATTCCTGATCTTCTGCTGCTGCT 1200
QY 1201 CGACTTGTGCTTCCATTTGTTCTGTTAAAGCCGAAAGGAGTAAAGAGGAACCTGT 1260
DB 1201 CGACTTGTGCTTCCATTTGCTGCTGTTAAAGCCGAAAGGAGTAAAGAGGAACCTGT 1260
QY 1261 CCATTGGCTGGGGAATATTAACCTTGTGATTAACAGACACTTAATATCTGAAAAA 1320
DB 1261 CCATTGGCTGGGGAATATTAACCTTGTGATTAACAGACACTTAATATCTGAAAAA 1320
QY 1321 ATGGCTTTGAATCTTTGGCAGTACTCATGACATTAAGAAATTTGCTGAACCTTATGCT 1380
DB 1321 ATGGCTTTGAATCTTTGGCAGTACTCATGACATTAAGAAATTTGCTGAACCTTATGCT 1380
QY 1381 GTTACTGATCAAAATCCAAATTAAGAAATCCATGCTTTAGAGTTGAGCTGCTTC 1440
DB 1381 GTTACTGATCAAAATCCAAATTAAGAAATCCATGCTTTAGAGTTGAGCTGCTTC 1440
QY 1441 AGCAGTGTGTAAGTTTCCAGATATGTGAGTGAAGACATGCCAATTTGCTGTA 1500

DB 1441 AGCAGTGTGTAAGTTTCCAGATATGTGAGTATGAAGACATGCCAATTTGCTGTA 1500
QY 1501 TCCCGTGAACAGATTTTATGTTATTTCCATGACAGACTGATTAACAGACTAGTAGAC 1560
DB 1501 TCCCGTGAACAGATTTTATGTTATTTCCATGACAGACTGATTAACAGACTAGTAGAC 1560
QY 1561 AATGAATTAAGAAAAATGATTAAGAAACAGCTCCAGCAATTTTGTACAGAGATCCCTTA 1620
DB 1561 AATGAATTAAGAAAAATGATTAAGAAACAGCTCCAGCAATTTTGTACAGAGATCCCTTA 1620
QY 1621 TCTGAATATCTGAGCAAGAAAAATTTTCTGTGAGCCACAGACACTATTTGTAACT 1680
DB 1621 TCTGAATATCTGAGCAAGAAAAATTTTCTGTGAGCCACAGACACTATTTGTAACT 1680
QY 1681 ATCCCGGAAATTTTACCCTAAATGCTTCTGTCTGTTAAATGAACTCTAGAGTGAAGTA 1740
DB 1681 ATCCCGGAAATTTTACCCTAAATGCTTCTGTCTGTTAAATGAACTCTAGAGTGAAGTA 1740
QY 1741 GCTCAGATGTAATGCTTGGTAAAGAAATTTGAGCTCCATCAAGCTGAACAGCTATGAG 1800
DB 1741 GCTCAGATGTAATGCTTGGTAAAGAAATTTGAGCTCCATCAAGCTGAACAGCTATGAG 1800
QY 1801 CTTCGAGCTGCAATTAACCAAGTCTATGTTGAGGTTTGTGCTGCTGCTTGAAG 1860
DB 1801 CTTCGAGCTGTAATTAACCAAGTCTATGTTGAGGTTTGTGCTGCTGCTTGAAG 1860
QY 1861 AATATTTAAACAGATGACAACTTTCTCAGTATTTAATCAGCTAGTACAGGCTCTAAA 1920
DB 1861 AATATTTAAACAGATGACAACTTTCTCAGTATTTAATCAGCTAGTACAGGCTCTAAA 1920
QY 1921 TATGAACAGATTTGATTAACCTGTTGAGTATTTTCTCAAAAACGTTAACTAAT 1980
DB 1921 TATGAACAAATTTGATTAACCTGTTGAGTATTTTCTCAAAAACGTTAACTAAT 1980
QY 1981 CAAAGATGCTGCTTTTCTTTTGGCATTTTAAATCTGAGTGCACATTAACAGTT 2040
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QY 2041 AGTCAGAGTTTGGCTGCTTTTGGACCTTATTTGCGTGCATGAGGATGTAATCTGAAG 2100
DB 2041 AGTCAGAGTTTGGCTGCTTTTGGACCTTATTTGCGTGCATGAGGATGTAATCTGAAG 2100
QY 2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAGCTCATTAAGCTGACATTTCCAAA 2160
DB 2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAGCTCATTAAGCTGACATTTCCAAA 2160
QY 2161 CAGAGAGAGAGATGAACACAAAAGTACAGATGAATTTTATGTTAGTACGCAATGAG 2220
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QY 2221 CGACCAATTTATGATGATGATCCCTTACAGGCTGCTGCTCTCTAAACCTGCTCA 2280
DB 2221 CGACCAATTTATGATGATGATCCCTTACAGGCTGCTGCTCTCTCTCTCTCTCA 2280
QY 2281 CTGGGAAATCTAGGCTTGAAGTGTGCAATTAATGCTCTTGCAAAAAGGCCACTGTGG 2340
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DB 2341 TTGAATTTGGGAAACCCAGACATCATGTGCAATTAATCTTTCAAAACATAGATCATC 2400
QY 2401 TTTAAAAATGGGATGATTTACGGAAGATATGTAACCTTCAAGATTAATGCAATTAAG 2460
DB 2401 TTTAAAAATGGGATGATTTACGGAAGATATGTAACCTTCAAGATTAATGCAATTAAG 2460
QY 2461 GAAATATCTGGCAAAATCAAGGCTTATCTTCAAGTATCTTTAGATGATGCTGTGA 2520
DB 2461 GAAATATCTGGCAAAATCAAGGCTTATCTTCAAGTATCTTTAGATGATGCTGTGA 2520
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Db 2521 ATCGGTGACTGTGTGGAGCTTATTGAGGTGTCGAAATTTCTACACTATTATGCAAAAT 2580
Qy 2581 CAGTGTAAAGAGGCGCTTGAAGGTGACCTGCACTTTAAACAGCCACACACTCCATGATG 2640
Db 2581 CAGTGTAAAGAGGCGCTTGAAGGTGACCTGCACTTTAAACAGCCACACACTCCATGATG 2640
Qy 2641 CTGAAAGACAAACAGAGGGGAAATATATGATGCGCGCATGATTTGTTTACAGCATCA 2700
Db 2641 CTGAAAGACAAACAGAGGGGAAATATATGATGCGCGCATGATTTGTTTACAGCATCA 2700
Qy 2701 TGTGCTGATGATTTGTGTGTCACCTTCATTTTGGAAATTTGGAGATGTCACAAATAGTAAT 2760
Db 2701 TGTGCTGATGATTTGTGTGTCACCTTCATTTTGGAAATTTGGAGATGTCACAAATAGTAAT 2760
Qy 2761 ATCATGCTTAAAGATGATGACACACTGTTTCATATAGATTTTGGACACTTTTGGATCAC 2820
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Qy 2941 CAGAGATGTTTAAAGAGCTTATCTAGCTATTTGGGACGACATGCGCATCTTTCATTAAT 3000
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Qy 3001 CTTTTCATGATGATGCTTGTGCTCGGAATGCGAAGCTCAATCTTTGATGATTTGCA 3060
Db 3001 CTTTTCATGATGATGCTTGTGCTCGGAATGCGAAGCTCAATCTTTGATGATTTGCA 3060
Qy 3061 TACATTTGAAAGACCTTACCTTATAGATTAACAGCAAGAGCTTTGGAGTATTTGATG 3120
Db 3061 TACATTTGAAAGACCTTACCTTATAGATTAACAGCAAGAGCTTTGGAGTATTTGATG 3120
Qy 3121 AAACAAATGATGATGACACACCATGCTGCTGAGACAAACAAATGATTTGATTTCCAC 3180
Db 3121 AAACAAATGATGATGACACACCATGCTGCTGAGACAAACAAATGATTTGATTTCCAC 3180
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Db 3181 ACAATTAAAGCATGCTTTGAACTGA 3207

RESULT 10
US-09-392-350-1
; Sequence 1, Application US/09392350
; Patent No. 6133032
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 BETA EXPRESSION
; FILE REFERENCE: RTS-0075
; CURRENT APPLICATION NUMBER: US/09/392,350
; CURRENT FILING DATE: 1999-09-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3213)
US-09-392-350-1

Query Match 14.0%; Score 448.2; DB 3; Length 3213;
Best Match Similarity 50.1%; Pred. No. 3,4e-121; Indels 106; Gaps 15;
Matches 1591; Conservative 0; Mismatches 1478;

Qy 58 ATCCTAGTAGAATGTTTACTTACCAATGGAGATGATGACTTAGAATGCTTCGCGAG 117

Db 88 ATACCTGTGATTTCCCTTTTGGCCACTGGGATTTATATCCAGTTGAGAGTACCTTCGGAA 147
Qy 118 GCTACGTTAATTAAGATAAGCATGATCTATTAAAGAAAGCAAGAAATACCTTCAT 177
Db 148 GCTACGTTAATTAATTAAGATAAGCATGATCTATTAAAGAAAGTACCAATTTCCAAATGTC 207
Qy 178 CAATCTTTCAAGATGATCTTCTTACATTTTGTGATGTTTACCAAGAAAGCAAGAAAG 237
Db 208 AACCTCTTAATGAGATTAATGATCTCTTATATGTTTGTGATGATGATGATGATGAT 267
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Db 268 GAGAGCTTGAAGATTAAGAAAGAGAGCTTGTGATGATGATGATGATGATGATGATGAT 327
Qy 298 AAAGTAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 357
Db 328 AAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 384
Qy 358 GCTATGCGATGCGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
Db 385 CTATATGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 444
Qy 418 CGAAGAAATATTTCTAATGTTTGTAAAGAGCTGTGATCTTAAGGATCTTAATTAACCT 477
Db 445 CGAAGAAATATTTCTAATGTTTGTAAAGAGCTGTGATCTTAAGGATCTTAATTAACCT 486
Qy 478 CATATAGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
Db 487 CTGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
Qy 538 CACATATATTAATTTGATTAAGGCAAAATATAGTGTGATTTGGTAAATGATTTCT 597
Db 547 TCCATCCCTAATACTTAAGATTAATCTTAATGAGGAAAGCTCATGATGATGATGAT 606
Qy 598 CCAATATGACAAACAGAGATTAATCTGTAATTAATCAACATGATGATGATGATGATGAT 657
Db 607 TTTGAAATGCTCCAGAGAGCTGTTTACCTTCAAGTCTCTTAATTAATGATGATGATGAT 666
Qy 658 GTAATGCTGAAAGCAATCAGAAAAAATCTGAAATGATGATGATGATGATGATGATGAT 717
Db 667 GTAATGATTAATGCAATC---CAAAAAGTTTGAATTAATGATGATGATGATGATGATGAT 723
Qy 718 AAATCTGTGTTTAAATATCAGGCAAGATTTTAAAGTGTGATGATGATGATGATGATGAT 777
Db 724 AGCCCTATG-----ATATGTTTGAAGTCAAGGAGGATGATGATGATGATGATGAT 765
Qy 778 TACTTCTGAAAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
Db 766 TATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 825
Qy 838 GAGAGATGCGCAATTTGATGCT---GATGCTAAAGAAAGCTCTAATCTCAATGCTG 892
Db 826 AGAGCCCTGCCCCATTTATATCTTGTGAAATGCTGCAAGATCAAGAAATGATGATGATGAT 885
Qy 893 CAATGATGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
Db 886 GAAATGATGCTATGAGGCTGCAATTAATGAAATTAATCTAATCTTCTTCCATTA 945
Qy 953 TGAATGGAATCATCTCAAAATCCCTTTGGGTTAATTAATGATGATGATGATGATGATGAT 1012
Db 946 CCACCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1005
Qy 1013 TTTCTTGTGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1072
Db 1006 GTCTTGTGTAAGGAAATTAATCTTAACAGAGAGAAAC--TGTAAAGTTCAATGTCAGCG 1063
Qy 1073 CAGATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1132
Db 1064 CTGTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
Qy 1133 GTTCCA---ATCCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189

Dh 1124 GGAATATGATCATATTGGATGAACCACTGGAATTTGATATTAATTTTGACTTAC 1183
Qy 1190 CTCTGCTGCTGCACTTTGCTTTTCCATT-----GTTCTGTTAAAGCCGAAAGGGTGC 1244
Db 1184 CAGAATGCTGCTGATTAATGTTTCTGTTATGAGTTTGGATTAAGTAAACGAGAGA 1243
Qy 1245 TAAAGGAAACACTGTCAT-----TGCCCTGGGAAATATTAACCTGTTG 1291
Db 1244 AATCAAGGAAATATTAATCCCTTAATATCAAGACATCAGGAAAGCTGAAAGTGC 1303
Qy 1292 ATTAACAGATACCTAGTATCTGAAATAATGGCTTGAATCTTTGGCCAGTACCTCATG 1351
Db 1304 ATTAATCTGAGGCTGGGTAATACATGTTTGACTTTAAAGCAATTAAGAACTG 1363
Qy 1352 GACTAGAAGATTTGCTGAACCTATGTTGTTACTGATCAAAATCAAAATTAAGAACTC 1411
Db 1364 GAGACATTAATTAATCAAGCTGATCTTCTGATGAACCTGAAAGAAATGTTGATC 1423
Qy 1412 CATGTTAGATTGGAGTTTGACTGTTCAAGCTGTGTAAGTTTCCAGATATGTCAG 1471
Db 1424 CATGGAACCTGTTCAACCAATCCATATCTGAAATGCAACAGCTTTCATGTTAAAT 1483
Qy 1472 TGATTGAAGAGCATGCCAATGTCGTATCCCGTGAAGAGAGATTAGTTATCCCATG 1531
Db 1484 TTCCAGAGATTAATAAACAACCTTATTAATCCCTTCGATTAAGATTATTAAGAAAG 1543
Qy 1532 CAGAGCTGATGATACAGACTAGAGACATTAATTAAGAAATAATGATTAAGAAAGC 1591
Db 1544 CAGCTAGATTTGAACAGAGATAGTCTATGTTCAAGCTCAAGGTGAAAGAAAGTTTC 1603
Qy 1592 TCC-----GAGCAATTTGTAACAAGATCTCTATCTGAATCACTGAGCAAGAG 1642
Db 1604 TTCTCTATTAAGAAATCTTGACAGGGATCCCTTGTCTCAAGCTGTGAAAGAAAGAA 1663
Qy 1643 AAGATTTTCTGAGGAGCCACAGC---ACTATGTGTAACTATCCCGAAATCTACCA 1699
Db 1664 TGGATCTTAATTTGGAATTTGCGAACAAGCTGCGAAGATTTTCCACATCACTGCCAA 1723
Qy 1700 AATTGCTTCTGCTGTTAAATGGAATCTAGAGATGAAGTGAAGTGAATGTACTGCTTG 1759
Db 1724 AATTACTGCTGCTCAATCAAGTGAATTAACCTTAGAGATGTTGCTCAAGCTTCAGGCCCTGC 1783
Qy 1760 TAAAGATTTGGCTCCCAATCAAGCCTGAACAGGCTATGAGCTTCTGATGCAATTAAC 1819
Db 1784 TTCAGATTTGGCTTAACCTGAGCCGCCGAGGAGCCTTAGAGCTTCGAAATTAACATATC 1843
Qy 1820 CAGATCTTAATGTTCCAGGTTTGTCTGTTGCTGCTTGAAGAAATATTTAAGATGACA 1879
Db 1844 CAGACAGATAGCTTCAGAGATATGCTGTAGGCTGCT---GCCAGATGATGATGAAG 1900
Qy 1880 AACTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAATAATGAACGATATTGGATA 1939
Db 1901 AACTTTCTCAATATCTTTTACACCTGTCAGTGAATTAATATGAGCTTTTCTTGATTT 1960
Qy 1940 AACTGCTTGTGATTTTACTCAAAAAGCGTTAATCAATCAAGATCGATCACTTTT 1999
Db 1961 GTGCCCTCTCTAGATCTTAATTAAGAAAGCACTTGATATGAGAGATAGGCAATTTTC 2020
Qy 2000 TCTTTTGGCAATTTAAATCTGAGATCACAATTAACAGTTACTCAGAGGTTTGGCTGC 2059
Db 2021 TATTTTGGCATCTTAGGTGAGAGTACATTCCTGCTCTCAGTACAAATTTGGGTGA 2080
Qy 2060 TTTTGGAGTCTATTGGCGTGACATGGAGATGATTTGAAGCACTTAATAGCAAGTTG 2119
Db 2081 TCTTTGAACATATCTGCCGGGAAAGTGGGCAATGAAGGCTTTCTTAAGCAGGTTG 2140
Qy 2120 AAGCTATGGAAGAGCTCATTAATCTGACATTTCTCAACAGAGAAAGAGATGAAA 2179
Db 2141 AAGCACTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2200
Qy 2180 CACAAAGGTACAGATGAAGTTTATGTTGAGCAAAATGGGGGCAACAGATTTCAAGTATG 2239
Db 2201 ACAGAGCCAAAGGGAAGAGGCAATGATACCTGTTTAAACAGAGTGTCTTACCGGGAAG 2260

Qy 2240 CTCTCAGGGCTTTCTGCTCTCTTAACCCCTCTCATAGCTGGGAAATCTCAGGCTTG 2299
Db 2261 CCTCTCTGACCTGCAAGTACCCCTGAAACCAATGTTATCTCTCAGAACTCTATGTTG 2320
Qy 2300 AAGAGTGTCAATTAATGCTCTTCTGCAAAAAGGCCACTGTGTTGAATGGGAAACCCAG 2359
Db 2321 AAAAGTGCAAAATACATGAGATTTCAAAATGAAGCCTTTGTGGCTGTGATACAAATGAAG 2380
Qy 2360 ACATCATGTCAGAAATTAATCTTTTCAAGAACATGAGATCATCTTTAAATAATGGGATGATT 2419
Db 2381 TATTTGGTGAAGATTCAGT-----TGAGTGAATTTTAAATAATGGTGAATGATT 2428
Qy 2420 TACGCAAGATATGCTAACCCCTCAGATTAATGCAATTAATGAAATAATCTGCAAAATC 2479
Db 2429 TACGACAGATATGTTGACACTCCAAATGTGGCTGTATGATTTTACTTGGAAAGAG 2488
Qy 2480 AAGTCTTGAATCTTCAATGTTAATCTTAATGATGTCATCAATCGGTGACTGTGGGAC 2539
Db 2489 CTGTTTGGATCTTGGATGTTGCTTATGGCTGTTTAAAGCAAGGAGATCGCTGGCC 2548
Qy 2540 TTATCAGAGTGTGAAATAATCTCACATTAATGCAATTCAGTGAAGAGGC---C 2596
Db 2549 TCATTAAGTGTGACACCTCTGAAACAAATGCTGACATTCAGCTGAAACATGACAAATG 2608
Qy 2597 TGAAGGTGACTGCAAGTTTAAACAGCCACACATCCATCAGTGGCTCAAAAGAGAAACA 2656
Db 2609 TGCTCTGAGAGAGCTTCAACAAAGATGCCCTTGAATCTGGCTTAAGAAATACAACT 2668
Qy 2657 AAGGGGAAATATTAATGATGGGCGCATGATTTGTTTACAGATCATGCTGATATTTGTTG 2716
Db 2669 CTGGGATGACCTCGAACGAGCATTTAGAGAAATTAACATGCTGCTGCTGCTGCTACTG 2728
Qy 2717 TTGCCACTTCAATTTGGGAATTTGAGATGTCACATTAATTAATCATGCTTTAAAGATG 2776
Db 2729 TGAATCTTAATGCTCTGGGATTTGGACAGCATGATGAACAATCATGCTCAAAAAA 2788
Qy 2777 ATGCAACACTGTTTCAATATGATTTTGGACACTTTTGGATCAACAGAGAAATAATTTG 2836
Db 2789 CTGGCAGCTCTTCCATATGACTTTGACATATTTTGGAAATTTCAATCTTAAGTTTG 2848
Qy 2837 GTTATTAACGAGAGCGCTGCGTTTGTGTAACAAGATTTCTTAATATGATTAAGTA 2896
Db 2849 GAATTAAGAGGAGAGAGGCTTTTATTTACTTACATTAATTTCAATGCTATTTCAAC 2908
Qy 2897 AAGAGCCCAAGATGCAACAAGAGAAATTTGAGAGTTTCAAGAGATGTTTACA 2956
Db 2909 AAGGAAAAACAGG-----AAATACAGAAAGATTTGGCGGTTCCGAGTGTGAGG 2962
Qy 2957 AAGCTTATTAATCTTATGCGGAGCATGCCAATCTCTTCAATAATCTTTCTCATATGTC 3016
Db 2963 ATGCATATCTGATTTTACAGCGGATGGGAATCTCTTCACTCTCTTTGGCGCTGATGT 3022
Qy 3017 TTGGCTCTGATATGCGAAGCTCAATCTTTGATGATATTAATGATCATTTCCAAAGACC 3076
Db 3023 TGAATGCAAGGCTTCTGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 3082
Qy 3077 TACCTTTAGATTAATACTGACAGAGGCTTTGAGATTTTCAAGAAACAAATGAATGATG 3136
Db 3083 TTGCATTTAGGGAAGATGAAAGAGCACTCAAAACAGTTTAAAGAAATTTGATGAGG 3142
Qy 3137 CACACCAATGAGTGTGAGCAACAACAAATGAGATTTGATCTTCAACATTAATGA 3191
Db 3143 CGCTCAGGGAAAGCTGGAATTAAGTAACTGAATGAGCCGACACAGTTTCGAA 3197

RESULT 11
US-09-194-640A-2
Sequence 2, Application US/09194640A
Patent No. 6482623
GENERAL INFORMATION:
APPLICANT: Van Hasebroeck, Bart
APPLICANT: Waterfield, Michael D.

Query Match	10.5%	Score 336.2	DB 3	Length 3866
Best Local Similarity	53.5%	Pred. No.2.9e-88		
Matches 804	Conservative	0	Matches 678	Indels 21
			Gaps	4
QY	1682	TCCCCGAATTCTTACCCAAATTCCTTCCTGTTAAATGGAACCTGAGATGAAGTAA	1741	
Db	1821	TCCGGAGGCGCTTACCCCGCGCTGCTGCTGTACCAAGTGAACAAGATGAGATGTGG	1880	
QY	1742	CTCAGATGTAAGTCTTGGTAAAGATGGCTTCCAATGAGCTTAAAGGCTATGAGC	1801	
Db	1881	CCCAATGCTTACCTGCTGTGCTCTGAGCGAGAGCTGCGGCTCTGAGCGCCCTGAGC	1940	
QY	1882	TTTCGGAATGCAATTACCCAGATCCTAATGTTGAGGATTTGGCTTTGGCTTTGAAA	1861	
Db	1941	TGCTAGACTTCAAGCTTCCCGATGGCCAGTAGGCTCTTGGCCATCAAGTGGCGGA	2000	
QY	1862	AATATTTAAGATATACAAACCTTCTCAGTACCTAAATCAGGTATACAGGACTAAAT	1922	
Db	2001	AAC---TGACGAGCATAGAGCTTCCAGTACCTGCTGAGCTGATGAGGTGCTCAAGT	2057	
QY	1922	ATGAACAGTATTTGGATTAACCTGCTGTGAGATTTTAACTGAAAACGTTAACTAATC	1983	
Db	2058	ACGAGTCTTACCTGGAGCTGCGAGCTGACCAATTTCTGCTGGACCGGCCCTGGCCAAC	2117	
QY	1992	AAAGATGGGTCACTTTTCTTTTGGCATTTAAATCTGAGATGACATTAACATTA	2041	
Db	2118	GCAAGATGGGCACCTCTTTCTGGGACCTCCGCTCCGAATGACCTGCGCTGTGG	2177	
QY	2042	GTCAGAGGTTTGGCGCTGCTTTTGGAGTCTTAATGCGGTCATGTCGATGATCTGAAC	2101	
Db	2178	CCTTGGCTTGGCGCTTCACTCTGAGGCTTACTGAGGGGACGACCCACACATGAAGG	2237	
QY	2102	ACCTTAATGCGCAAGTTGAGCTATGAGAAAGCTCAATTAAGTGAATGACATTTCTAAC	2161	
Db	2238	TGCTGATGAGCAGGGGGAGAGACTGACCAAACTGAAGCCCTGATATCACTTGGTCAAC	2297	
QY	2162	AAGAGAAAGATGAAAACAACAAAGTACAGATGAAGTTTATGTTAGTGAACAAATGGCG	2221	
Db	2298	TGAGCTCTCAAGAAAGCCCCCAAGCCCCAGACCAAGAGACTGATGACTTGTGACATGGCG	2357	
QY	2222	GACCGATTTTATGATGATGCTCTCCAGGGCTTTCGTCTCTCTCTAACCCTGCTATCAG	2281	
Db	2358	AGGAGGCTTACTTAAAGGCCCTTTCGCCACTGTGACCTCCACTGACCCCAAGCACCCTGC	2417	
QY	2282	TGGGAATCTCAGGCTTGAAGATGTCGAAATATGTCTTCTGCAAAAAGCCACTGTGT	2341	
Db	2418	TGGCTGAAGTCTGGGTGAGCAGTGTACCTTCAATGAGTCCAAATGAAAGCCCTGTGGA	2477	
QY	2342	TGAATTTGGGAAGACCAGACATCATGTGCAATTAATCTTTCAAGAACATGATCATCT	2401	
Db	2478	TCATGTACAGCAAGAGAG-----GCAGCAGCGCGGAGCGTGGGCACTCATCT	2528	
QY	2402	TTAAAAATGGGGATGATTTACGGCAAGTATGCTAACCCCTCAATATTTGGCATATGG	2461	
Db	2529	TTAAGAAAGGGAAATGACTCCGGCAGGACATGCTGACCCTGCAATATGCTCAGTCTAGG	2588	
QY	2462	AAAATATCTGCAAAATCAAGSTCTTGATCTTCAATTTTACCTTATGATGTCTGCAA	2521	
Db	2589	ACGTCTGTGAACACGAGAGGGGCTGACCTGAAGATGACCCCTATAGTGTCTCCCA	2648	
QY	2522	TGGTGAATGTGGGACTTATCGAGGTGTGAAGAAATTTCAACATTAATGAGATTC	2581	
Db	2649	CCGGGAGCCGACAGGCTCATTTAGGGGTGATCCGTTTCAAGACACATGCGCAACATCC	2708	
QY	2582	A---GTGAAAGGAGGCGCTGAAGGTGACATGCAATTAACGCCACACACTCATAGT	2638	
Db	2709	AACCTCAACAGAGCAACATGGCAGCCAGCCGCTTCAACAGAGATGCTGTCAACT	2768	
QY	2639	GGCTCAAAAGCAAGAACAAAGGGGAAATATATGATGCGGCACATGATTTGTTTACAGAT	2698	
Db	2769	GGCTGAAGTCCAAAGAACCCGGGGAGGCGCTCGATTCAGCATATGAGAGTTTACCTCT	2828	
QY	2699	CATGTGCTGATATTTGTGTTCCACTTCAATTTTGGGAATGAGATGCTCAATATGTA	2758	

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Db      2829  CCTGCGCTGGCTATTGTGTGGCCACATATGTGCTGGGCAATTGGGCAATGGGACACGCCACA 2888
QY      2759  ATATCATGTTAAAGATGATGAGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATC 2818
Db      2889  ACATCATGATCCGAGAGAGTGGGACGCTGTTCCACATTTGATTTTGGCCACTTTTGGGGA 2948
QY      2819  ACAAGAGAAAAAATTTGGTTATTATGAAGAGAGCGCGCTGTTGTTTGGACACAGATT 2878
Db      2949  ATTTCAGACCAAGTTTGGAAATCAACCGCGAGCGCTGTCCATTCATCCTCACTAGCACT 3008
QY      2879  TCTTAATAGTATTAGTAAGAGGACCCCAAGATGCAAAAGACAAGAAATTGAGAGT 2938
Db      3009  TTGTCATGTGATTCAGCAGG3-----GAAAGACTAATAATAGTAGAAGAAATTGAACGT 3062
QY      2939  TTCAGAGATGCTGTTACAGGCTTATCTAGCTATTTCGGCAGCATGCCAATCTCTTCAATA 2998
Db      3063  TCGGGGGGTACTGTGAAGAGGCCCTACACACATCTCGGGCCGCCACGGGCTTCTCTCC 3122
QY      2999  ATCTTTTCTCATGATGCTTGCTTGCTTGAATGCCAGAACTGCAATCTTTTGATGATTA 3058
Db      3123  ACCCTTTTGCCCTGATCGGGCGGCGAGGCGCTGCTGAGCTGACCTGCCAAGACATCC 3182
QY      3059  CATCATTTCCAAAAGACCTTAGCTTTAATATAAATGACCAAGGCTTTGGAGATTTC 3118
Db      3183  AGTATCTCAAGACTCCCTGGCACTGGGGAAACAGAGGAGGAGCACTAAGCACTCC 3242
QY      3119  TGAACAATAATGATGATGACACACCATGCTGGCTGGACAAACAAAATGATTTGATCTTCC 3178
Db      3243  GAGGGAAGTTTAAAGAAAGCCCTCCGTAGAGCTGGAAACCAAGTAGAATGGCTGGCC 3302
QY      3179  ACA 3181
Db      3303  ACA 3305

RESULT 13
US-08-777-405A-1
: Sequence 1, Application US/08777405A
: Patent No. 5858753
: GENERAL INFORMATION:
: APPLICANT: Chantry, David
: APPLICANT: Hoekstra, Meri F.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: No. 5858753el Lipid Kinase
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall O'Toole Garstein Murray & Borun
: STREET: 6300 Sears Tower/233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/777,405A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5858753and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/33441
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ. ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5220 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..3327
US-08-777-405A-1

Query Match 10 5%; Score 336.2; DB 2; Length 5220;
Best Local Similarity 53.5%; Pred. No. 3.5e-88;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

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1682 TCCCGGAATTTACCAAAATGCTTCTGTCTTTAAATGAACTCTAGAGTGAAGT 1741
1820 TCCCGAGGCGCTAGCCCGGCTGCTGCTGTCAACCAAGTGAACAAAGCATGAGATG 1879
1742 CTCAGATGCTGCTTGTGTAAGATGGCTTCCAAATCAAGCTGAACAGGCTATGAGC 1801
1880 CCCAGATGCTTACCTGCTGTGCTCTGCGAGCTGCCCTCTGAGCGCCCTGAGC 1939
1802 TTCTGACCTGCAATTCACCAATCCATATGATTCGAGTTTGTGCTGCTTGA 1861
1940 TCTTACACTTCAAGCTTCCCGATTCGACGTAAGCTCTTCCGATCAAGTGTGCGGA 1999
1862 AATATTAAAGATGACAACTTCTCAGTACCTTAATGAGTGAAGTACTAAAT 1921
2000 AAC--TGACGACGATGAGCTGTTCAGTACCTGCTGACGCTGAGTGTCTCAAGT 2056
1922 ATGACAGATTTTGAATACCTGCTGTGATTTTACTCAAAAAGCTTAATATC 1981
2057 AGCAGTCTTACCTGAGCTGAGCTGACCAAAATTCCTGAGACCGGCTGACCAAC 2116
1982 AAGGATCGCTCTTTTCTTTGGCATTTAAATCTGAGATGACACATTAACAGTTA 2041
2117 GCAAGATCGGCACTTCTTTCTTGGCACTCCGCTCCGAGATGCAAGTCCGTG 2176
2042 GTGAGAGTTTGGCTCTTTTGGAGTCTTATTCCTGATGCTGATGAGTGTGAAGC 2101
2177 CCTGCGCTTCCGCTCATCTGAGGCTACTGACAGGCGACACCAACCATGAAG 2236
2102 ACCTTAATAGGCAAGTGAAGCTTATGAAAAGCTTAACTTACAGTCAATCTCAAC 2161
2237 TGCTGATGAAGCAGGAGGAGCACTGAACAACTGAAGGCTTAATGACTTCTCAAGC 2296
2162 AAGGAAAGAGATGAACACAAAGATGACATGAATTTTATGAGCAATGCGGC 2221
2297 TGAAGCTCAGAAAGACCCCAAGCCCAAGACCAAGAGCTGATGCACTTGTGATGCGGC 2356
2222 GACCAATTTATGATGCTCTCCAGGCTTCTGCTCTTAAACCTTGTCTATCAGC 2281
2357 AGGAGGCTTACTAGAGCCCTCTCCCACTGCACTTCCCACTCCACCCAGCACTGCG 2416
2282 TGGGAATCTCAGGCTTGAAGTGTGCAATTTATGCTTCTGCAAAAAGGCACTGTGT 2341
2417 TGGCTGAGTCTGCTGAGAGCTGACCTTATGATGCACTCCAAAGTGAAGCCCTGTGA 2476
2342 TGAATTTGGAGAACCCAGACATCATGTGCAATTTCTTTCAGAACATGAGATCATCT 2401
2477 TCATGTACAGCAACGAGG-----GCAAGGACGCGCGGCACTGTGGGCACTCATCT 2527
2402 TTAATAATGGGATGATTTACGCAAGATATGCTAACCTTCAAGTTATTCGATTAATG 2461
2538 TTAAGAACGGGATGACCTCCGAGAGACATGCTGACCTGAGATGATCCAGCTCATG 2587
2462 AAAATATCTGGCAAAATCAAGCTTGTGATCTTCAATTTTACTTTATGAGTGTGTCA 2521
2588 AGCTCTGTGGAAGCAGAGGCTGACCTGAGATGAACCCCTTATGCTGTCTCCCA 2647
2522 TGGTACTGTGTGGACCTTATGAGAGTGTGAGAAATCTCAGCATATATCAGATTC 2581
2648 CCGGAGACGCAACAGGCTTATGAGGTGTACTCCGTTTACACCATTCGCAATCTC 2707

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2582 A--GTGTAAGAGAGGCTTGAAGGTGCTGACGATTTAAAGCCACACACTCCATGAT 2638
2708 AACTCAACAGAGCAATGCGACCCACAGCGGCTTCAACAGAGTCCCTGTCTCACT 2767
2639 GGTTCAAAGCAAGAACAGGAGGAGAAATATATGATGCGGCCCATGATTTGTTACAGAT 2698
2768 GGTGAAGTCCAAAGACCCGAGGAGGAGCCCTGATTCAGACCATGAGAGTTCACCTCT 2827
2699 CATGCTGATATATGTTGTTGCCACTTCAATTTTGGATTTGAGATGTCACAAATGTA 2758
2828 CTTGCTGCTGATTTGTGTGCGCACATATGTGCTGGGCAATGGGATTCGAGACGCA 2887
2759 ATATCATGTTAAGATATGACACCTTTCATATATGATTTTGGACACTTTTGGATC 2818
2888 ACATCATATCCAGAGAGTGGCGAGCTGTTCCACATTTGATTTTGGCCACTTTTGGGGA 2947
2819 ACAAGAAAGAAATTTGTTATTAAGAGAGCGGCTCCGTTGTTTGAACAAAGTT 2878
2948 ATTTCAGACCAAGTTTGAATCAACCCGAGCGGTCCATTCCTCACCTATGACT 3007
2879 TCTTAATAGTATTTAGTAAAGAGCCCAAGATGCAAAAGCAAGATTTGAGAGGT 2938
3008 TTGTCATGTGATTCAGCAGG-----GAAGACTAATATATGAGAAATTTGAACGT 3061
2939 TTCAAGAGATGTTTAAAGGCTTATCTAGCTATTCGAGAGATGCAATCTCTCATTA 2998
3062 TCCGGGCTACTGTGAAAGGCTTACACCATCTGCGGCGCAAGGCTTCTTCTCTCC 3121
2999 ATCTTTTCTCANTGATGCTGCTGGAATCCAGACATGCAATCTTTTGAATGATATG 3058
3122 ACCTCTTGTCCCTGATGCGGCGGCGAGGCTGCTGATGCTCTCAAGACATCC 3181
3059 CATACATTCGAAAGACCTTAGCTTTAGATTAATCTAGCAAGAGCTTTGAGATATTC 3118
3182 AGTATCTAAGAGCTCCCTGCACTGGGCAAAACAGAGAGGAGCACTGAACACTTCC 3241
3119 TGAACAAATGAATGATGACACCATGATGCTGCAACAAATGATGATGATTC 3178
3242 GAGTGAAGTTTAAAGAACCTTCGTGAGAGCTGGAACCAAGTGAATGACTGCTGCC 3301
3179 ACA 3181
3302 ACA 3304

```

RESULT 14

US-08-977-871A-1
Sequence 1, Application US/08977871A

Patent No. 5882910

GENERAL INFORMATION:

APPLICANT: Chantry, David
APPLICANT: Hoeftre, Neil F.

APPLICANT: Holzman, Douglas A
TITLE OF INVENTION: No. 5882910el Lipid Kinase

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESS: Marshall O'Toole Gerstein Murray & Borun
STREET: 6100 Sears Tower/233 South Wacker Drive

CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/977.871A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/777,405

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..3327
US-08-977-871A-1

Query Match 10.5%; Score 336.2; DB 2; Length 5220;
Best Local Similarity 53.5%; Pred. No. 3.5e-88;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

QY 1682 TCCCGGAAATTCACCCAAATGCTTCTCTTTAAATGAACTCTAGAGATGAAATAG 1741
DB 1820 TCCCGGAGGGCTAGCCCGGCTGCTGTGTACCAAGTGAACAGACATGAGAGATGG 1879
QY 1742 CTGAGATGTACTGCTGTGTAAAGATTGGCCTCAATCAAGCCTGAACAGCTATGAGAC 1801
DB 1880 CCGAGATGCTCTACCTGCTGTGCTCCGCGGAGAGCTGCCGCTCTAGAGCCCTGTGAGC 1939
QY 1802 TTCTGAGCTGCAATTAACCCAGATCCATGATGAGTTTGGCTGTTCCGCTGTGAGAA 1861
DB 1940 TGTATAGCTTCACTTCCGATTTCCGATTCGAGCTCTTCCGCTTAACTGCTGCGGA 1999
QY 1862 AATATTTAAACAGATGACAACTTTCTCAGTACCTAATTCAGTACAGTACTAAAT 1921
DB 2000 AAC--TGAGGAGAGATGAGCTGTCCAGTACCTGCTGAGCTGTGCAAGTCTCAAGT 2056
QY 1922 ATGAAACAGTATTTGAGTAACTGCTGTGAGATTTTACTCAAAAAGCGTTAACTAATC 1981
DB 2057 ACAGATGCTTACCTGAGCTGAGCTGACCAAAATTCCTGCTGAGACCGGCGCTGAGCAAC 2116
QY 1982 AAGGATGCGTCACTTTTCTTGGCATTTAAATCTGAGATGACAAATTAACAGTTA 2041
DB 2117 GCAAGATCGGCTTCTTCTTCTGCACTCCGCTCCGAGATGACAGTCCGCTGCTGG 2176
QY 2042 GTGAGAGTTTGGCTGCTTGTGAGTCTTATGCGGTGATGGATGTATCTGAGC 2101
DB 2177 CCTGGGCTTCGGCTCTCATCTGAGGCTTACTGAGGGGACACCCACCAATGAAAG 2236
QY 2102 ACCTTATATGCGCAAGTTGAGGCTATGAGAAAGCTCATTAACCTTGACTGACATTTCAAC 2161
DB 2237 TGCTGATGAAAGCGGGGGAAGCACTGAGCAAACTGAAAGCGCTGAAATGACTTGTCAAGC 2296
QY 2162 AAGAGAGAAGATGAAACCAAAAGGTACAGATGAAATTTTATGTTGAGCAATGCGGC 2221
DB 2297 TGAAGCTCTGAAAGACCCCAACCCCAAGCAAGAGGCTGATGACATTTGTGATCGGC 2356
QY 2222 GACCAATTTTCAATGATGCTCTCCAGGGCTTTGTCTCTCTTAAACCTGCTCATCAGC 2281
DB 2357 AAGAGCGCTTACCTAGAGGCGCTCTCCACCTGCACTGCCACCTGCAACCCAGACCTGTC 2416
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QY 2342 TGAATTTGGGAAACCAAGCATATGTCAGAAATTAATCTTTTCAAGCAATGATGATCATCT 2401
DB 2477 TCATGTACAGCAACGAGAG-----GCAAGCAGCGGCGGACGCTGGGCGATCATCT 2527

QY 2402 TTAAAAATGGGAGTATTTTACGGCAAGATATGCTAACCTTCAGATTATTCGATTATGG 2461
DB 2528 TTAAAGAACGGGATGATGACCTCCGGAGAGCATGCTGACCTCGAGATGATCCAGCTATGG 2587
QY 2462 AAAATATCTGCAAAATCAAGTCTTGTATTTGAAATGTTAATCTTATGATGATGTCTCAA 2521
DB 2588 ACGTCTGTGAAAGCAGAGAGGCTGTGACCTGAGATGACCCCTATATGCTGCTCCCA 2647
QY 2522 TCGGTGCTGTGAGGACCTATGAGGTGTGAGAAATTCACATATATAGAGATTC 2581
DB 2648 CCGGAGACCGCAAGGCTTATTTAGGTGTACTCCGTTAAGACACATGCCAACAATCC 2707
QY 2582 A---GTGTAAGAGAGGCTTGAAGGTGCACTGACGATTTAAACAGCAACACCTCATAGT 2638
DB 2708 AACTCAACAAAGACATATGAGCCACAGCCGCTTCAACAAAGATGCTCCTGCTCACT 2767
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DB 2768 GGTGAAAGTCCAAAGAACCCGGGGAGGCGCTGTGATGACCATTTGAGAGATTCACTCT 2827
QY 2699 CATGTGCTGATATTTGCTTGGCCACCTTCACTTTTGGAAATTTGAGATCGTCAATATGTA 2758
DB 2828 CTTGTGCTGCTATTTGTGTGGCCACATATGTGCTGTGGCATTTGGCGACAGCGACA 2887
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QY 2819 ACAAGAAAGAAATTTGTTATTAACGAGAGCGCTGCGTTTGTGACAAAGAT 2878
DB 2948 ATTTCAGACCAAGTTTGAATCAACCGGAGCGGTGCCATTCATCTCATTATGACT 3007
QY 2879 TCTTAATGATGATTAATTAAGAGCCCAAGATGCAACAAAGAAATTTGACAGAT 2938
DB 3008 TTGTTCATGATGATTCAGCGG-----GAGACTATATATATGAGAAATTTGAACGGT 3061
QY 2939 TTGAGAGATGTTGTTCAAGAGCTTATCTAGCTATTTGCGGAGATGCAATCTCTGATA 2998
DB 3062 TCCGGGCTACTGTGAAGGCTTACACATCTGCGGCGCCGCTTCTTCTCC 3121
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QY 3059 CATACATTTGAAGAGACCTTATCTATGATTAATCTAGCAAGAGGCTTTGAGATTTCA 3118
DB 3182 AGTATCTCAAGAGCTCTCTGGAACCTGGGAAAAAGAGAGGAGCACTGAACACTTCC 3241
QY 3119 TGAACAAATGATGATGACACCATGTGTGGCTGCAACAAAAATGGAATTTGATCTTCC 3178
DB 3242 GAGTGAAGTTTAAGAGAGCTTCTGTGAGAGCTGAAAAACAAAGTGAATCTGCTGCCCC 3301
QY 3179 ACA 3181
DB 3302 ACA 3304

RESULT 15
US-09-225-951-1
Sequence 1, Application US/09225951
Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Weri F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589e1 Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall O'Toole Gerstein Murray & Borum
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

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      ZIP: 60606
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/225,951
      FILING DATE:
      CLASSIFICATION:
      ATTORNEY/AGENT INFORMATION:
      NAME: No. 5985589and, Greta E.
      REGISTRATION NUMBER: 35,302
      REFERENCE/DOCKET INFORMATION:
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (312) 474-6300
      TELEFAX: (312) 474-0448
      TELEX: 25-3856
      INFORMATION FOR SEQ. ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 5220 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 196..3327
      US-09-225-951-1

Query Match      10.5%; Score 336.2; DB 2; Length 5220;
Best Local Similarity 53.5%; Pred. No. 3.5e-88;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

      1682 TCCCGCAATTCCTCCCAATTCCTGCTGCTTTAAATGAGAACTTAGAGATGAAGTAG 1741
      1820 TCCCGAGGCGCTGAGCCGCGTCTGCTGCTGACCAAGTGAACAGCATAGAGATGTGG 1879
      1742 CTCAGATGTAAGTCTGTTGTTAAAGATTGGCTTCCCAATTAAGCTTGAAGCTTAGAGC 1801
      1880 CCCAGATGCTTACTGCTGCTGCTGCTGCTGCGGAGCTGCCGCTCTGAGCGCCCTGAGC 1939
      1802 TTCGAGCTGCAATTAACCAATCCATAGGTTGAGGTTTGTGCTGCTGCTAGAAA 1861
      1940 TGCTAGACTTCAAGCTTCCCGATTCGCAAGTACGCTGCTGAGTGTGCTCAAGT 1999
      1862 AATATTTAAGATGACAAATCTTCTCACTACCTTAATCAAGTACTAGTACAGTAAAT 1921
      2000 AAC--TACGAGACATGAGCTGCTTCCAGTACCTGCTGAGTGTGACAGGTCTCAAGT 2056
      1922 ATGAACAGTATTGGATTAACCTGCTTGTGAGATTTTACTCAAAAAAGCTTAATATC 1981
      2057 ACGACTCTTACCTGAGCTGAGCTGAGCTGACCAAAATTCCTGTGAGCCGGCCCTGGCCACC 2116
      1982 AAGAGATGCTTACTTTTCTTTTGGCAATTTAAATCTGAGATGACCAATAAAGATT 2041
      2117 GCMAATGCGGCACCTTCTTTCTGACACTCCGCTCCAGATGACGTCGGCTGGGTGG 2176
      2042 GTCAAGGTTTGGCTGCTTTTGAAGTCTTATGCTGATGCTGATGAGATGATCTGAAGC 2101
      2177 CCTGCGCTTCCGCTTCTGCTGAGGCTTACTGCAAGGGGCAAGCAACCAACATGAAAG 2236
      2102 ACCTTAATAGGCAAGTTGAGGCTTANGAAAGTCAATTAATCTGATGACATTTCAAAAC 2161
      2237 TCGTATGTAAGGAGGGGAGGCACTGAGAAACTGAAGGCCCTGATGACTTGTGTAAGC 2296
      2162 AAGAGAGAAAGATGAACAACAAGATACAGATGAAGTTTATGTTAGCAAAATGCGGC 2221
      2297 TGAGCTCTCAGAAAGACCCCAAGCCCAAGCAAGAGAGCTGATGACCTGTGATCGGCG 2356
      2222 GACCAATTTTCATGATGCTCTCAGGGCTTTCTGCTCTTAAACCTGTCTCATAGC 2281
      2357 AGGAGGCTTACTAGAGGCGCTTCCCACTGCAAGTCCCACTGACCCAGCAACCCTTGC 2416

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      2282 TGGAAATCTCAGGCTTGAAGATGTGCAATTTATGCTTTGCAAAAAGCCACTGTGT 2341
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      2477 TCATGTACGCAACGAGAG-----GCAGGAGGGGGGCGCGGTGGGATCATCT 2527
      2402 TTAATAATGGGATGATTTACGGCAAGATATGCTAACCTTCAAGTTATTCGCAATTATGG 2461
      2528 TTAAGACGGGATGACCTCCGCGAGGACATGCTGACCTGAGATGATTCAGCTCATGG 2587
      2462 AAAATATCTCGCAAAATCAAGGCTTTGATCTTGAATGTTACCTTATGATGCTGTCAA 2521
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      2522 TGGGTGACGTGTGGGACTTATCGAGTGTGAGAAATTCACACTATATATGACATTC 2581
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      2582 A---GTGAAGAGAGCCCTGAAGGTGACCTGACGTTTAACAGCCACACTCCATCACT 2638
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      2768 GGCTGAAGTCCAAAGAACCGGGGAGCCCTGATGAGCATTGAGAGTTTACCTCT 2827
      2699 CATGTCTGATATATGTGTGTGACCTTCAATTTTGGAAATGAGATGCTGACATATGA 2758
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      2888 ACATCATGATCCGAGAGAGTGGGAGCTGTTCACATGATTTTGGCACTTCTGGGGA 2947
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      2948 ATTTCAAGACCAAGTTTGAATCAACCGGAGGTGTCCATTCATCTCACTATGACT 3007
      2879 TCTTAATAGTATATGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGT 2938
      3008 TTGTCAATGTGATTCAAGAGG-----GAAGCTAATTAATGAGAAATTTGAACGCT 3061
      2939 TTCAGAGATGTGTTAAGGCTTATCTAGCTATTTGGCAGCATGCCAATCTCTCAATTA 2998
      3062 TCCGGGCTACTGTGAAGGCTTAACACATCTGCGCGCCAGCGGCTTCTTCTCC 3121
      2999 ATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGTGATATTTG 3058
      3122 ACCCTTTTCCCTTATGAGGCGGCGAGGCTGCTGAGCTGAGCTGCTCCAAAGACATCC 3181
      3059 CATCATTTGAAAGACCTTACTTTAGATTAATACTGACAAAGAGCTTTGAGATTTCA 3118
      3182 AGTATCTTAAGGACTCCCTGACACTGGGAAAAAGAGGAGGAGCACTGAAGCACTTCC 3241
      3119 TGAACAATATGATGATGACCAACATGCTGCTGAGCAACAAAATGATATGATCTTCC 3178
      3242 GAGTGAATTTAAGCAACCCCTCGGTGAGAGCTGTGAACCAAAAGTGAATGAGGTGCGCC 3301
      3179 ACA 3181
      3302 ACA 3304

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Search completed: November 7, 2003, 13:16:14
 Job time : 156.839 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:07:07 ; Search time :40.233 Seconds
(without alignments)
16024.736 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207
Sequence: 1 ATGCCTCCAGACCATCATC.....AGCAGCATGCTTGACGTA 3207

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
26: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3207	100.0	3207	14	AA051155
2	3202.2	99.9	3498	15	AA057012
3	3008.6	93.8	3412	14	AA051156
4	3008.6	93.8	3424	24	AB159523
5	3008.6	93.8	3424	24	AB159523
6	519.2	16.2	741	21	AA02190
7	448.2	14.0	3213	21	AA05690
8	448.2	14.0	3213	24	ABV78026

9	448.2	14.0	3213	24	AA514366	CDNA encoding huma
10	408.8	12.7	412	25	ABX37274	Bovine EST associa
11	336.2	10.5	3387	19	AAV16533	CDNA encoding mamma
12	336.2	10.5	3668	21	AA13154	Human phosphatidyl
13	336.2	10.5	3668	24	ABR84750	Human CDNA differe
14	336.2	10.5	3668	24	AA514363	CDNA encoding huma
15	336.2	10.5	5220	19	AAV31340	Human phosphatidyl
16	336.2	10.5	5220	20	AA159532	CDNA sequence enco
17	336.2	10.5	5220	21	AA232882	Human PI 3-kinase
18	323.4	10.1	3525	24	ABR84381	Human CDNA differe
19	297.4	9.3	3773	23	ABU07215	Drosophila melanog
20	288.8	9.0	5162	20	AAV74104	Human G-protein re
21	288.8	9.0	5162	21	AA286814	Human p120 regulat
22	288.8	9.0	5397	24	AB159522	Human phosphatidyl
23	288.8	9.0	5397	24	AB159522	CDNA encoding huma
24	285	8.9	4134	17	AA758545	Human phosphatidyl
25	285	8.9	4137	17	AA758545	Human phosphatidyl
26	277.6	8.7	3808	19	AAV05634	Human phosphatidyl
27	277.6	8.7	3808	20	AAV74100	Porcine phosphatidyl
28	277.6	8.7	3808	21	AA286813	Porcine G-protein
29	262.6	8.2	4074	22	AA137431	Pig p120 regulator
30	262.6	8.2	4074	22	ABR07289	Human musculoskele
31	262.6	8.2	4074	22	ABR07290	Human pancreatic c
32	262.6	8.2	4074	22	AAK89934	Human G-protein
33	262.6	8.2	4074	22	AAK89935	Human digestive sy
34	262.6	8.2	4074	25	ABX60419	CDNA encoding nove
35	233.6	7.3	1074	23	AA573988	CDNA encoding nove
36	232.8	6.9	5285	18	AA780199	DNA encoding novel
37	218.4	6.8	5061	19	AAV42920	phosphatidyl inosi
38	218.4	6.8	5061	25	ABT17093	CDNA encoding a hu
39	198.2	6.2	4491	23	AA571517	Androgen-independe
40	198.2	6.2	4878	24	ABR59725	DNA encoding novel
41	183	5.7	5990	24	ABR62570	Novel human coding
42	173	5.4	4498	23	AA569360	Rat sequence diffe
43	173	5.4	4747	22	ABR08693	DNA encoding novel
44	173	5.4	4747	22	AAH95523	Human PI3-kinase h
45	148.4	4.6	170	24	AB136640	Human protein enco
						Human colon tumour

ALIGNMENTS

RESULT 1	
AA051155	
ID	AA051155 standard; cDNA; 3207 BP.
AC	AA051155;
XX	
DT	25-MAR-2003 (updated)
DT	09-JAN-2003 (updated)
DT	12-APR-1994 (first entry)
XX	
DE	p110 cDNA.
XX	
KW	Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW	antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW	platelets; neurorphil activity; 3-phosphorylated phosphoinositides;
se.	
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	1.3207
FT	CDS
FT	Location/Qualifiers
FT	1.3207
FT	/*tag= a
FT	/note= "PI3- kinase p110"
XX	
PN	W09321328-A1.
XX	
PD	28-OCT-1993.
XX	
PF	13-APR-1993; 93WO-GB00761.
XX	
PR	13-APR-1992; 92GB-0008135.

QY 1621 TCTGAATCACTAGACAGAGAAAGATTTCTGTGAGCCACAGACACTATGTGTAAT 1660
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 Db 1741 GCTCAGATGTAAGTGTGTAAGATGAGCTTCATCAACAGCTGAGAGAGATGAG 1800
 QY 1801 CTCTTGACATGCAATTAACCAAGATCTATGATGAGGTTTGTCTGTGTTAGAA 1860
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 Db 2221 CGACCGATTTTCAATGATGCTCTCCAGGCTTTCTGTCTCTTAAACCTGCTCATCAG 2280
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 Db 2281 CTGGGAATCTCAGGCTTGAAGAGTGCAGATTAATGCTCTGCAAAAAGGCCACTGTGG 2340
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 Db 2341 TTGAATTTGGAGAACCCAGACATCATGTCAAGATTAATCTTTCAAGACATGAGATCATC 2400
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 Db 2401 TTTAAAAATGGGATGATTTAAGGCAAGATATGCTAACCTTCAAGATTTTGCATTAAG 2460
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Db 2701 TGTGCTGATATTTGTGTGCACTTCAATTTTGGAAATGAGATCGTCAATATAGTAAT 2760
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 Db 2761 ATCATGGTTAAACATGATGACCAACGTTTCATATATGATTTTGGACACTTTTGGATCAC 2820
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 QY 3121 AACAATATGATATGACACCACTGTGCTGAGACACAAATATGATTTGATCTTCAC 3180
 Db 3121 AACAATATGATATGACACCACTGTGCTGAGACACAAATATGATTTGATCTTCAC 3180
 QY 3181 ACAATTAGCAGATGCTTTGAATGCA 3207
 Db 3181 ACAATTAGCAGATGCTTTGAATGCA 3207

RESULT 2
 AA057012
 ID AA057012 standard: cDNA to mRNA, 3498 BP.
 XX
 AC AA057012;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-AUG-1994 (first entry)
 XX
 DE Pedins 3-kinase 110 kD catalytic subunit cDNA.
 XX
 KW 110 kD catalytic subunit, phosphatidyl inositol 3-kinase;
 KW transformation; Schizosaccharomyces pombe; mit promoter; choline;
 KW Pedins 3-kinase; assay; detection; cell growth; regulation; cancer;
 KW blood vessel plaques; ss.
 XX
 OS Bos taurus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3207
 FT /-tag= a
 FT /product= p110
 XX
 PN W09403609-A1.
 XX
 PD 17-FEB-1994.
 XX
 PF 05-AUG-1993; 93WO-GB01651.
 XX
 PR 05-AUG-1992; 92GB-0016654.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Goode NT, Nurse PM, Parker PUJ, Waterfield MD;
 XX
 DR WPI; 1994-065697/08.
 DR P-PSDB; AAR46294.

XX Eukaryotic cells transformed with mammalian phospholipid or
 PT protein kinase DNA - useful in assays for compounds involved in
 PT cell growth regulation and for treating cancers
 XX
 PS Disclosure; Fig 1; 71pp; English.

XX This sequence encodes the 110 kD catalytic subunit of the phosphatidy-
 CC inositol (PtdIns) 3-Kinase. This sequence was transformed into
 CC Schistosomacromyces pombe cells under the regulatory control of the
 CC mnt promoter in an embodiment of the invention. In the presence of
 CC thiamine the promoter is inactive and the cells carrying the PtdIns
 CC catalytic subunit plasmid grow as the parental strain. In the absence
 CC of thiamine the mnt promoter functions and the PtdIns 3-kinase
 CC catalytic subunit is induced. PtdIns activity is substantially
 CC increased under these conditions. Cells containing constructs such as
 CC this, are useful in assays for detecting compounds involved in cell
 CC growth regulation. It is also used as the basis for detecting
 CC compounds for treating cancers and the formation of blood vessel
 CC plaques.
 CC (updated on 25-MAR-2003 to correct PN field.)
 CC
 XX

Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T; 0 other;

Query Match 99.9%; Score 3202.2; DB 15; Length 3498;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3204; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 61 CTAGTGAATGTTTACTTACCAATGGATGATAGTACTTTAGATGCTTCGTGAGGCT 120
 QY 121 ACGTTAATAGATTAAGCATGAACTATTAAAGACAGAAATACCCCTCCATCAA 180
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Db 661 ATTGCTGAAGCAATCAGAAAAAACTCGAAGTATGTTGCTATATCTGAACAACTAAAA 720
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 Db 1501 TCCCGTGAACAGAGATTTAGTTATTCCTCATGAGACTGAGTAAAGACTAGCTAGAGAC 1560
 QY 1561 AATGAATTAAGAAATGATTAAGAAACAGCTCCAGCAATTTGTACAGAGATCTCTTA 1620
 Db 1561 AATGAATTAAGAAATGATTAAGAAACAGCTCCAGCAATTTGTACAGAGATCTCTTA 1620
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 QY 1681 ATCCCGGAAATTTCAACCAATTTCTGTGTTTAAATGAACTTTAAGATGAAGTA 1740
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 QY 1741 GCTCAGATGACTGTTGTTAAAGATTTGCTTCAATCAAGCTGAACAGGCTATAGAG 1800

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Db      1741 GCTCAGATGTAAGTCTTGTTAAAGATGGCTCCAACTCAACCCCTGAAACAGGCTATGAG 1800
Qy      1801 CTTCGAGCTGCAATTAACCCAGATCCTATGTTGAGAGTTTTCGTTGGTCTTAGAA 1860
Db      1801 CTTCGAGCTGCAATTAACCCAGATCCTATGTTGAGAGTTTTCGTTGGTCTTAGAA 1860
Qy      1861 AATATTTAAACAGATGACAAACCTTCTCAGTACCTTAATTCAGCTAGTACAGGTACTAAA 1920
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Qy      1921 TATGAACAGTATTTGGATAACCTGCTGTGAGATTTTCTCAAAAAGGGTAACTAAAT 1980
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Qy      1981 CAAGAGATGCTGCTCTTTTCTTTGGCAATTTAAATCTGAGATGCAATTAACAGTT 2040
Db      1981 CAAGAGATGCTGCTCTTTTCTTTGGCAATTTAAATCTGAGATGCAATTAACAGTT 2040
Qy      2041 AGTCAGAGTTTGGCTGCTTTTGGAGTCTATTCCTGATGCTGAGATGTAATCGAAG 2100
Db      2041 AGTCAGAGTTTGGCTGCTTTTGGAGTCTATTCCTGATGCTGAGATGTAATCGAAG 2100
Qy      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAAGCTGATTAACCTGACATCTCCAA 2160
Db      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAAGCTGATTAACCTGACATCTCCAA 2160
Qy      2161 CAAGAGAGAGAGATGMAACACAAAAGTACAGATGAGTTTATGAGCAATGCGG 2220
Db      2161 CAAGAGAGAGAGATGMAACACAAAAGTACAGATGAGTTTATGAGCAATGCGG 2220
Qy      2221 GACCCAGATTTATGATGATGCTCTCCAGGGCTTTCTGTCTCTCTTAAACCTGCTCATCAG 2280
Db      2221 GACCCAGATTTATGATGATGCTCTCCAGGGCTTTCTGTCTCTCTTAAACCTGCTCATCAG 2280
Qy      2281 CTGGGAAATCTGAGGCTTGAAGATGTCGAATTAATGCTCTTGGCAAAAAGGCGCAGCTGAG 2340
Db      2281 CTGGGAAATCTGAGGCTTGAAGATGTCGAATTAATGCTCTTGGCAAAAAGGCGCAGCTGAG 2340
Qy      2341 TTGAATTTGGAGAACCCACATCATGTCAGATTAATCTCTTCAAGAACATAGAGATCATC 2400
Db      2341 TTGAATTTGGAGAACCCACATCATGTCAGATTAATCTCTTCAAGAACATAGAGATCATC 2400
Qy      2401 TTTAAAAATGGGGAATTTACGCGCAAGATATGCTAACCCCTCAAGTATTTGCGCAATTATG 2460
Db      2401 TTTAAAAATGGGGAATTTACGCGCAAGATATGCTAACCCCTCAAGTATTTGCGCAATTATG 2460
Qy      2461 GAAAAATATCTGGCAAAATCAAGGCTTGAATCTTGAATTTGAATTTGAGATGCTGCTCA 2520
Db      2461 GAAAAATATCTGGCAAAATCAAGGCTTGAATCTTGAATTTGAATTTGAGATGCTGCTCA 2520
Qy      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCTCACACTATTAATGCGAGAT 2580
Db      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCTCACACTATTAATGCGAGAT 2580
Qy      2581 CAGGTGTAAGAGGCTTGAAGGTCATGCACTGATTTAAACGCGCACACCTCCATCAGTGG 2640
Db      2581 CAGGTGTAAGAGGCTTGAAGGTCATGCACTGATTTAAACGCGCACACCTCCATCAGTGG 2640
Qy      2641 CTCAAGACAGAGAAACAGGGGGAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
Db      2641 CTCAAGACAGAGAAACAGGGGGAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
Qy      2701 TGTGCTGATATTTGTGTGCCACTTCAATTTGGGAAATTTGAGATGTCACAAATGTAAT 2760
Db      2701 TGTGCTGATATTTGTGTGCCACTTCAATTTGGGAAATTTGAGATGTCACAAATGTAAT 2760
Qy      2761 ATCATGTTAAAGATGATGACAACTGTTCTATATAGATTTTGAACACTTTTGGATCAC 2820
Db      2761 ATCATGTTAAAGATGATGACAACTGTTCTATATAGATTTTGAACACTTTTGGATCAC 2820
Qy      2821 AAGAGAGAAAAATTTGGTTATTAAGAGAGGCGCGCTTGTGTTGACACAAATTTTC 2880
Db      2821 AAGAGAGAAAAATTTGGTTATTAAGAGAGGCGCGCTTGTGTTGACACAAATTTTC 2880

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Qy      2881 TTATATGATATTAAGTAAAGAGCCCAAGATGCACAAAAGCAAGAGATTTGAGAGTTT 2940
Db      2881 TTATATGATATTAAGTAAAGAGCCCAAGATGCACAAAAGCAAGAGATTTGAGAGTTT 2940
Qy      2941 CAGGAGATGTGTTACAGGCTTATCTTATTTGGCAGCATGCCAATCTTTCAATAAAT 3000
Db      2941 CAGGAGATGTGTTACAGGCTTATCTTATTTGGCAGCATGCCAATCTTTCAATAAAT 3000
Qy      3001 CTTTCTCATATAGATGCTTGGCTGTGGAATGCCAAGCTCCATCTTTATATATATGCA 3060
Db      3001 CTTTCTCATATAGATGCTTGGCTGTGGAATGCCAAGCTCCATCTTTATATATATGCA 3060
Qy      3061 TACATTCGAAGAACCTTACCTTTAGATTAACCTGAGCAAGAGGCTTTGGAGTATTCATG 3120
Db      3061 TACATTCGAAGAACCTTACCTTTAGATTAACCTGAGCAAGAGGCTTTGGAGTATTCATG 3120
Qy      3121 AAACAAATGATGATGACACACCATGCTGAGAACAAACAAATGATTTGATCTTCAC 3180
Db      3121 AAACAAATGATGATGACACACCATGCTGAGAACAAACAAATGATTTGATCTTCAC 3180
Qy      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207
Db      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207

RESULT 3
AA051156
ID   AA051156 standard; cDNA, 3412 BP.
XX
XX   AA051156;
AC
XX
XX   25-MAR-2003 (updated)
DT
XX   12-APR-1994 (first entry)
DE
XX
XX   Human p110 cDNA.
KW
XX
XX   Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW
XX
XX   antiproliferative; cell proliferation; inhibition; prophylaxis; therapy;
KW
XX
XX   platelets; neutrophil activity; 3-phosphorylated phosphoinositides;
KW
XX
XX
OS   Homo sapiens.
FH
XX
XX   Key      Location/Qualifiers
FT
XX   CDS      1..3207
FT
XX           /*tag= a
FT
XX           /note= "PI3- kinase p110"
PN
XX
XX   WO9321328-A1.
PD
XX
XX   28-OCT-1993.
PF
XX
XX   13-APR-1993; 93WO-GB00761.
PR
XX
XX   13-APR-1992; 92GB-0008135.
PA
XX
XX   (LUDW-) LUDWIG INST CANCER RES.
PI
XX
XX   Hiles ID, Fry MD, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI
XX
XX   Panayotou G, Volinia S, Gout I;
XX
XX
XX   WPI. 1993-351736/44.
DR
XX
XX   P-FSDB; AAR43342.
XX
XX
XX   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
XX
XX   activity, useful for controlling cell proliferation
XX
XX
XX   Claim 7, Fig 16; 146pp; English.
CC
XX
XX   Southern blot analysis was performed using a bovine cDNA probe contg.
CC
XX
XX   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC
XX
XX   from a cDNA library constructed from mRNA isolated from the human

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QY	1	TTGGCTCCAAAGCCATCATCGGTGAACTGTGGGGCATTCACCTTGAATGCTCCCAAGATC	60
Db	1	ATGGCTCCAAAGCCATCATCGGTGAACTGTGGGGCATTCACCTTGAATGCTCCCAAGATC	60
QY	61	CTAGTAGAATGTTTACTACCAATGGAGTAGTACTGACTTTAGAAATGCTCCCGTAGGGCT	120
Db	61	CTAGTAGAATGTTTACTACCAATGGAGTAGTACTGACTTTAGAAATGCTCCCGTAGGGCT	120
QY	121	ACGTTAATAACGATAAAGCATGAATATTTTAAAGAAAGCAAAATAATCCCTCCATCAAA	180
Db	121	ACATTAGTAATATAAGCATGAATATTTTAAAGAAAGCAAAATAATCCCTCCATCAAA	180
QY	181	CTTCTTCAAGATGAATCTCTTCAACATTTTCGTAGTGTACCCAGAAGCAAGAAAGGAA	240
Db	181	CTTCTTCAAGATGAATCTTACATTTTCGTAGTGTATCCCAAGAAAGCAAGAAAGGAA	240
QY	241	GAAATTTTGTAGTAACAGAGCACTTGTGACCTTGGCTTTTCAACCCCTTTTAAAA	300
Db	241	GAAATTTTGTAGTAACAGAGCACTTGTGATCTTGGCTTTTCAACATTTTAAAA	300
QY	301	GTAATTGAACCACTAGGCAACCGTGAAGAAAGATCTCAATCGAATAATGTGTGCT	360
Db	301	GTAATTGAACCACTAGGCAACCGTGAAGAAAGATCTCAATCGAATAATGTGTGTCT	360
QY	361	ATCGGCAATGCCAGTGTGTGAATTGATATGTGTTTAAAGATCCAGAAAGTACAGGACTCCGA	420
Db	361	ATCGGCAATGCCAGTGTGCGAATTGATATGTGTTTAAAGATCCGAAATACAGGACTCCGA	420
QY	421	AGAAATATTCCTCAATGTTTGTAAAGAAAGCTGTGGATCTTAGGGATTTAAATTCACCTCAT	480
Db	421	AGAAATATTCCTTAATGTTTGTAAAGAAAGCTGTGGATCTTAGGGATCTTAAATTCACCTCAT	480
QY	481	AGTAGAGCAATGTATGTTTTTATTCCTCCAAATGTGAATCTTCAACAGAACTGCCAAAGCAC	540
Db	481	AGTAGAGCAATGTATGTCTATCCGCCACATGTGAATCTTCAACAGAGCTGCCAAAGCAC	540
QY	541	ATAATATATAAATGTGAATTAAGGGCAATATAAGTGTGATTTGGGTATATAGTTTCTCCA	600
Db	541	ATAATATATAAATGTGATAGGGCCAAATATATGTGTGATTTGGGTATATAGTTTCTCCA	600
QY	601	AATAATGACAAACAGAACTATCTTGAAATTCACCATGACTGTGTGCCAGAAACAAGTA	660
Db	601	AATAATGACAAACAGAAATATACCTGAAATTCACCATGACTGTGTGCCAGAAACAAGTA	660
QY	661	ATTGCTGAAGCAATCAGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAATTTAAA	720
Db	661	ATTGCTGAAGCAATCAGAAAAAACTGGAAGTATGTTGCTATCATCTGAACAATTTAAA	720
QY	721	CTCTGTGTTTAGAATATCAGGGCAAGTATTTTAAAGTGTGAGTGTGATGTAATAC	780
Db	721	CTCTGTGTTTAGAATATCAGGGCAAGTATTTTAAAGTGTGAGTGTGATGTAATAC	780
QY	781	TTTCCTAGAAAAATATCTCTGTAGTCAAGTATAGTATATMAAGACGTGTATATATCTTGGG	840
Db	781	TTTCCTAGAAAAATATCTCTGTAGTCAAGTATAGTATATMAAGACGTGTATATATCTTGGG	840

[illegible]

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Db      1861 AATATTTAAGATGACAAACTTCTCAGTATTTAATGAGTAGTACAGGTCCTAAAA 1920
Qy      1921 TATGAACAGTATTTGGATAACCTGCTTGAGATTTTAACTCAAAAAAGCGTTAACTAAT 1980
Db      1921 TATGAACAGTATTTGGATAACCTGCTTGAGATTTTAACTCAAAAAAGCGTTAACTAAT 1980
Qy      1981 CAAAGATGCTGACCTTTTCTTTTGGCAATTTAAATCTGAGATGCAACAATAAAGAGTT 2040
Db      1981 CAAAGATGCTGACCTTTTCTTTTGGCAATTTAAATCTGAGATGCAACAATAAAGAGTT 2040
Qy      2041 ACTCAGAGGTTGGCCCTGTTTGGAGTCTCTATTTGCCGTCATGTGGGATGTAATCTGAAG 2100
Db      2041 ACCCAGAGGTTGGCCCTGTTTGGAGTCTCTATTTGGGTCATGTGGGATGTAATTTGAAG 2100
Qy      2101 CACCTTAATAGGCAAGTTGAGGCTATGSAAGAGCTATTAACCTGACGACATCTTCAAA 2160
Db      2101 CACCTTAATAGGCAAGTTGAGGCAATGSAAGAGCTATTAACCTGACGACATCTTCAAA 2160
Qy      2161 CAAAGAGAGAGATGAAAACACAAAAGGTACAGATGAAGTTTAACTTGAAGCAATGCGG 2220
Db      2161 CAGGAGAGAGAGATGAAAACAAAAGGTACAGATGAAGTTTAACTTGAAGCAATGCGG 2220
Qy      2221 GCACGAGATTTATGAGATGCTCTCCAGGCTTTCTGCTCTCTAAACCTGCTCATCG 2280
Db      2221 GCACGAGATTTATGAGATGCTCTCCAGGCTTTCTGCTCTCTAAACCTGCTCATCG 2280
Qy      2281 CTGGGAAATCTCAGGCTTGAAGAGTGTCCGATTTATGCTTTCGCAAAAAGGCGCAGTGG 2340
Db      2281 CTAGGAAATCTCAGGCTTGAAGAGTGTCCGATTTATGCTTTCGCAAAAAGGCGCAGTGG 2340
Qy      2341 TTGAATTTGGAGAACCCGACATCATGTGAGATTTACTCTTTCAGAACATAGATCATC 2400
Db      2341 TTGAATTTGGAGAACCCGACATCATGTGAGATTTACTCTTTCAGAACATAGATCATC 2400
Qy      2401 TTTAAAAATGGGAGATTTAGGCAAGTATGCTAACCTTCAAGATTTATGCTAATATG 2460
Db      2401 TTTAAAAATGGGAGATTTAGGCAAGTATGCTAACCTTCAAGATTTATGCTAATATG 2460
Qy      2461 GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTTCGAATGTACCTTATGAGATGTCGTA 2520
Db      2461 GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTTCGAATGTACCTTATGAGATGTCGTA 2520
Qy      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCTACACTAATATGAGAT 2580
Db      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCTACACTAATATGAGAT 2580
Qy      2581 CAGTGTAAAGAGGCTTGAAGAGTGTGACGCTTTAAACGCAACACTCCATAGTGG 2640
Db      2581 CAGTGTAAAGAGGCTTGAAGAGTGTGACGCTTTAAACGCAACACTCCATAGTGG 2640
Qy      2641 CTCAAGACAAAGAACAGGGGGAATATATGATGCGGCATGATTTGTTTACAGATCA 2700
Db      2641 CTCAAGACAAAGAACAGGGGGAATATATGATGCGGCATGATTTGTTTACAGATCA 2700
Qy      2701 TGTGCTGATATTTGTGTCACCTTCAATTTGGGAATTTGAGATGTCACAATAGTAT 2760
Db      2701 TGTGCTGATATTTGTGTCACCTTCAATTTGGGAATTTGAGATGTCACAATAGTAT 2760
Qy      2761 ATCATGTTAAAGATGATGACACATGTTTCAATATGATTTTGAACACTTTTGGATAC 2820
Db      2761 ATCATGTTAAAGATGATGACACATGTTTCAATATGATTTTGAACACTTTTGGATAC 2820
Qy      2821 AAGAAAGAAAAATTTGTTATTAAGAGAGGCGCGGTTTGTGTTTGAACCAAAATTT 2880
Db      2821 AAGAAAGAAAAATTTGTTATTAAGAGAGAGCGTGGCAATTTGTTTGAACAGGATTT 2880
Qy      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGCAAAAAGCAAGAAATTTGAGAGTTT 2940
Db      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGCAAAAAGCAAGAAATTTGAGAGTTT 2940
Qy      2941 CAGGAGATGTGTATACAGGCTTATCTAGCTATTTGGCGAGCATGCAATCTCTCAAT 3000
Db      2941 CAGGAGATGTGTATACAGGCTTATCTAGCTATTTGGCGAGCATGCAATCTCTCAAT 3000

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Qy      3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGATGCAATCTTTGATGATATGCA 3060
Db      3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGATGCAATCTTTGATGATATGCA 3060
Qy      3061 TACATTCGAAGAACCTTACCTTTAGATMAAACTGACCAAGAGCTTTGGAGTATTCATG 3120
Db      3061 TACATTCGAAGAACCTTACCTTTAGATMAAACTGACCAAGAGCTTTGGAGTATTCATG 3120
Qy      3121 AAACAAATGAATGATGACACCATGCTGCTGACCAAAAAATGATTTGATCTTCAC 3180
Db      3121 AAACAAATGAATGATGACACCATGCTGCTGACCAAAAAATGATTTGATCTTCAC 3180
Qy      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207
Db      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207

RESULT 4
ABL59523
ID ABL59523 strand: cDNA, 3424 BP.
XX
AC ABL59523;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme;
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW chromosome 3q26.3; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200227028-A1.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-US30366.
XX
PR 28-SEP-2000; 2000US-0676052.
XX
PA (ATAT-) ATRACIN TECHNOLOGIES INC.
XX
PI Skinner MK, Patton JL, Chaudhary J;
XX
DR WPI: 2002-402054/43.
XX
PT Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action
XX
PS Example 1: Page 82-83; 113pp; English.
XX
CC The present invention describes a method for identifying tumour
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilised on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;

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Dp	2113	CACCTGAAATAGGCAAGTCAGGCAATGGAAGAGCTCAATTAACCTTAACGACATTTCTCAA	2172
Qy	2161	CAGAGGAAGAAAGATGAAACACAAAAGCTACAGATGAAGTTTATGTTAGCAAAATGCGG	2220
Dp	2173	CAGGAGAGAAAGATGAAACACAAAAGGTAACAGATGAAGTTTATGTTAGCAAAATGAGG	2232
Qy	2221	CGACAGATTTATCATGATGCTCTCCAGGGCTTCTGTCTCCCTTAACCGTCGTCATACG	2280
Dp	2293	CGACAGATTTATCATGATGCTCTCCAGGGCTTCTGTCTCCCTTAACCGTCGTCATACG	2292
Qy	2281	CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGTCTTCGCAAAAGGCCACTGTGG	2340
Dp	2293	CTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTAATGTCTTCGCAAAAGGCCACTGTGG	2352
Qy	2341	TTGAATTTGGAGAACCCCGACATCATCTGCAGATTAATCTCTTTCAGAACATGAGATCATC	2400
Dp	2353	TTGAATTTGGAGAACCCCGACATCATCTGCAGATTAATCTCTTTCAGAACATGAGATCATC	2412
Qy	2401	TTTAAAAATGGGAGATTTTACGGCAAAATATGCTAACCCCTCAGATTAATTCGATTAATG	2460
Dp	2413	TTTAAAAATGGGAGATTTTACGGCAAAATATGCTAACCCCTCAGATTAATTCGATTAATG	2472
Qy	2461	GAAAAATATCTGGCAAAATCAAGGTCCTTGATCTTCGAAATGTACCTTAATGATGTCTGCA	2520
Dp	2473	GAAAAATATCTGGCAAAATCAAGGTCCTTGATCTTCGAAATGTACCTTAATGATGTCTGCA	2532
Qy	2521	ATCGGTGACTGTGGGACTTATCGAGGTGTGAGAAAATTCTCACATATATATGACAGATT	2580
Dp	2533	ATCGGTGACTGTGGGACTTATCGAGGTGTGAGAAAATTCTCACATATATATGACAGATT	2592
Qy	2581	CAGGTGAAGGAGGCTTAAAGTGCATCTGCAGTTTAAACAGCCACACACTCATAGTGG	2640
Dp	2593	CAGGTGAAGGAGGCTTAAAGTGCATCTGCAGTTTAAACAGCCACACACTCATAGTGG	2652
Qy	2641	CTCAAAACAAGAACAAAGGCGGAAATATATATGATCGGCGCATCGATTTGTTTAAACAGATCA	2700
Dp	2653	CTCAAAACAAGAACAAAGGCGGAAATATATATGATCGGCGCATCGATTTGTTTAAACAGATCA	2712
Qy	2701	TGTGCTGAGATATGTTGTTGCCACTTCAATTTTGGGAATTTGAGATTCGTCAAAATGTAAT	2760
Dp	2713	TGTGCTGAGATATGTTGTTGCCACTTCAATTTTGGGAATTTGAGATTCGTCAAAATGTAAT	2772
Qy	2761	ATCATGTGTTAAAGATGATGACCAACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2820
Dp	2773	ATCATGTGTTAAAGATGATGACCAACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2832
Qy	2821	AAGAAGAAAAAATTTGGTTATTAATAAGAGGCGGCTGCTGTTGTTGACACAAGATTTTC	2880
Dp	2833	AAGAAGAAAAAATTTGGTTATTAATAAGAGGCGGCTGCTGTTGTTGACACAAGATTTTC	2892
Qy	2881	TTAAATAGTATTTAGTAAAGAGCCCAAGATATGCAAAAGACAAAGAAATTTGAGAGGTTT	2940
Dp	2893	TTAAATAGTATTTAGTAAAGAGCCCAAGATATGCAAAAGACAAAGAAATTTGAGAGGTTT	2952
Qy	2941	CAGAGATGTGTTCAAAGGCTTATATCTATGCTATTTGCGACGATGCGAATCTCTTCATTAAT	3000
Dp	2953	CAGAGATGTGTTCAAAGGCTTATATCTATGCTATTTGCGACGATGCGAATCTCTTCATTAAT	3012
Qy	3001	CTTTTTCATATGATGCTGTCGCTGCGAATGCAAACTGCAATCTTTTGAATATTTGCA	3060
Dp	3013	CTTTTTCATATGATGCTGTCGCTGCGAATGCAAACTGCAATCTTTTGAATATTTGCA	3072
Qy	3061	TACATTCGAAAGACCCCTAGCTTTTATGATTAATACTGAGCAAGAGCTTTGAGATATTTCATG	3120
Dp	3073	TACATTCGAAAGACCCCTAGCTTTTATGATTAATACTGAGCAAGAGCTTTGAGATATTTCATG	3132
Qy	3121	AAACAAATGAAATGATGCAACCATGTGTGCTGCAACAACAAAATGATGATGATCTTCCAC	3180
Dp	3133	AAACAAATGAAATGATGCAACCATGTGTGCTGCAACAACAAAATGATGATGATCTTCCAC	3192
Qy	3181	ACAATTAAGACGATGCTTTGAACCTGA	3207
Dp	3193	ACAATTAAGACGATGCTTTGAACCTGA	3219

ID	AA514365 standard; cDNA, 3424 BP.
XX	AA514365;
XX	12-MAR-2002 (first entry)
XX	cDNA encoding human p110alpha isoform of PI3-kinase.
XX	Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform;
XX	LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
XX	autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
XX	Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
OS	Homo sapiens.
PH	Key
FT	Location/Qualifiers
FT	CDS
FT	13..3219
FT	/*tag= a
XX	/product= "p110alpha isoform of PI3-kinase"
PN	W0200185986-A2.
XX	
PD	15-NOV-2001.
XX	
XX	10-MAY-2001; 2001WO-US15065.
PF	
XX	10-MAY-2000; 2000US-203346P.
PR	
XX	(ICOS-) ICOS CORP.
PA	
XX	Sadhu C;
PI	
XX	WPI: 2002-075252/10.
DR	P-ESDB; AAU09687.
PT	Identifying a modulator of p110delta polypeptide binding to SH3
PT	domain-containing polypeptides e.g. LASP-1, comprising allowing the
PT	binding partners to interact in the presence and absence of a test
PT	compound
XX	
XX	Example 1; Page 55-60; 85pp; English.
PS	
XX	The present invention relates to identifying a modulator of the
CC	phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC	the catalytic subunit via a SH3 domain-containing polypeptide such as
CC	LASP-1. Also described are methods of assaying the specific binding
CC	affinity of the PI3-kinase binding partner. Such modulators are useful
CC	for the treatment of diseases characterised by the undesirable or
CC	excessive activity of PI3Kdelta. For example the modulators can be used
CC	for inhibiting the growth or proliferation of cancer cells
CC	(e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC	Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC	arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC	autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
CC	bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC	dermatoses (e.g. contact dermatitis), central or peripheral nervous
CC	system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC	and Type I diabetes mellitus. The present sequence encodes for human
CC	p110alpha isoform of PI3K.
XX	
XX	Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;
SO	
Query Match	93.8%; Score 3008.6; DB 24; Length 3424;
Best Local Similarity	96.1%; Pred. No. 0;
Matches 3083; Conservative	0; Mismatches 124; Indels 0; Gaps 0;
07	1 ATGGCTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 60
08	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 120
09	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 180
10	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 240
11	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 300
12	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 360
13	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 420
14	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 480
15	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 540
16	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 600
17	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 660
18	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 720
19	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 780
20	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 840
21	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 900
22	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 960
23	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1020
24	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1080
25	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1140
26	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1200
27	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1260
28	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1320
29	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1380
30	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1440
31	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1500
32	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1560
33	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1620
34	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1680
35	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1740
36	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1800
37	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1860
38	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1920
39	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 1980
40	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2040
41	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2100
42	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2160
43	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2220
44	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2280
45	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2340
46	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2400
47	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2460
48	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2520
49	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2580
50	ATGCTTCCAGACCATCATCATGAGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC 2640

```

Oy      1  ATGCTCCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC  60
        |||||
Db      13  ATGCTCCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCCCCCAAGATC  72

```


QY 61 CTAGTAGAATGTTTACTACCAATGGATGATGACTTTAGATGCTTCGGAGGCT 120
| | | | |
Db 73 CTAGTAGAATGTTTACTACCAATGGATGATGACTTTAGATGCTTCGGAGGCT 132
| | | | |
QY 121 ACGTAAATGAAGATGAAGATGATTTAAGAGCAAGAAAAATACCTCTCCATCA 180
| | | | |
Db 133 ACATTAGTAATTAAGCATGAACTATTAAAGAGCAAGAAAAATACCTCTCCATCA 192
| | | | |
QY 181 CTTCTCAAGATGAATCTTTCTACATTTTCCGTAAGTTTACCAAGAGCAAGAAAA 240
| | | | |
Db 193 CTTCTCAAGATGAATCTTTCTACATTTTCCGTAAGTTTACCAAGAGCAAGAAAA 252
| | | | |
QY 241 GAATTTTGTGAGAAACAAGACGACTTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300
| | | | |
Db 253 GAATTTTGTGAGAAACAAGACGACTTTGTGACCTTGGCTTTTCAACCTTTTAAAA 312
| | | | |
QY 301 GTAATTGAACCAAGTAGCAACCGTGAAGAAAAATCTCAATCGAGAAATTTGGTTTGT 360
| | | | |
Db 313 GTAATTGAACCAAGTAGCAACCGTGAAGAAAAATCTCAATCGAGAAATTTGGTTTGT 372
| | | | |
QY 361 ATCGGATGCCAGTGTGTGAATTCGATTCGTTAAAGATCCAGAGTAGACAGACTTCCGA 420
| | | | |
Db 373 ATCGGATGCCAGTGTGTGAATTCGATTCGTTAAAGATTCGTAAGTAGACAGACTTCCGA 432
| | | | |
QY 421 AGAAATATTCGAAATGTTTGTAAAGAGCTGTGATCTTTAGGGATCTTAAATTCACCTCAT 480
| | | | |
Db 433 AGAAATATTCGAAATGTTTGTAAAGAGCTGTGATCTTTAGGGATCTTAAATTCACCTCAT 492
| | | | |
QY 481 AGTAGAGCAATGATGTTTATCTCTCCAAATGTGAATCTTACAGAACTGCCAAAGCAC 540
| | | | |
Db 493 AGTAGAGCAATGATGTTTATCTCTCCAAATGTGAATCTTACAGAACTGCCAAAGCAC 552
| | | | |
QY 541 ATATATATATATGATGATTAAGGCAATTAATAGTGGATTTGGATATGTTCTCCA 600
| | | | |
Db 553 ATATATATATATGATGATTAAGGCAATTAATAGTGGATTTGGATATGTTCTCCA 612
| | | | |
QY 601 AATTAATGCAAAAGAGTAACTCTGAAATCAACCTGACTGTGCGAAGCAAGTA 660
| | | | |
Db 613 AATTAATGCAAAAGAGTAACTCTGAAATCAACCTGACTGTGCGAAGCAAGTA 672
| | | | |
QY 661 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAAACAATAAA 720
| | | | |
Db 673 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAAACAATAAA 732
| | | | |
QY 721 CTTCTGTGTTTGAATATCAGGCAAGTAATTTTAAAGGTGTGATGATGAATAC 780
| | | | |
Db 733 CTTCTGTGTTTGAATATCAGGCAAGTAATTTTAAAGGTGTGATGATGAATAC 792
| | | | |
QY 781 TTCCTAGAAAAATATCCCTCTGAGTCAATAGTATATAGAAAGCTGTATTAATGCTTGG 840
| | | | |
Db 793 TTCCTAGAAAAATATCCCTCTGAGTCAATAGTATATAGAAAGCTGTATTAATGCTTGG 852
| | | | |
QY 841 AGGATGCCCAATTTGATGCTGATGCTAAGAAAGCTCTATTTCTCAATGCGCATGAGC 900
| | | | |
Db 853 AGGATGCCCAATTTGATGATGCTAAGAAAGCTCTATTTCTCAATGCGCATGAGC 912
| | | | |
QY 901 TGTGTTTACATGCTCATATTTCCAGACCATCTCCACAGCTAAGGCAATATATGATGGA 960
| | | | |
Db 913 TGTGTTTACATGCTCATATTTCCAGACCATCTCCACAGCTAAGGCAATATATGATGGA 972
| | | | |
QY 961 GAAACATCTACAAATCCCTTTGGGTTATTAATAGTGAATGCACTCAATTAATAATTTCTTGT 1020
| | | | |
Db 973 GAAACATCTACAAATCCCTTTGGGTTATTAATAGTGAATGCACTCAATTAATAATTTCTTGT 1032
| | | | |
QY 1021 GCAACCTATGATGATTAATTTCCAGACATGACAGATTTATGTTGCAACAGATAC 1080
| | | | |
Db 1033 GCAACCTATGATGATTAATTTCCAGACATGACAGATTTATGTTGCAACAGATAC 1092
| | | | |
QY 1081 TACCATGAGAGAAACCTTATGTGATATGTGAACACTCAAAAGATACCTGTTCCAAAT 1140
| | | | |
Db 1093 TACCATGAGAGAAACCTTATGTGATATGTGAACACTCAAAAGATACCTGTTCCAAAT 1152
| | | | |

QY 1141 CCCAGGTGATATGATATGCTGAATTAAGATATATATACATTCCTGATCTTCTGCTGCT 1200
| | | | |
Db 1153 CCCAGGTGATATGATATGCTGAATTAAGATATATATACATTCCTGATCTTCTGCTGCT 1212
| | | | |
QY 1201 CGACTTGGCTTCCATTTGTTCTGTTAAAGGCCGAAAGGGTGTAAAGAGAACTGCT 1260
| | | | |
Db 1213 CGACTTGGCTTCCATTTGTTCTGTTAAAGGCCGAAAGGGTGTAAAGAGAACTGCT 1272
| | | | |
QY 1261 CCATTGGCTGGGAAATATTAACCTGTTGATTAACACATATCTATGATCTGAAAA 1320
| | | | |
Db 1273 CCATTGGATGGGAAATATTAACCTGTTGATTAACACACACTCTATGATCTGAAAA 1332
| | | | |
QY 1321 ATGGCTTGAATCTTTGGCCGATACCTCATGAGCATGAAGATTTGCTAACCTATTGT 1380
| | | | |
Db 1333 ATGGCTTGAATCTTTGGCCGATACCTCATGAGATTTGAAGATTTGCTAACCTATTGT 1392
| | | | |
QY 1381 GTTACTGATCAAAATCCAAATTAAGAAATCCATGTTTGAAGTTGAGTTGACTGCTTC 1440
| | | | |
Db 1393 GTTACTGATCAAAATCCAAATTAAGAAATCCATGTTTGAAGTTGAGTTGACTGCTTC 1452
| | | | |
QY 1441 AGCAGTGTGTAAAGTTTCCAGATATGTCAGATGTTGAAGAGCAATGCTGCTGA 1500
| | | | |
Db 1453 AGCAGTGTGTAAAGTTTCCAGATATGTCAGATGTTGAAGAGCAATGCTGCTGA 1512
| | | | |
QY 1501 TCCCGTGAAGCAGATTTAGTATTTCCCATGAGGACTGAGTAAGACACTAGAGAC 1560
| | | | |
Db 1513 TCCCGAAGGAGGATTTAGTATTTCCCATGAGGACTGAGTAAGACACTAGAGAC 1572
| | | | |
QY 1561 AATGAATTAAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACAGAGATCTCTCA 1620
| | | | |
Db 1573 AATGAATTAAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACAGAGATCTCTCA 1632
| | | | |
QY 1621 TCTGAATCACTGAGCAAGAAAGATTTTCTGTGAGGCAAGACATATGTTGTAATCT 1680
| | | | |
Db 1633 TCTGAATCACTGAGCAAGAAAGATTTTCTATGAGGCAAGACATATGTTGTAATCT 1692
| | | | |
QY 1681 ATCCCGGAAATTTCAACCAATTTGCTTGTCTGTTAAATGAACTCTAGAGTGAATGA 1740
| | | | |
Db 1693 ATCCCGGAAATTTCAACCAATTTGCTTGTCTGTTAAATGAACTCTAGAGTGAATGA 1752
| | | | |
QY 1741 GCTCAGATGATAGCTGTTGTTAAAGATTTGGCTCTCAATCAAGCTGAAACAGGCTATGAG 1800
| | | | |
Db 1753 GCTCAGATGATAGCTGTTGTTAAAGATTTGGCTCTCAATCAAGCTGAAACAGGCTATGAG 1812
| | | | |
QY 1801 CTTCTGAGCTCAATTAACCAATCTATAGTGTGAGCTTTTGTGCTTGGCTGTGA 1860
| | | | |
Db 1813 CTTCTGAGCTCAATTAACCAATCTATAGTGTGAGCTTTTGTGCTTGGCTGTGA 1872
| | | | |
QY 1861 AATATATTAACAGATGACAACTTTCCAGTACTAATTCAGTATGACATGACTAAAA 1920
| | | | |
Db 1873 AATATATTAACAGATGACAACTTTCTCAGTATTAATTCAGTATGACATGACTAAAA 1932
| | | | |
QY 1921 TATGAACATGATTTGGATTAACCTGCTGTGATGATTTTACTGAAAGAGCATGACTAAT 1980
| | | | |
Db 1933 TATGAACATGATTTGGATTAACCTGCTGTGATGATTTTACTGAAAGAGCATGACTAAT 1992
| | | | |
QY 1981 CAAGAGATGAGTCACTTTTCTTTTGGCATTTAAATCTGAGATGCAATTAACAGCT 2040
| | | | |
Db 1993 CAAGAGATGAGTCACTTTTCTTTTGGCATTTAAATCTGAGATGCAATTAACAGCT 2052
| | | | |
QY 2041 AGTCAGAGTTTGGCTGCTTTTGGAGTCCATATGCGGAGTGTGGGATGATCTGAAG 2100
| | | | |
Db 2053 AGTCAGAGTTTGGCTGCTTTTGGAGTCCATATGCTGATGTGGGATGATTTGAAG 2112
| | | | |
QY 2101 CACCTTAATAGCAGAGTTGAGGCTATGAAAAAGCTCATTAAGTGAATGACATTTCTCAA 2160
| | | | |
Db 2113 CACCTTAATAGCAGAGTTGAGGCTATGAAAAAGCTCATTAAGTGAATGACATTTCTCAA 2172
| | | | |
QY 2161 CAGAGAGAGAGATGAAAAACAAAAAGTACAGATGAAGTTTATGTTGAGCAAAATGAGG 2220
| | | | |
Db 2173 CAGAGAGAGAGATGAAAAACAAAAAGTACAGATGAAGTTTATGTTGAGCAAAATGAGG 2232
| | | | |
QY 2221 CGACAGATTTCAATGATGCTCTCCAGGCTTTCTGTCTCTTAACCTGCTCATCAG 2280
| | | | |


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Db 2233 CGACCGAATTTTCATGATGCGCTTACAGGGCTGCTGCTCCCTTAAACCCTGCTCATCAA 2292
Qy 2281 CTGGGAATCTCAGGCTTGAAGAGTGTGCAATTATGCTCTTGCAGAAAAGGCACTGTGG 2340
Db 2293 CTAGGAACCTCAGGCTTAAAGAGTGTGCAATTATGCTCTTGCAGAAAAGGCACTGTGG 2352
Qy 2341 TTGAATTGGAGAACCCAGACATCATGTCAAGTACTCTTGCAGAACATGAGATCATC 2400
Db 2353 TTGAATTGGAGAACCCAGACATCATGTCAAGTACTCTTGCAGAACATGAGATCATC 2412
Qy 2401 TTTAAATTTGGGATGATTTACGGCAAGATATGCTAACCCCTTCAATTTATTCGCAATTATG 2460
Db 2413 TTTAAATTTGGGATGATTTACGGCAAGATATGCTAACCCCTTCAATTTATTCGCAATTATG 2472
Qy 2461 GAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTAACCTTATGAGATGCTGCA 2520
Db 2473 GAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTAACCTTATGAGATGCTGCA 2532
Qy 2521 ATCGGTGATCTGTGTGGGACTTATCGAGGTGTGAGAAATTCCTCACTATATGAGATTT 2580
Db 2533 ATCGGTGATCTGTGTGGGACTTATGAGGTGTGAGAAATTCCTCACTATATGAGATTT 2592
Qy 2581 CAGGTAAAGAGGCTTGAAGAGTGTGCACTGCAATTAAACAGCCACACACTCATCATGTGG 2640
Db 2593 CAGGTAAAGAGGCTTGAAGAGTGTGCACTGCAATTAAACAGCCACACACTCATCATGTGG 2652
Qy 2641 CTCAAGCAAGAACAGGGGGAAATATATGATGGGCACTGCAATTGTTTACAGATCA 2700
Db 2653 CTCAAGCAAGAACAGGGGGAAATATATGATGGGCACTGCAATTGTTTACAGATCA 2712
Qy 2701 TGTGCTGATATTTGTGTGCTCCACTTCAATTTGGGAAATTTGAGATGCTGCAATATGAT 2760
Db 2713 TGTGCTGATATTTGTGTGCTCCACTTCAATTTGGGAAATTTGAGATGCTGCAATATGAT 2772
Qy 2761 ATCTGTTAAAGATGATGCAACATGTTTCAATATGATTTTGGACACTTTTGGATCAC 2820
Db 2773 ATCTGTTAAAGATGATGCAACATGTTTCAATATGATTTTGGACACTTTTGGATCAC 2832
Qy 2821 AAGAGAAAAAATTTGTTTAAACGAGAGGCGGTGCTGTTTGTGACACAGATTTTC 2880
Db 2833 AAGAGAAAAAATTTGTTTAAACGAGAGGCGGTGCTGTTTGTGACACAGATTTTC 2892
Qy 2881 TTTATAGTATTTAGTAAGAGCCCAAGAAATGACAAAGACAGAGATTTGAGAGGTTT 2940
Db 2893 TTTATAGTATTTAGTAAGAGCCCAAGAAATGACAAAGACAGAGATTTGAGAGGTTT 2952
Qy 2941 CAGAGATGTTTGAAGAGCTTATCTAGCTAATTTGGAGACATGCAATCTTCTATTAAT 3000
Db 2953 CAGAGATGTTTGAAGAGCTTATCTAGCTAATTTGGAGACATGCAATCTTCTATTAAT 3012
Qy 3001 CTTTTCGATGATGCTGTGCTGCGAAATGCGCAAAATCTGCAATTTTGTATGATTTGCA 3060
Db 3013 CTTTTCGATGATGCTGTGCTGCGAAATGCGCAAAATCTGCAATTTTGTATGATTTGCA 3072
Qy 3061 TACATTCGAAGAGCCCTAGCTTATGATTAACCTAGCAAGAGGCTTTGAGATTTGATG 3120
Db 3073 TACATTCGAAGAGCCCTAGCTTATGATTAACCTAGCAAGAGGCTTTGAGATTTGATG 3132
Qy 3121 AAAACAATGATGATGACACCATGTGCTGCAACAAAAATGATGATCTTCCAC 3180
Db 3133 AAAACAATGATGATGACACCATGTGCTGCAACAAAAATGATGATCTTCCAC 3192
Qy 3181 ACAATTAAAGAGATGCTTTGAACTGA 3207
Db 3193 ACAATTAAAGAGATGCTTTGAACTGA 3219

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RESULT 6
 AAA02190
 ID AAA02190 standard; cDNA; 741 BP.
 XX
 AC AAA02190;

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XX 19-MAY-2000 (first entry)
DT Human colon cancer cell line polynucleotide sequence SEQ ID NO:2181.
XX
DE Human; colon cancer; tumour; diagnosis; gene expression product;
XX probe; detection; cancerous state; metastasis; identification;
XX breast cancer; oestrogen receptor-positive breast cancer; therapy;
XX oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO958675-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10602.
XX
PR 14-MAY-1998; 98US-0085426.
PR 15-MAY-1998; 98US-0085537.
PR 15-MAY-1998; 98US-0085636.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.
XX
PA (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J,
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamsom G, Drmanac R, Citrenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Steiche-Crain B;
XX WPI: 2000-126369/11.
XX
DR Polynucleotide library used to determine cancerous states of mammalian
XX cells -
XX
PT Claim 1; Page 850; 1097pp; English.
XX
PS
XX
XX AA00010 to AA02716 represent polynucleotides isolated from cDNA
XX libraries constructed from human colon cancer cell lines. The present
XX invention also describes a method of detecting differentially expressed
XX genes correlated with a cancerous state of a mammalian cell, comprising
XX detecting at least one differentially expressed gene product in a test
XX sample derived from a cell suspected of being cancerous, where detection
XX of the differentially expressed gene product is correlated with a
XX cancerous state of the cell from which the test sample was derived.
XX The polynucleotide sequences can be used in a method for detecting
XX differentially expressed genes correlated with a cancerous state of a
XX mammalian cell. The polynucleotides can also be used as probes for
XX detecting and mapping related genes. They can be used in diagnosis and
XX prognosis of diseases and disorders (e.g. identification of
XX pre-metastatic or metastatic cancerous states, stages of cancer, or
XX responsiveness of cancer to therapy). This is particularly for breast
XX cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
XX negative breast cancer, lung cancer, and colon cancer.
XX
SQ Sequence 741 BP; 221 A; 137 C; 154 G; 208 T; 21 other;

```

Query Match 16.2%; Score 519.2; DB 21; Length 741;
 Best Local Similarity 89.0%; Pred. No. 6.3e-134;
 Matches 633; Conservative 0; Mismatches 69; Indels 9; Gaps 7;

```

Qy 2182 CAAAAGTACAGATGAGATTTTATGTTGAGCAATGCGGACACAG-ATTTCATGATGC 2240
Db 18 CAAAGGTACAGATGAGATTTTATGTTGAGCCATGAGGAGACAGAAATTTATGATGC 77
Qy 2241 TCTCCAGGCTTTC-TGTCTCTCTTAAACCCTGCTATCAGCTGGGAAATCTAGGCTTG 2299
Db 78 TCTACAGGCTTCTGTTCTCTTAAACCCTGCTATCAGCTGGGAAATCTCAGCTTG 137
Qy 2300 AAGAGTGCAGATTTATGCTCTTGCAGAAAAGGCACTGTGTTGATTTGGAGAACCCAG 2359

```

Query Match	14.0%	Score 448.2	DB 21	Length 3213
Best Local Similarity	50.1%	Prod. No. 8.3e-114		
Matches 1591	Conservative 0	Mismatches 1478	Indels 106	Gaps 15
<p>Example 1; Column 43-50; 34pp; English.</p> <p>This invention describes a novel antisense compound (I) 8-30 nucleobases in length targeted to a start codon or nucleobases 4-3174 of the coding region of human p13 kinase p13beta (II), in which (I) specifically hybridizes with and inhibits the expression of (II). The products of the invention have cytosolic, antiinflammatory and antiinfective activity. (I) is useful for inhibiting the expression of (II) in human cells or tissues. The antisense compound can be utilized for diagnostics, therapeutics, prophylaxis and as research reagents and kits. The antisense compounds may also be useful for prophylactically, e.g., to prevent or delay infection, inflammation or tumor formation. The antisense compounds are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding (II).</p>				
Sequence	3213 BP	979 A	612 C	704 G
			918 T	0 other
Query	Match	14.0%	Score 448.2	DB 21
Best Local Similarity	50.1%	Prod. No. 8.3e-114		
Matches 1591	Conservative 0	Mismatches 1478	Indels 106	Gaps 15
58	ATCTAGTAGAATGTTTACTACCAAAAGGGATATGTGACTCTTACATGCTCCGTGAG	117		
88	ATACCTGGAGATTCCTTTGGCCACTGGATTTATATCCAGTTGAGGACTCGGAAA	147		
118	GCTAGCTTAATACGATTAAGCATGAACTATTTAAAGACAAAGAAATACCTCCAT	177		
148	GCTACCAATTCCTATATTAAAGCAATGTATGGAAGCAAGTTCAATTAACCAATGTC	207		
178	CAACTCTTCAGATGAATCTTCTTACATTTTCTAGTGTTTCCCAAGACGAAGAAG	237		
208	AACTCTTATGATATGTGACTCCATATATGTTCCATGTTGATCAGATCGCTGATAT	267		
238	GAGAAATTTTGGATGAAGAAAGACGACTTTGTGACCTGGCTTTTCAACCTTTTA	297		
268	GAGGACTTGAAGATGAACAGAGACTCTGTATGTCAACCTTTTCTTCCAGTTCTC	327		
298	AAAGTAATTGAACACAGTAGGCAACCTGTAAGAAAGATCCCATCGAAGATGTGTTT	357		
328	AAATTAGTCACAGAAAGTTGTGACCCAGGGGAAA--ATTAGACTCAAAATTTGAGTC	384		
358	GCTATGCGATGCCAGTGTGTGAATTCGATAGTGAAGATCCAGAGTACAGGATTC	417		
385	CTTATAGGAAGAGTGTGATGATTTGATCTTGAAGATCCGAAAGTAAATGATTT	444		
418	CGAAGAAATNTGTCATGTTTGAAGAAGCTGGATCTTAGGATCTTATTCACCT	477		
445	CGAAGAAAAATGCGAAATTCACG--GAAAAAATTCCTGTCA	486		
478	CATAGTAGACGATGATGTTTATCTCCAAATGTAGATCTTACCCAGACCTGCCAAG	537		
487	CTTGTGGATGTTCTTGATGATGACTGTGCTAAACAAACATTCACACAGATGACGA	546		
538	CACATATATTAATTGATGAAGAAGGCAATATATAGTGATTTGGTATATAGTTCT	597		
547	TCCATCCCTGAAACTTAGAAGATAACTTATGGGGAAAGCTCATCTGATGCTTTCAT	606		
598	CCAAATATGACAAACAGATATCTGAAATTAACAATGATGATGTGTGCGAAGCA	657		
607	TTTGAAATGTCGAGGACGTTTATAGCTTCATAGTCTCTCTATATGAATCCTATCAA	666		
658	GTAATGTGGAAGCAATCAGAAAAAAATCGAAGTATGTTGATCATCTGACAACTA	717		
667	GTAATGATGTTGGCAATC--CAAAAGTTTGATCTTACATGGAAGAAATGAAGTT	723		
718	AAACTGTGTTTGAATATCAGGCAAGTATATTTAAAGTGTGTGATGATGAA	777		
724	AGCCCTATG-----ATTATGTTGCAAGTCAGCGGAGAGTAGAA	785		
778	TACTTCCTAGAAAAATATCTCTGATCAGTATTAAGTATATTAAGAGCTGATATATCTT	833		
766	TATGTTTTCGATCATCCTCAATTCAGTTCCAGTATATCCGAACTGTGTATGAC	822		

QY 838 GGGAGATGCCAATTTGATGCT-----GATGCTAAGAAAGCCTCTATTTCTCAACTGC 892
DB 826 AAGGCCCTCCCATTTTATCTGTGGAATGCTGCAAGATCAAGAAAATGATGAACAA 885
QY 893 CAATGAGCTGTTTACAAATGCCATCATATTTCCAGAGCATCTCCAGAGCTAGCCCATATA 952
DB 886 GAAATGATGGCTTAAGAGCTGCCATTAATTCGAAATTCATCTAATCTTCTCTTCATTA 945
QY 953 TGAATGAGAAAATCTACAAAATCCCTTGGGTTATTAATAGTCAGTCAGATATAAAA 1012
DB 946 CCACCAAGAAAACAGAAATATTTCTCATGTTTGGGAAAATACAAACCTTTCCAAAT 1005
QY 1013 TTCTTTTGTCCAACTTATGTAATGTAATATTCGACACTGCAAGATTTATGTTGAA 1072
DB 1006 GTCTTGCTTAAGGAAATTAACCTTAACAGAGGAAAC--TGTAAAGTTCATGTCAGGG 1063
QY 1073 CAGGTATCTACATGAGAGAAACCTTATGATATATGTAACACTCAAGAGTACCTT 1132
DB 1064 CTGGCTTTTTCATGCTAGCTGAGCTCTGTGTAACCATCGTAAGCTCAGAGTATCAG 1123
QY 1133 GTTCCA---ATCCAGGTGAAATGAATGGCTGAATTAACATATATCATTTCTGATCTTC 1189
DB 1124 GAAAAAATGATCATATTTGGAATGAACCACTGGAATTTGATATTAATTTGTGACTTAC 1183
QY 1190 CTGCTGCTGCTGACTTTCCTTTCCATTT---GTCTGTTAAGCCGGAAGGGTGC 1244
DB 1184 CAGGAATGCTCGATATGTTTGTGTTATGACAGTTTGGATAAAGTAAACAGAA 1243
QY 1245 TAAAGGAACACTGTCAT-----TGCCCTGGGGAATATAAACTTGTTG 1291
DB 1244 AATCAACGAAACATATTAATCCCTTAATATCAGACATCAGGAAAGCTGGAAGTGC 1303
QY 1292 ATTACACAGATACCTAGTATCTGNAAAATGCGCTTGAATCTTGGCCAGTACCTCATG 1351
DB 1304 ATTATCTGTAGCTGGGTAATAGATGCTTTTGACTTTAAGACAACTGAGACTG 1363
QY 1352 GACTGAAAGATTTGCTGAACCTTATGTTGTTATCTGATCAATCCAAATGAAGAACTC 1411
DB 1364 GAGACATATATTAACACAGCTGCTTTCATTTCTGATGACCTCGAAGAAATGTTGATC 1423
QY 1412 CATGTTTAGAGTTGAGTTGACTGTTGACGAGTGTGTAAAGTTTCCAGATATGTCAG 1471
DB 1424 CATGGAACCTGTTCAAACAAATTCATATCTGAAATGCAACAGCTTGCATGTTAAAT 1483
QY 1472 TGATTTGAGAGCATGCAATTTGCTGTATCCCGTGAACAGAGATTTAGTTATCCCATG 1531
DB 1484 TTCCAGAAATTAATAAAACAACCTTATATTAACCTCCCTTCATTAAGATTAATGAAGG 1543
QY 1532 CAGGACTGAGTAACAGACTAGTAGACATGAATTAAGAAAATGATTAAGAAACAGC 1591
DB 1544 CAGCTGAGATTCAGACAGTATAGTCTAATGTCTCAAGTGAAGTGAAGAAAGTTTC 1603
QY 1592 TCC-----GAGCAATTTGTACAGGATCTCTATCTGAAATCACTGAGCAAGACA 1642
DB 1604 TTCTGTATTAAGAAAATCTTGAACAGGATCCCTTGTCTCAACTGTGTGAAAATGAAA 1663
QY 1643 AAGATTTTCTGTGAGCCACAGAC---ACTATTTGTATCTATCCCGGAATTTCAACCA 1699
DB 1664 TGGATCTTATTTTGACTTTGCAACAGACTGCGGAGAGATTTTCCACATATCATGCGAA 1723
QY 1700 AATTCCTTCTGTCTGTTAATGGAACCTTGAAGATGAATAGCTCAGATGTACTGCTGG 1759
DB 1724 AATTACTGCTGTCAATCAAGTGAATTAACCTTGAAGATGTTGCTCAGGCTCAGGGGCTGC 1783
QY 1760 TAAAGATTTGGCTTCAATCAAGCTGGAACAGGCTATGAGCTTCTGGACTGCAATTAAC 1819
DB 1784 TTCAATTTTGGCTTAAACTGCCCGCGGAGGCCCTGAGCTTCTGGAATTTCAACTATC 1843
QY 1820 CAGATCTATGCTGAGGTTTGTGCTGCTGCTGTTGAAAATATTTAATCAAGATGACA 1879
DB 1844 CAGACACATGATGTTGAGAAATATGCTGTAAGCTGCT---GCCACGATGATGATGAAG 1900
QY 1880 AACTTTCATAGTAACTTAATTCAGTAGTACAGTACTAATAATATGAACAGTATTTGATA 1939

DB 1901 AACTTTCATATATCTTTTACAACTGTGCAAGTGTAAATAATAGACCTTTCTTGAT 1960
QY 1940 AACTGCTGTGATTTTATCTCAAAAAGCGTTAACTATCAAGATTCGCTCACTTT 1999
DB 1961 GTGCCCTCTCTAGATTTCTTAATGAAGAGCACTGTGTAATGAGGATAGGCGATTTTC 2020
QY 2000 TCTTTTGGCATTTAAATCTGAGATGCAACATTAATAACAGTTAGTACAGAGTTTGGCTGC 2059
DB 2021 TATTTTGGCATTTAGTGCAGAAAGTGCACATTTCTGCTGTCTCATGATCAATTTGGTGTCA 2080
QY 2060 TTTTGGAGTCTATTTGCGGTGATGTGGAGTATCTGAAGCCTTAATAGGCAAGTTG 2119
DB 2081 TCTTGAAGCATACGCGGGAGAGTGGGCAATGAAGATGCTTTCTTAAGCAGGTTG 2140
QY 2120 AGGCTATGGAAGAGCTCATTAACCTGACTGACATCTCAACAAAGAAAGATGAAA 2179
DB 2141 AAGCACTCAATTAAGTTAAACCTTTAAATAGTTATCAAACTGAAATGCGTGAAGTTAA 2200
QY 2180 CACAAAGGTAAGATGAAGTTTATGTTAGCAAAATGCGGCAACAGATTTATGATG 2239
DB 2201 ACAGAGCCAAAGGAGAGAGCCATGATCCTGTTTAAACAGAGTCTTACCGGGAAG 2260
QY 2240 CTCTCCAGGGCTTTCTGTCTCCTCTAAACCTGTCATCAGCTGGGAAATCTCAGGCTTG 2299
DB 2261 CCCTCTGACCTGCACTGACAGTCAACCGTGAACCAATGTTATCTCTCAAGAACTCTATGTTG 2320
QY 2300 AAGATGTGCAATTAATGCTTTGTCAAAAGGCCACTGTGCTGTAATGGAGAACCAAG 2359
DB 2321 AAAAGTGAATAATGATGATTCGAAATGAAACCTTTGTGCTGTATACAAATACAGG 2380
QY 2360 ACATCATGTCAGAAATTAATCTTCTTGAAACAAATGACATCATCTTTAAATGGGGAATG 2419
DB 2381 TATTTGGAGGATTCAGT-----TGAGTGAATTTTAAATGCTGTGATGAT 2428
QY 2420 TAAGGCAAGATATGCTAAACCTTCAGATTAATGCAATTAAGAAAATCTGGCAAAATC 2479
DB 2429 TACGACAGGATATGTTGACATCCAAATGTTGCGCTTATGATTTTACTGTGAAGAAAG 2488
QY 2480 AAGCTTGTGATTTGAAATGTTTACTTATGATGATGCTGTCAATCGGTGACTGTGGGAC 2539
DB 2489 CTGCTTTGATCTTGGATGTTGATGTTGCTTATGCTGTATGCAACAGAGATGCTCTGGCC 2548
QY 2540 TTATGAGGTGGTGAAGAAATCTCACTATTAATGCAATTCAGTGTAAAGAGGC---C 2596
DB 2549 TCATTTGAAGTTGTGACCTCTGAAACAAATGCTGACATTCAGCTGAACAGTACAAATG 2608
QY 2597 TGAAGGTGCACTGCACTTTTAAACAGCCACACACTCCTCAGTGCCTCAAGAACAGAAACA 2656
DB 2609 TGGCTGTGACAGACGCTTCAACAAAGATGCTTCTGGAATCTGAAATTCATCAACT 2668
QY 2657 AAGGGAAATATATGATCGGCGCATCGATTTGTTTACACGATCATGTGCTGTGATGTTG 2716
DB 2669 CTGGGGATGACCTGGAACCGACCATTTAGGAATTTACATGCTGCTGCTGCTGCTGCTG 2728
QY 2717 TTGCCACTTGATTTTGGGAATTTGAGATGCTGCAATAGTAATATCATGTGTTAAAGT 2776
DB 2729 TAGCTTCTTATGCTTGGATGTTGTCACAGACATAGTGAACATCTGCTGCTCAAAAAA 2788
QY 2777 ATGCAACATGTTTCAATATGATTTTGGACACTTTTGGATCACAAGAAAAAATTTG 2836
DB 2789 CTGGCAGACTCTTCACTTACATTTGACATATTTCTTGGAAATTTCAAACTTAAGTTTG 2848
QY 2837 GTTATTAACGAGAGCGCTGCTGTTGTTTGTGACACAAGATTTCTTAATAGTATTA 2896
DB 2849 GCATTTAAAGGAGAGATGCTTTTATTTCTTACTATGATTTATCATTCATGCAATTTCAAC 2908
QY 2897 AAGAGCCCAAGATGACAAAGACAGAGAAATTTGAGAGTTTCAGAGATGTTGTTCA 2956
DB 2909 AAGGAAAAACAG-----AAATACAGAAAGTTTGGCGGATTCGCGAGTGTGTGAGG 2962
QY 2957 AAGCTTATCTAGCTATTTGCGAGCATGCGCAATCTTCTCATTAATCTTTCTCAATGATGC 3016

Db 2963 ATGCATATCTGATTTTACGACGCGATGGGATCTCTTCACTCTCTTGGCTGATGT 3022
Oy 3017 TTGGCTCGAATGCGCAGAACTGCATCTTTTGTATGATATTTGCATTCATTCGAAAGACCC 3076
Db 3023 TGACTGCGAGGCTTCTCTGATCTACATCTGCAAGATATTAAGATCTTAAGGACTCTC 3082
Oy 3077 TAGCTTTAGATATAAATGAGCAAGAGCTTTGAGATTTTCAATGAACAAATGAATGATG 3136
Db 3083 TTGCATTTAGGAAGAGTGAAGAAAGCACTCAACAGTTTAAGCAAAAATTTGATGAGG 3142
Oy 3137 CACACCATGCTGCTGCGACACAAATGATTTGATCTTCCACACATTTAAGCA 3191
Db 3143 CGCTCAGGAAGAGCTGACTTAAAGTGAAGTGAAGTGGCCACACAGTTTGGAA 3197

RESULT 8
ABV78026
ID ABV78026 standard; DNA; 3213 BP.
XX
AC ABV78026;
XX
DT 12-NOV-2002 (first entry)
XX
DE Hypoxia-regulated protein coding sequence #46.
XX
KM Cytosolic; vasoregulatory; tranquilizer; antiatherosclerotic; gene therapy;
KM anti-inflammatory; vulnereary; gynecological; ophthalmological; vaccine;
KM hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KM ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KM pre-eclampsia; atherosclerosis; inflammatory condition; wound healing;
KM inflammation; erythropoiesis; hair loss; human; gene; ds.
XX
OS Homo sapiens.
XX
PN MO200246465-A2.
XX
PD 13-JUN-2002.
XX
PF 10-DEC-2001; 2001MO-GB05458.
XX
PR 08-DEC-2000; 2000GB-0030076.
PR 08-FEB-2001; 2001GB-0003156.
PR 25-OCT-2001; 2001GB-0025666.
XX
PA (OXFORD BIOMEDICA UK LTD.
PI white J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI Rayner WN;
XX
WPI: 2002-627238/67.
XX
PS Claim 37; Page 363-364; 538pp; English.
XX
CC The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/protome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV7873-ABV78116
CC and ABP65061-ABP65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating hypoxia-regulated
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,

CC retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss.
XX
SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;
Query Match 14.0%; Score 448.2; DB 24; Length 3213;
Best local similarity 50.1%; Pred. No. 8.3e-114;
Matches 1591; Conservative 0; Mismatches 1478; Indels 106; Gaps 15;
Oy 58 ATCCATAGATGATTTTACTACCAATGGGATGATGACTTTGAAATGCTCCGTGAG 117
Db 88 ATACCTGCGATTTCTCTTGGCCACTGGGATTTATATCAAGTGGATACCTTGGGAA 147
Oy 118 GCTACGTTAATACATTAAGCATGAATCTATTAAAGAGCAAGAAATACCTCCAT 177
Db 148 GCTACCATTTCTTATATTAAGAGATGTTAAGAGCAAGTTCAATTTCCCAATGTTT 207
Oy 178 CAATCTTTCAGATGAATCTTACATTTTCTGATGTTTACCCAGAGCAAGAGG 237
Db 208 AACCTCTTATGATGATATGACTCTATATGTTTGCATGTTGAATCAGACTGTTAT 267
Oy 238 GAAGATTTTGTGATGAAACAAAGACGCTTGTGACCTTGGCTTTTCAACCTTTTA 297
Db 268 GAGAGCTTGAAGATGAACAGAGACTCTGATGTCAGACCTTTTCTCAGTTCTC 327
Oy 298 AAGATATTGAACCACTAGGCAACCGTGAAGAAAGAAATCTCAATGAGATTGTTT 357
Db 328 AATTTAGTGAACAGAAAGTTGTGACCCAGGAGAAA--ATTAGATCTCAAAATTTGAGTC 384
Oy 358 GCTATGCGCATGCGACATGCTGTAATCGATATGTTAAGATCAGAGATGACGACTTC 417
Db 385 CTTATAGGAAGAGCTGCTGATGATTTGATTTCTTGAAGATCTCGAATGATTAATTT 444
Oy 418 CGAAGAAATATTTCTCAATGTTTGTAAAGAGCTGTGATTTAGGATCTTAATCACCT 477
Db 445 CGAGAGAAATTCGCAAAATTCAGGA-----GGAAAAATCTGTCTCA 486
Oy 478 CATATGAGCAATGATGTTTATCTTCCAAATGTGATCTTCCAGAGATGCCAAG 537
Db 487 CTGTGGGATTTGTTGTGATGAGCTGTGCTAAACAAATATCCACAGAGATGAACCA 546
Oy 538 CACATATATTAATTAATGATTAAGGCAATATAGTGTGATTTGGGATATGTTCT 597
Db 547 TCCATCCCTGAATCTTAGAGATTAATCTTATGCGGAAAGCTCATGTGTTCTAT 606
Oy 598 CCAATATATGACAAACAGAGATATCTGTAATTAACCATGCTGTGCGCAGAACAA 657
Db 607 TTTGAAACCTGCGAGAGCTGTTAGCTTCAAGTGTCTCTTAATATGAAATCTATCAA 666
Oy 658 GTAATTTGTCGAAGCATGAGAAAGAAATCTGAGATGTTGCTATCATCTGAACAACCTA 717
Db 667 GTAATTTGATTTGGCAATC---CAAAAGCTTGTGATATTCATGGAAGAAATGAGATT 723
Oy 718 AAATCTGTGTTTGAATATCAGGCAAGTATATTTAAAGTGTGATGATGAA 777
Db 724 AGCCCTTAG-----ATATGCTTGAAGTCAAGGCGGAGATAGAA 765
Oy 778 TACTTCCTGAAATAATCTCTGAGTGAATTAAGTATTAAGAACTGTATATGCTT 837
Db 766 TATGTTTGTGATCATCTAATTCAGTTCCAGTATATCCGAACTGTGATGAAC 825
Oy 838 GGGAGATGCCCAATTTGATGCT-----GATGCTAAAGAAAGCTCTATCTTCAACTGC 892
Db 826 AGAGCCCTCCCATTTTACTTGTGATGATCTGCAAGATCAAGAAATGATAGAACAA 885
Oy 893 CAATGACCTTTTACAAAGCATATTTCCAGAGCATCTCCAGAGTACGCCATATA 952
Db 886 GAATATTTGCCATTAAGCTGCGCATTAATTCGAATTTCTTCTTCATTA 945
Oy 953 TGAATGAGAAACATTAACAAATCCCTTGGTTATTAATGATGCTCAGATTAATAA 1012
Db 946 CCACCAAGAAACAGCAATTAATTTCTCATGTTTGGAAATTAACACCTTTCCAAATTT 1005

QY 1013 TTCTTTGTGCACTTGTGCAATGTAAATTTGAGACATTTGACAGATTTATGTTGAA 1072
DB 1006 GTCTTGATTAGGGAATATACTTAACACAGAGAAAC--TGTAAAGTTCACTGTCAGGG 1063
QY 1073 CAGGTATCAACCATGGAGGAAACCTTATGTGATATGTGAACCTCCAAAGATACCTT 1132
DB 1064 CTGGTCTTTTTCATGTGATCTGAGCTCTGTGTAAACCATGTAGCTCGAGGTATCAG 1123
QY 1133 GTTCCA---ATCCAGGTGGAATGAAATGCTGAATTAACGATATATCATTCCTGATCTTC 1189
DB 1124 GGAAAAATGATCATATTTGGAAATGAACCATGGAATTTGATATATTTATTTGACTTAC 1183
QY 1190 CTGCTCTGCTGACCTTTGCTTTCCATT---GTTCTGTAAAGCCGAAAGGCTGC 1244
DB 1184 CAGAAATGCTCATATATGTTTGTCTGTATGCACTTTTGATGATTAAGTAAACCAAGA 1243
QY 1245 TAAAGAGAACACTGTCCAT-----TGCCCTGGGAAATATATACTTGTTC 1291
DB 1244 AATCAACGAAATATATTAATCCCTTAATATATCAGACCATCAGAAAGCTGAAAGTGC 1303
QY 1292 ATTACACAGATATCTAGTATCTGAAAAATGCTTTGAATCTTTGGCCAGTACTCATG 1351
DB 1304 ATTATCTGTAGCTGGTAAATAGATGTTTGTACTTTAAAGACATTTGAGAACTG 1363
QY 1352 GACTAGAGATTTGCTGAACCTTATGTTGTTACTGATCAAAATCCAAATTAAGAACTC 1411
DB 1364 GAGACATATATATTAACACCTGGTCTTCACTTCTGATGAATCGAAAGAAATGTTGATC 1423
QY 1412 CATGTTTAAGTTGGAGTTTGACTGTTAGCAGATGTGTAAGTTTCCAGATATGTCAG 1471
DB 1424 CAATGGAACTGTTCAACAAATCCATATATGAAATGCAACAGCTTTGCATGTTAAAT 1483
QY 1472 TGATTGAAAGCATGCGCAATTTGCTGTATCCCGTAGAGAGATTTAGTATTTCCCATG 1531
DB 1484 TTCCAGAGAAATAAAAACAACCTTATTTATTTACCTCCCTTCGATAGATTTATGAAAAG 1543
QY 1532 CAGGACTGATACAGACTAGCTAGAGACATGAAATTAAGAAAAATGATAAGAACAG 1591
DB 1544 CAGCTGAGATTCAGACGATGATAGTCTAATGTGTCAAGTGAAGTGGAAAAAAGTTTC 1603
QY 1592 TCC-----GAGCAATTTGTACAGATCTCTTATCTGAATCACTGAGCAAGAGA 1642
DB 1604 TTCTGTATTTGAAAGAAATCTTGGACAGGATCCCTGTCTCAACGTGTGAAAAAGAAA 1663
QY 1643 AAGATTTCTGTGAGCCACAGAC---ACATTTGTATTAATTCGCGAAATTTCTAACCA 1699
DB 1664 TGGATCTTATTTGACTTTGCGACAAAGCTGCCGAGAGATTTTCCCAATATCATGCCAA 1723
QY 1700 AATGCTTCTGTCTGTAAATGGAATCTAGAGATGAAGTAGCTCAGATGTACTGCTTG 1759
DB 1724 AATTACTGTCTCATATCAAGTGGAAATTAATCTTAGAGATGTTGCTCAGCTTCAGGGCTGC 1783
QY 1760 TAAAAATTTGGCTCCAAATCAAGCCCTGAACAGGCTATGAGCTTCTGAGCTGCATTAAC 1819
DB 1784 TTCAATTTGGCTTAAACCTGCCCCCGGAGGCTCTAGAGCTTCTGGAATTTCACTATC 1843
QY 1820 CAGATCTTAATGAGGTTTGTGCTGCTGCGGCTTAAAAAAATTTTAACAGATGAGA 1879
DB 1844 CAGACAGATGACTTGGAAATATGCTGTAGGCTGCT---GGACAGATGAGTGAAG 1900
QY 1880 AACTTTTCTCAGTACCTTAATTCAGTAGTACAGTACTAAATATGAACAGATTTGGATA 1939
DB 1901 AACTTTTCTCAATATCTTTTAACTGTGTCAAGTGTAAATATGAGCTTTTCTTGAT 1960
QY 1940 AACTGCTGTGATTTTACTCAAAAAAGCGTTAACTATCAAGAGATGCTCACTTTT 1999
DB 1961 GTGCCCTCTCTAGATTTCTATTAGAAAGCACTTGTAAATCGAGAGATGAGGAGTTTC 2020
QY 2000 TCTTTTGGCATTTAAATCTGAGATGACAAATAAACAGTTAGTCAGAGATTTGGCTGC 2059
DB 2021 TATTTTGGCATTTAGGTGAGAGTGCACATTTCTGCTGTCTCAGTACAAATTTGGTGTCA 2080
QY 2060 TTTTGAAGTCTTAATTTGCGGTGATGTGGATGTATCTGAAGCACTTAATAGCAAGTTG 2119

DB 2081 TCCTTAAGCATCTCCCGGGAAAGTGTGGGCACATGAAGTCTTTCAACAGGTTG 2140
QY 2120 AGGCTATGAAAAAGCTCATTTAACTTACGTACATTTCTCAACAGAGAAAGAGATGAA 2179
DB 2141 AAGCACTCAATATGTTAAAACTTTAAATAGTTTATCAAACTGAATGCCGTGAAGTTAA 2200
QY 2180 CACAAAAGGTACAGATGAAGTTTATGTTGAGCAATGGCGGCAACGAAATTTGATGATG 2239
DB 2201 ACGAGCCAAAGGAAAGGAGGCCATGCTATACCTGTTTAAACAGAGTCTTACCGGAAAG 2260
QY 2240 CTCTCGAGGCTTTCTGTCTCTTAACCTGCTCATCAGCTGGGAAATCTCAGGCTTG 2299
DB 2261 CCCTCTCTGACCTGACAGTCAACCCCTGAACCAATGTGTATTCCTCAGAAATCTATGTTG 2320
QY 2300 AAGAGTGTGAATATATGTTCTTCTGCAAAAAAGCCACTGTGTGTAATTTGGAGAACCCAG 2359
DB 2321 AAAAGTCAAAATACATGAAATCCAAATGAAGCTTTGTGGCTGTATCAATTAACAAAG 2380
QY 2360 ACATCATGTCAATTAATCTTTCAAGAACATGAGTCAATCTTTAAATTTGGGATGAT 2419
DB 2381 TATTTGTAGGATTCAGT-----TGAGTGAATTTTAAATAATGTGATGAT 2428
QY 2420 TACGCCAAGATATGCTAACCTTCAGATTAATTCGATTAAGAAAAATATCTGCAAAATC 2479
DB 2429 TACGACAGATATGTTGACATCCAAATGTGGCTTATGATTTACTCTGGAAGAAAG 2488
QY 2480 AAGCTCTTATCTTGAATGTTTAACTTATGATGTCTGCAATCGGTGACTGTGGAGC 2539
DB 2489 CTGATTTGATCTTGGATGTTGCTTATGTGCTTATGCTTACCAAGAGATCCCTCTGCGC 2548
QY 2540 TTATGAGGTGTGAAATTTCTACACTATATATGAGTTAGTGTAAAGAGGC---C 2596
DB 2545 TATTTGAATTTGAGACCTTGAACCAATTTGCTGACATTCAGCTGAAACATGACATG 2608
QY 2597 TGAAGGTGCACTGCAAGTTTAAACAGCCACACACTCCATCAGTGGCTCAAGAACAA 2656
DB 2609 TGGCTGTGACAGAGCTTCAACAAAGATGCCCTTCTGAACTGGCTTAAGATATCAACT 2668
QY 2657 AAGGGGAATATATATGATGCGGCATGCAATTTGTTTACACAGATGCTGTGATTTGTG 2716
DB 2669 CTGGGATGACCTGACACGAGCAATTTGAGAAATTAACATGCTGTGCTGTGCTACTGTG 2728
QY 2717 TTGCCACCTCAATTTTGGGAATTTGAGATGTGCACAAATGTAAATATCAAGTAAAGATG 2776
DB 2729 TAGCTTCTTATGCTCTGGATTTGTGACAGCATATGATCAACATCATGCTCAAAAAA 2788
QY 2777 ATGACAACTGTTTATATATAGATTTTGGACACTTTTGGATCACAAGAAAGAAAAATTTG 2836
DB 2789 CTGGCAGCTCTTCCACATGATGCTTTGACATATTTCTTGAAATTTCAATCTAAGTTG 2848
QY 2837 GTTATTAACGAGAGCGGCTGCTTTGTTTGAACAAGATTTCTTAATATGATTAAGTA 2896
DB 2849 GCATTAAAGGAGAGAGGCTTTTATTTCTTACTATGATTAATTCATCATGTCAATCANC 2908
QY 2897 AAGGAGCCCAAAATGCAAAAGACAAGAAATTTGAGAGTTTACAGAGATGTGTACA 2956
DB 2909 AAGGAAAAACAGG-----AAATACAGAAATTTTGGCCGGTTCCGCCAGTGTGTGAGG 2962
QY 2957 AAGCTTATCTAGCTATTTGGGACAGTGCCAATCTCTTCAATAATCTTTTCTCAAGATGC 3016
DB 2963 AAGCATATCTGATTTTACAGCGGCAATGGGAATCTTTATCATCTCTCTTTGGCTGATGT 3022
QY 3017 TTGGCTCTGGAATGCCAGAACTGCAATTTTGTATGATATTCATACATTTGAAAAGCCC 3076
DB 3023 TGACTGACAGGCTTCTCAATCTCATCATCAAGATATACAGATCTTAAGGACTCTC 3082
QY 3077 TAGCTTATGATTAATCTAGCAAGAGGCTTTGAGATATTTATGAAACAAATGATGATG 3136
DB 3083 TTGCATTTAGGGAAGGTAAAGAGAGCACTCAACAGTTTAAGCAAAATTTGTGTAGG 3142
QY 3137 CACACCATGTGTGCTGACCAACAAAATGATTTGATCTTCCACCAATTAAGCA 3191

Db 3143 CGCTCAGGAGGAGCTGACTACTAAAGTGAAGTGGATGGCCACACAGTTGGAA 3197

RESULT 9

AA514366

ID AA514366 standard; cDNA; 3213 BP.

AC

AA514366;

XX 12-MAR-2002 (first entry)

DE cDNA encoding human p110delta isoform of PI3-kinase.

XX

XX Human: phosphatidylinositol 3-kinase; PI3K; p110delta isoform;

KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS Homo sapiens.

PH Key 1.3213 Location/Qualifiers

PT CDS /tag= a

PT /product= "p110delta isoform of PI3-kinase"

XX MO200185986-A2.

XX 15-NOV-2001.

XX 10-MAY-2001; 2001WO-US15065.

XX 10-MAY-2000; 2000US-203346P.

XX (ICOS-) ICOS CORP.

XX Sadhu C;

XX WPI: 2002-075252/10.

DR P-PSDB; AAU09688.

XX

PT Identifying a modulator of p110delta polypeptide binding to SH3

PT domain-containing polypeptides e.g. LAMP-1, comprising allowing the

PT binding partners to interact in the presence and absence of a test

PT compound

XX

XX Example 1: Page 63-68; 85pp; English.

XX

XX The present invention relates to identifying a modulator of the

XX phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to

XX the catalytic subunit via a SH3 domain-containing polypeptide such as

XX LAMP-1. Also described are methods of assaying the specific binding

XX affinity of the PI3-kinase binding partner. Such modulators are useful

XX for the treatment of diseases characterized by the undesirable or

XX excessive activity of PI3Kdelta. For example of cancer cells

XX for inhibiting the growth or proliferation of cancer cells

XX (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,

XX Hodgkin's lymphoma, leukemias), inflammatory diseases (e.g. rheumatoid

XX arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),

XX autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory

XX bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory

XX dermatoses (e.g. contact dermatitis; central or peripheral nervous

XX system inflammatory disorders (e.g. meningitis), bacterial pneumonia,

XX and Type I diabetes mellitus. The present sequence encodes for human

XX p110delta isoform of PI3K.

XX

XX Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

XX

Query Match 14.0%; Score 448.2; DB 24; Length 3213;

Best Local Similarity 50.1%; Pred. No. 8.3e-114;

Matches 1591; Conservative 0; Mismatches 1478; Indels 106; Gaps 15;

XX

58 ATCTCTAGAGATGTTTACTACCAATGGGATGATAGTACTTGAATGCTCCGTGAG 117

Db 88 ATACCTGTGATTTTCCTTTGGCCACTGGGATTTATATCCATGTGAGTACTCGGAA 147

Qy 118 GCTACGTTATATACGATTAAGCATGAACTATTAAAGACAGAAATACCTCTCCAT 177

Db 148 GCTACGATTTCTTATATTAACGATGTTATGGAAGGATTCACAAATACCAATGTT 207

Qy 178 CACTTTCTTCAAGATGAATCTTTTACATTTTCGTAAGTGTATACCAAGACAGAAAG 237

Db 208 AACCTCTTATGGAATATGAGCTCTATATGTTTGTGATGTGATACAGACGCTGTATAT 267

Qy 238 GAGAAATTTTGTATGAAACAAGACGACTTGTGACCTTGGCTTTTCAACCTTTTAA 297

Db 268 GAGAGCTTGAAGATGAAACAGAAAGCTGTGATGTGACGCTTTCTTCCAGCTTCC 327

Qy 298 AAAGTAAATTTGAAACGATGAGCAACCGTGAAGAAAGATCCTCAATCGGAATGTTT 357

Db 328 AATATTGTACAAAGAGTTGTGACCCAGGGGAAA---ATTGACTCAAAAATTTGAGT 384

Qy 358 GCTATGCGATGCCAGTGTGTGTAATTCGATATGTTTAAAGATCCAGAGTAGAGACTTC 417

Db 385 CTATATGAGAAAGGTCTGATGATGATTTGATTCCTTGAAGAGATCTGAAATATGAA 444

Qy 418 CGAAGAAATATTCGATGATGTTGTAAAGAGCTGTGATCTTAGGATCTTAATTCAC 477

Db 445 CGAAGAAATATTCGCAAAATTCAGCGA-----GGAAAAATCCTGTCA 486

Qy 478 CATAGTAGAGCAATGATGTTATCTCTCAATGTGAATCTTACAGAGCCCAAG 537

Db 487 CTGTGGGATGTCCTGATGAGCTGCTGCTAAACAAATATCCAGAGCATGAACA 546

Qy 538 CACATATATTAATTAATTTGATTAAGGCAAAATATAGTGTGATTTGGTAAATGTTCT 597

Db 547 TCCATCCCTGAAAACCTTGAAGATTAACCTTATGAGGGGAAAGCTCATGAGCTTCAT 606

Qy 598 CCAATATGACAAACAGAGTACTCTGAAAATCAACCATGATCTGTGCCAGAACAA 657

Db 607 TTGAAAACCTGCCAGACGTTTGTAGCTTCAAGTGTCTCTAATATGAATCTTATCAA 666

Qy 658 GTAATTCCTGAGCAATCAGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTA 717

Db 667 GTAAATGAATGGCAATC---CAAAAAGTTGACTTATTCATGAGGAGAAAGATGAA 723

Qy 718 AACTCTGTGTTTGAATATCAGGCAAGATATTTTAAAGGTGTGATGTATGA 777

Db 724 AGCCCTATG-----ATTATGTGTCAGAGTCACGGAGAGATGAA 765

Qy 778 TACTTCCAGAAAAATATCTCTGAGTCAGTATATGATATTAAGAGCTGTATATGCTT 837

Db 766 TATGTTTGTGATCATCTCAATTCAGTTCCAGTATATCCGAACTGTGTATGAAC 825

Qy 838 GGGAGATGCCCAATTTGATGCT---GATGCTAAAGAAAGCCTTATCTCAACTGC 892

Db 826 AGAGCCCGCCCATTTATCTTGTGAAAGCTGCAAGATCAAGAAATATGATGAACA 885

Qy 893 CAATGAGCTGTTTATCAATGCCATCATATTCACAGCGATCTCCACAGTACGCCATATA 952

Db 886 GAAATGATGGCCATAGAGCTGCCATTAATGCAATTAATCTTATCTTCTTCCATTA 945

Qy 953 TGAATGAGAAACATCTACAAATCCCTTGGGTATTAATATGTCACCTCAGATTAATA 1012

Db 946 CCACCAAAABAAACAGAAATTTTCTCATGTTTGGAAAAATTAACACCTTTCAAAT 1005

Qy 1013 TTTCTTGTGCAACCTATGTGAATGTAAATATTCGAGACATTCACAAAGATTTATGTT 1072

Db 1006 GTCTTGTTAAGGAAATTAACCTTAACACAGAGGAAAC--TGTAAAGTTCAATGAGG 1063

Qy 1073 CAGTATTCACATGAGAGAAACCTTATGATATATGTAAGTGAACCTCAAGAGTACTT 1132

Db 1064 CTGCTCTTTTCTTATGATGATGAGCTCTGTGTAACATTCGTAACTCAGAGTATCAG 1123

Qy 1133 GTTCCA---ATCCAGGTGAATGAATGAGCTGATTAATGATATATATCTCTGATCTTC 1189

Db 1124 GGAATAATGATCATATTTGAAATGAACCACTGGAATTTGATATTAATTTGACTTAC 1183

1190 CTCTGCTGCTGCACTTTCCTTCCATT-----GTTCTGTAAAGCCGAAAGGCTGC 1244
1184 CAGAAATGGCTCATTATGTTTGTCTGTATGCAAGTTTGGATTAAGTAAAGCAAGA 1243
1245 TAAAGAGACAGTCAT-----TGCCCTGGGGAATATATAACTTGTG 1291
1244 AATCAAGCAAACTATTAATCCCTCTAATAATACAGACATCAGAAAGCTGGAAGTGC 1303
1292 ATTACACAGATCCTAGTATCTGGAAGAAATGGCTTGAATCTTTGGCCAGTACCTCAG 1351
1304 ATTATCTGTAGGTGGGTAAATACATGTTTGAATTTAAAGCAATTTAGAACTG 1363
1352 GACTAGAGATTTGCTGAACCTTATGGTTACTGTGATCAATCCAAATTAAGAAATC 1411
1364 GAGACATATATATACACAGCTGCTTCATTTCTGTATGAATCGAAGAAATGTGAATC 1423
1412 CATGTTAAGTTGAGTTGACTGCTGTCAGCTGTGTAAGTTTCCAGATATGTCAG 1471
1424 CAATGGAACTGTTCAAACAAAATCAATATCTGMAATGCAACAGCTTGCATGTTAAAT 1483
1472 TGATTAAGAGCATGCAATTGTGCTGTATCCCGTAAGCAGATTTAGTTATTTCCATG 1531
1484 TTCCAGAGAAATAAAAACAACCTTATTTACCTCCCTTCGATTAAGATTTAGAAAAG 1543
1532 CAGGACTGATGACAGACTAGTACAGACAAATTAAGAGAAATGATTAAGAAACAGC 1591
1544 CAGCTGAGATTGCAACAGATGATAGTCTAATGTGCAAGTCGAGGTGGAAGAAATGTT 1603
1592 TCC-----GAGCAATTTGTACACAGATCTCTATGTGAATCACTGACCAAGAG 1642
1604 TTCTGTATTAAGAAATCTTGACAGGATCCCTGTCTCAACTGTGGAAGAAATGAAA 1663
1643 AAGATTTCTGAGGACCAAGAC---ACTATGTGTAATCTATCCCGAAATTTCTACCA 1699
1664 TGGATCTTATTTGACTTTGCGAAGACCTGCGAAGATTTTCCACAACTACCTCCAA 1723
1700 AATGCTTGTCTGTTAAATGAGACTCTAGAGATGAAGTACTGATGCTGCTGG 1759
1724 AATTACTGCTGTCATCAAGTGAATAACTTGAAGATGTGCTGAGCTTCAGGCGCTGC 1783
1760 TAAAGATTTGGCTCCAAATCAACGCTGAACAGGCTATGAGCTTCTGAGCTGCAATTACC 1819
1784 TTCAGATTTGGCTTAACTGACCCCGGAGGCGCTAGAGCTTCTGGAATTTCAATATAC 1843
1820 CAGATCTTATGTTGAGGTTTGTGTTGCTGCTAGGAAATATTTTAAACAGATGACA 1879
1844 CAGACCAATGCTTCCAGAAATATGCTGAGGCTGCT---GCGACAGATGAGTGAAG 1900
1880 AACTTCTCAGTAACTTAATTCAGTACAGTACTTAATAATTAAGACATTTTGGATA 1939
1901 AACTTCTCAGTAACTTTTCAACTGCTGCAAGTGTAAATATGAGCTTTTCTTGAT 1960
1940 AACTGCTGTGAGATTTTACTCAAAAAGCTTAACTAATCAAAAGATCGCTACTTT 1999
1961 GTGCCCTCTCTAGATTTCTATTAAGAAAGCACTTGTATCGAGAGATAGGCAAGTTTC 2020
2000 TCTTTTGGATTTAAATCTGAGATGCAATTAACATGTTAGTCAAGATTTGGCTGTC 2059
2021 TATTTTGGATCTTAAAGTGAAGGACATTTCTGCTGCTCAAGCAATTTGGGTGA 2080
2060 TTTTGGAGTCTTATGCGCTGACATGAGATGATCTGAAGCACTTAAATAGCAAGTTCG 2119
2081 TCTTTGAAGCATACGCTCCGGGGAAGTGTGGGCACTGAAGATGCTTTCTAAGCAGCTTG 2140
2120 AGGCTATGGAAGAGCTCATTAATCTGACTGACATTTCTAAACAGAGAAAGAGATGAAA 2179
2141 AAGCACTCAATAGTAAAGAACTTAAATAGTTTAACTCAAGATGCGGTGAAGTTAA 2200
2180 CACAAAGGTACAGATGAAGTTTATGAGCAAAATGGCGGACCAAGTTTCAATGATG 2239
2201 ACAGAGCCAAAGGAGGAGCCATGCAATCTGTTTAAACAGAGTGTCTACCGGGAAG 2260

2240 CTCTCAGGCTTCTCTGCTCTCTTAACCTGCTCATGAGTGGAAATCTCAGGCTTG 2299
2261 CCTCTCTGACCTGCAAGTCAACCTGCAACCATGTGTATCTCTCAGAACTCTATGTTG 2320
2300 AAGATGTGCAATATATGCTCTTCTGCAAAAAGCCACTGTGTTGAATTTGGAGAACCCAG 2359
2321 AAAAGTCAAAATCAATGAAATCCMAAATGAAAGCTTTGTGGCTGTATACAAATTAACAGG 2380
2360 ACATCATGTCAATTAATCTTTCAACAACAATGATCAATCTTTAAATAATGGGAGATG 2419
2381 TATTTGTGAGATTAAGT-----TGAGATGATTTTAAATAATGGATGAT 2428
2420 TACGCAAGATATGCTAACCTTCAGATTAATTCGATTAATGCAAAATATCTGCAAAATC 2479
2429 TACGACAGATATGTTGACACTCAATATGTGGCTGTATGATTTACTCTGGAAGAAAG 2488
2480 AAGCTTTGATCTTGAATGTTTACCTTATGATGTCTCAATCGGTGACTGTGGGAC 2539
2489 CTGGTTTGGATCTTCGATGTTGCTTATGCTGTTTACCAACAGAGATCGCTGTGGCC 2548
2540 TTATGAGGTGGTGAAGAAATTTCTCAACATTAATGCAATTCAGTGAAGAGAGC---C 2596
2549 TCAATTAAGTGTGAGCACCTCTGAACCAATGCTGACATTCAGCTGAACAGTGAAGATG 2608
2597 TGAAGGTGCACTGCACTTAAACAGCCACACACTCCATCAGTGGCTCAAGACAGACA 2656
2609 TGGCTGCTGACAGAGCTTCAACAAAGATGCCCTTGTGAATCTGCTTAAAGATACAACT 2668
2657 AAGGGAAATATATGATGCGGCCATGATTTGTTTACAGATCATGTGCTGATTTGTG 2716
2669 CTGGGATGACCTGCAACGAGCATGAGAAATTTCACTGCTGCTGCTGCTACTGTG 2728
2717 TTGCCACCTCAATTTTGGGAATTTGAGATGTCACAAATGTAATATCATGTTTAAAGATG 2776
2729 TAGCTTCTTATGCTCTTGGATTTGACAGACATATGTAACAACATCATGTCMAAAAA 2788
2777 ATGCAAACTGTTTCAATATATAGATTTTGGACACTTTTGGATCAACAAAGAAATAATTTG 2836
2789 CTGGCCAGCTCTTCCACATTTGACTTTGGACATATTTCTTGAAATTTCAATCTAAGTTTG 2848
2837 GTTATTAACGAGAGCGGCTGCGGTTTGTGTAACAACAGATTTCTTAATATGATTAATA 2896
2849 GCATTAAGAGGAGGAGGAGTCTTTTATTTACTTACATATGATTTCAATGATCATTAAC 2908
2897 AAGGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGGTTTACGAGATGTGTTACA 2956
2909 AAGGAAAAACAG-----AATTAACAAGAAAGTTTGGCGGTTCCGCCAGTGTGTGAGG 2962
2957 AAGCTTATCTAGCTATTCGGGACAGATGCCAATCTCTTCAATAATCTTTCTCAATGATGC 3016
2963 ATGCATATCTGATTTTACGAGCGCATGGAAATCTTCTTCACTCTCTTTGGCGTGAATG 3022
3017 TTGGCTTGGGAATGCGCAAGCTCAATCTTTTGTATGATATTTGCAATATTCGAAGAACCC 3076
3023 TGAATGCAAGGCTTCTGTAATCACAATCAGTCAAGATATACATGATTTAGAGACTGTC 3082
3077 TAGCTTTAGATTAATACTGACAGAGGCTTTGGATTTTCAAGAAATGAATGATG 3136
3083 TTGCATTTGGGGAAGATGAAGAAAGCACTCAAAACAGTTTAAAGCAAAATTTGATGAGG 3142
3137 CACACATGAGTGGCTGACCAAAATAATGATTTGATCTTCCACAAATTTAGCA 3191
3143 CCTCAGGGAAGCTGAGACTTAAATGTAACATGAGATGGCCACACAGTTCCGAA 3197

RESULT 10
ABX37274
ID ABX37274 standard; cDNA, 412 BP.
XX
XX ABX37274;
AC
XX
XX
DT 20-FEB-2003 (first entry)
XX

PR 19-JUL-1999; 99US-0357070.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowsett LM;
 XX WPI; 2000-282691/24.
 DR P-PSDB; AAY8372.
 XX
 PT New antisense compounds targeting nucleic acids encoding human PI3
 PT Kinase p110 delta useful for treating a disease or condition associated
 PT with PI3 Kinase p110 delta expression, e.g. rheumatoid arthritis,
 PT asthma
 XX
 PS Example 13; Column 45-52; 35bp; English.
 XX
 CC This sequence represents a nucleotide sequence encoding the delta
 CC catalytic subunit of human phosphatidylinositol 3 Kinase. Phosphatidyli
 CC inositol 3 kinases (PI3K) act as downstream effectors of hormone and
 CC growth factor receptors, and have been implicated in growth factor
 CC mediated cell transformation, mitogenesis, protein trafficking, cell
 CC survival and proliferation, and many other cellular activities. PI3K is a
 CC heterodimer, consisting of a 110kD catalytic subunit (p110), and an 85kD
 CC regulatory subunit (p85). The invention relates to antisense
 CC oligonucleotides which target the p110 delta mRNA of PI3K. The antisense
 CC oligonucleotides specifically hybridize with various regions of the PI3K
 CC mRNA sequence, and inhibit the expression of PI3K. The antisense
 CC oligonucleotides may be used to treat an animal, particularly human,
 CC oligonucleotides may be used to treat a disease or condition associated
 CC with the expression of PI3K, e.g. rheumatoid arthritis or asthma. The
 CC treatment works through the modulation (preferably inhibition) of the
 CC expression of PI3K. The antisense oligonucleotides may also be used for
 CC research and diagnostics, in pharmaceutical compositions and
 CC formulations, in the preparation of kits for detecting the level of PI3K
 CC in a sample, and as prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation. Antisense oligonucleotides, which are
 CC able to inhibit gene expression specifically, are used to elucidate the
 CC function of particular genes, and to distinguish between functions of
 CC various members of a biological pathway.
 CC
 XX Sequence 3868 BP; 800 A; 1190 C; 1141 G; 737 T; 0 other;
 SQ
 Query Match 10.5%; Score 336.2; DB 21; Length 3868;
 Best Local Similarity 53.5%; Pred. No. 1.4e-92;
 Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

QY 2102 ACCCTTAATGAGCAAGTGGAGCTATGAGAAAAGCTATTAACTGACTGACATTCGCAAC 2161
 DB 2238 TGCTGATGAGACAGAGGGGAGACCTGAGCAAACTGAGAGCCCTGATATGACTTCGCAAGC 2297
 QY 2162 AAGAGAAAGAGATGAAACACAAAAGGTACAGATGAAGTTTATGTTGAGCAAAATGCGGC 2221
 DB 2298 TGAGCTTCGAGAAAGACCCCAAGCCCAAGACCAAGAGACTGATGACTTGTGATGCGGC 2357
 QY 2222 GACCAAGATTTGATGATGATGATCTCTCCAGGCTTTGCTCTCTCTTAAACCCCTGCTATGAC 2281
 DB 2358 AGAGAGCCCTAGTACAGCCCTCTCCACCTGCACTGCCACTCGACCCAGCACCTTGC 2417
 QY 2282 TGGGAATCTCAGCGCTTGAAGAAGTGCATTTATGCTTTCGCAAAAAGGCCACTGTGGT 2341
 DB 2418 TGGCTGAAGTTCGCTGAGAGAGTCACTTCATGAGACTCCAAAGTGAAGCCCTGTGGA 2477
 QY 2342 TGAATTTGGAGAACCCAGACATCATGTGCAATTAATCTCTTTTCAGAACTATGATCATCT 2401
 DB 2478 TCATGTACGCAACGAGAGG-----GACGAGAGGGGGGCAAGCGGCATCATCT 2528
 QY 2402 TTAATAATGGGATGATGATTTACGCAAGATATGCTTAACTCTTATGATTTGCAATATGG 2461
 DB 2529 TTAAGAAGGGATGATGATCTCCGAGAGCATGCTGACCTGAGATGATCCAGCTCATGG 2588
 QY 2462 AAAATCTGGCAAAATCAAGTCTTGAATCTTGAATGTTTACCTTATGATGATCTGTCAA 2521
 DB 2589 ACCTCTGTCGAAAGCAGAGGGGCTGACCTGAGATGACCCCTTATGCTGCTGCCCA 2648
 QY 2522 TCGGTACGCTGTGGGACTTATGAGAGTGTGAATTTCTCACTATATATGACATTC 2581
 DB 2649 CCGGGAGCCGACAGGCTTATGAGTGTATCTCGTTACAGACATGACCAATCC 2708
 QY 2582 A---GTGAAGAGGCTGAAAGGTGACCTGCAAGTTTAAAGCCACACCTCCATCAGT 2638
 DB 2709 AATCTCAACAAAGACCAATGCGACCAACGCCCTTCAACAAAGATCCCTGCTCACT 2768
 QY 2639 GGCTCAAAAGACAAACAAAGGGGAAATATATATGAGGCGCATGATTTGTTACAGAT 2698
 DB 2769 GGCTGAAGTCCAAAGAACCGGGGAGGCGCTGATTCAGCATTTGAGAGATTCACCTCT 2828
 QY 2699 CATGTGCTGATATATGTTGTTGCCACTTCAATTTGGAAATGAGATGCTCACAAATGTA 2758
 DB 2829 CCTGTGCTGATATGTTGTTGCCACTATATGCTGCTGCGCATTTGGGATCGGACAGCA 2888
 QY 2759 AATCATGTTTAAAGATGATGAGCAACTGTTTCAATATGATTTGGACACTTTTGGATC 2818
 DB 2889 ACATCATGATCCGAGAGAGTGGCAGCTGTTCCACATTTGATTTGGCCACTTTCGGGGA 2948
 QY 2949 AATTCAAAGACCAAGTTTGAATCAACCGGAGCGTTCATTCCTCATCGTACGACT 3008
 DB 2879 TCTTAATGATATGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGT 2938
 QY 3009 TTGTCATGATGATGACAGGG-----GAGACTAATATATGAGAAATTTGAACGT 3062
 DB 2939 TTCAGAGATGTTTAAAGGCTTATCTAGCTATTTGGGAGATGCCAATCTTTCAATA 2998
 QY 3063 TCCGGGGCTACTGTGAAGGGCTTACACCATCTCGGGGCCACGGGCTTCTTCTCTCC 3122
 DB 2999 ATCTTTTCTCAATGATGCTTGGCTCTGCAATGCCAAGACTGCAATCTTTGATGATATG 3058
 QY 3123 ACTCTTTTCCCTGATGCGGGGGGAGGCTCTGAGCTCACTGCTCCAAAGACATCC 3182
 DB 3059 CATACATTGGAAGACCCCTAGCTTTAGATTAAGTGAAGAGAGGCTTTGAGATTTGA 3118
 QY 3183 AGTATCTCAAGGCTCTCTGAGCACTGGGAAAAAGAGAGAGGACATGGAAGCATCTCC 3242
 DB 3119 TGAACAAATGAATGATGACACATGATGCTGCAACAAATATGATTTGATCTTCC 3178
 QY 2042 GTCAAGAGTTTGGCTGCTTTTGGAGTCCATTTGGCGTGCATGAGATGATCTGAGC 2101
 DB 2118 GCAAGATCGGCACTTCTTTTGGGACCTCCGCTCCGAGATGCAAGTCCGCTGGTGG 2177
 QY 2042 GTCAAGAGTTTGGCTGCTTTTGGAGTCCATTTGGCGTGCATGAGATGATCTGAGC 2101
 DB 2178 TCCCTGCTTGGCTGCTCATCTGAGAGGCTTACGAGGAGGACCAACCATGATGAGG 2237

QY 3179 ACA 3181
 DB 3303 ACA 3305

RESULT 13
 ABR84750
 ID ABR84750 standard; cDNA, 3868 BP.
 AC ABR84750;
 XX
 DT 14-AUG-2002 (first entry)
 DE Human cDNA differentially expressed in granulocytic cells #1321.
 XX
 XX Human; se; granulocytic cell; DNA chip; bacterial infection;
 KM viral infection; parasitic infection; protozoal infection;
 KM fungal infection; sterile inflammatory disease; psoriasis;
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KM adult respiratory distress syndrome; inflammatory bowel disease;
 KM Crohn's disease; ulcerative colitis; periodontal disease;
 KM granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 PN W0200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PE 03-OCT-2001; 2001WO-US30821.
 XX
 PR 03-OCT-2000; 2000US-237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 PI Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
 DR WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 PS
 PS Claim 1; SEQ ID No 1321; 114pp: English.

reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease, also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and MS is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 3868 BP, 800 A; 1190 C; 1141 G; 737 T; 0 other;
 SQ

Query Match 10.5%; Score 336.2; DB 24; Length 3868;
 Best Local Similarity 53.5%; Pred. No. 1,4e-82;
 Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

QY 1682 TCCTCCGAATTTCTACCCCAATTTGCTTCTGTTAAATGGAACCTAGATGAAGTAG 1741
 DB 1821 TCCCGAGGCGCTAGCCCGGCTGCTGTCGTCACCAAGTGAACAAGATGAGATGTGG 1880
 QY 1742 CTCAGATCTACTGCTTGTGTAAGAATGGCTCCCAATCAAGCTGACAGCTATGAGC 1801
 DB 1881 CCGAGATGCTTACCTGCTGTGCTCTGCGGAGCTGCCGTCTAGCGCGCTGAGC 1940
 QY 1802 TTCTGAGATGCAATTACCCCAATCTATGTTGCAAGTTTGTGCTTGTGCTTGA 1861
 DB 1941 TGCTAGACTTACGCTCCCGATTTGCCACGATGAGCTCCCTTGCATCAAGTGTGCGGA 2000
 QY 1862 AATATTTACAGATGACCAAACTTTCTCAGTACCTATTCAGTACGATGACGATCAAT 1921
 DB 2001 AAC---TGACGAGAGATGAGCTGTTCCAGTACCTGCTGACGATGAGTGTCTCAAGT 2057
 QY 1922 ATGAAAGATATTTGATTAACCTGCTTGTGATTTTAACTCAAAAACGTTAACTATC 1981
 DB 2058 ACGAGTCTTACCTGACGTCGAGCTGACCAATTTCTGCTGAGCCGGCCCTGGCAAC 2117
 QY 1982 AAAGATGCGTCACTTTTCTTTGGCATTTAAATCTGAGATGACATTAACAGTTA 2041
 DB 2118 GCAAGATGCGCACTTCTTTTCTGCACTCCGCTCCGATACAGTGTGCGGTGG 2177
 QY 2042 GTCAGAGTTTGGCGCTCTTTTGGAGTCTTATGCGCGGATGAGGATGATGTAAGC 2101
 DB 2178 CCTGCGCTTGGCGCTTATCTGAGGCTTATCTGACGGGAGGACCAACCAATGAGG 2237
 QY 2102 ACCTTAAATAGGCAAGTTGAGGCTATGGAAGGCTCATTAATCTGACATTTCTCAAC 2161
 DB 2238 TGCTGATGAGACAGGGGAGGAGCACTGAGCAAACTGAAAGGCCCTGAATGACTTCAAGC 2297
 QY 2162 AAGGAAAGAGATGAACAACAAGATGATGAAGTTTATGTTAGGCAAAATGCGGC 2221
 DB 2298 TGAAGCTTCAAGAAACCCCAAGCCCAAGCAAGGAGCTGATGCACTTGTGACGCGC 2357
 QY 2222 GACCAAGTTTCATGAGATGCTCTCCAGGCTTGTGCTCTCTTAAACCTGCTCATAGC 2281
 DB 2358 AGAGAGCTTCTTGAAGGCTCTCCCACTGCAAGTCCCACTGACCCAGCAACCTGTC 2417
 QY 2282 TGGGAAATCTCAGGCTTGAAGATGCAATTAATGTTCTGCAAAAAGGCCAATGTGT 2341
 DB 2418 TGGCTGAAGTCTGGGTGAGCAAGTCACTTCAATGAGCTCCAGATGAACCCCTGTGGA 2477
 QY 2342 TGAATTTGGGAAACCAAGACATATGTCAAGATTAATCTTTTCAAGAACATGAGATCTT 2401
 DB 2478 TCAATGTACCAACAGAGG-----GACAGCAAGCGGAGGCTGAGGTGGCATCTT 2528
 QY 2402 TTAATAATGGGAGATGATTTACGGCAAGATATGTAACCTTCAGATTAATTCGATTAAG 2461
 DB 2529 TTAAGAAAGGAGATGACCTCCGACAGACATGCTGACCTGCGAGATATCACTCAATGG 2588
 QY 2462 AAAATATCTGGCAAAATCAAGGCTTGTGATCTTGAATGTTACCTTATGATGTCTGTCAA 2521
 DB 2589 ACGTCTGTGAGAGCAGAGAGGCTGACCTGAGATGACCCCTTATGCTGCTCCCA 2648

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OY 2522 TCGGTGACTGTGTGGACCTTATGAGGTGGTGAATTTCTCACTATATGCAATTC 2581
DB 2649 CCGGGGAGCCGACAGGCTCATTTGAGTGTGTTACTCCGTTACAGACCATGCGCAATCC 2708
OY 2582 A---GTGTAAGAGGCGCTGAAAGTGCACATGAGTTAACAGCCACACACTCATAGT 2638
DB 2709 AACTCAACACAGAACATGCGACGACAGCGGCTTCAACAGAGATGCGCTGTCACT 2768
OY 2639 GGCTCAAGACAGAACAGGCGGAATATATATGCGGCGCATGATTTGTTACAGAT 2698
DB 2769 GGCTGAAGTCCAGAGAACCGGGGAGGCGCTGAGTCAGCCATTGAGAGTTGACCCCT 2828
OY 2699 CATGTGCTGATATTGCTGTGCGACCTTCATTTGGGAATTGAGATGTCACAACTA 2758
DB 2829 CCGTGGCGGCTATTTGTGTGCGACATATGTCTGGGATGGCATGGCGACAGCGACA 2888
OY 2759 ATATGATGTTAAAGATGAGCAACTGTTTCATATGATTTTGGACACTTTTGGATC 2818
DB 2889 ACATCATGATCCGAGAGAGTGGGAGCTGTTCCACATTGATTTTGGCCACTTTTGGGGA 2948
OY 2819 ACAGAGAGAAAAATTGGTTATTAACAGAGCGCGTGGCTTTGTTGACACAAGAT 2878
DB 2949 ATTCAAGACCAAGTTTGGATATCAACCGGAGCGTGTCCATTCTCTACCTACGACT 3008
OY 2879 TCTTAATGATGATTAGTAAGAGCCCAAGATGACAAAGACAGAGATTTGAGAGT 2938
DB 3009 TTGTCCATGTGATTGACAGAGG-----GAGACTAATTAATGTAAGAAATTTGAACGT 3062
OY 2939 TTCAGAGATGTGTCAAGGCTTATCTAGCTATTTGGCGAGCATGCCAATCTTTCATTA 2998
DB 3063 TCCGGGCTACTGTGAAGGCGCTACACATCTCGGCGGCGCCACGCGCTTCTTCTCC 3122
OY 2999 ATCTTTCTCAATGATGCTTGGCTCTGGAATGCGCAAGATCGCAATCTTTGATGATTTG 3058
DB 3123 ACCTCTTGGCCGTGATCGGGCGGCGAGCGCTGCTGAGCTGAGTCTCCAAAGACTCC 3182
OY 3059 CATTCATTCAGAAAGACCTTGAATTAATGATTAAGTGAAGAGGCTTGGAGTATTTCA 3118
DB 3183 AGTATCTTCAGAGACTCCCTGCGACTGGGAAACAGAGAGGAGGCACTGAAGCACTTCC 3242
OY 3119 TGAAGACAAATGATGATGACACCATGTGCTGAGACAAACAAATGATTTGATCTCC 3178
DB 3243 GAGTGAAGTTTAAGAGAGCCCTCCGTGAGACTGGAACAAAGTGAATGCGTGGCC 3302
OY 3179 ACA 3181
DB 3303 ACA 3305

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PD 15-NOV-2001.
PF 10-MAY-2001; 2001WO-US15065.
PR 10-MAY-2000; 2000US-203346P.
XX (ICOS-) ICOS CORP.
XX Sadhu C;
PI WPI: 2002-075252/10.
DR P-PSDB; AAU09685.
XX
XX Identifying a modulator of p110delta polypeptide binding to SH3
PT domain-containing polypeptides e.g. Lasp-1, comprising allowing the
PT binding partners to interact in the presence and absence of a test
PT compound.
XX
XX Example 1; Page 43-48; 85pp; English.
XX
XX The present invention relates to identifying a modulator of the
CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC the catalytic subunit via a SH3 domain-containing polypeptide such as
CC Lasp-1. Also described are methods of assaying the specific binding
CC affinity of the PI3-kinase binding partner. Such modulators are useful
CC for the treatment of diseases characterized by the undesirable or
CC excessive activity of PI3Kdelta. For example the modulators can be used
CC for inhibiting the growth or proliferation of cancer cells
CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC dermatoses (e.g. contact dermatitis; central or peripheral neuritis,
CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC and Type I diabetes mellitus. The present sequence encodes for human
CC p110delta isoform of PI3K.
XX
XX Sequence 3868 BP; 800 A; 1190 C; 1141 G; 737 T; 0 other;
SQ

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Query Match 10.5%; Score 336.2; DB 24; Length 3868;
Best Local Similarity 53.5%; Pred. No. 1.4e-82;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

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OY 1682 TCCCGCAATCTTACCAAAATGCTTCTGTCTTAATGAACTGAGATGAGTAG 1741
DB 1821 TCCCGAGGCGCTAGCCGCGTGTCTGTCACCAAGTGAACAGACATGAGATGCG 1880
OY 1742 CTCAGATGTACTGCTTGTGAAGATTTGGCTCCATCAAGCGCTGACAGGCTATGAGC 1801
DB 1881 CCCAGATGCTTACTCTGTGCTCTGCGCGAGAGCTGCCCTCTGAGGCCCTTGAGGC 1940
OY 1802 TTCTGAGCTGCAATTTACCCGATCTTATGTTGAGGTTTGTCTGCTTACGAA 1861
DB 1941 TGTAGACTGTAGCTTCCCATTTGCCAGTAGGCTCCTTGCCATCAAGTGGTGGCA 2000
OY 1862 AATATTAAAGATGACAAATTTCTCAGTACTTAATCACTAGTACTAGTACTAAAT 1921
DB 2001 AAC---TACGAGCATGAGCTGTTCAGTACTGCTGACCTGTGAGGTTGCACT 2057
OY 1922 ATGAACAGTATTGGATTAAGCTGTTGAGATTTTCTCAAAAACGTTAATAATC 1981
DB 2058 AGAGTCTTACTGAGTACGAGTGAACAAATTTCTGTGAGCCGGGCTTGAGACC 2117
OY 1982 AAAGATGCTGCTACTTTTCTTTGSCATTTAAATTCGAGTGAACATTAACAGTTA 2041
DB 2118 GCAAGATGCGCACTTCTTTCTGACCTCCGCTCGAAGTGAAGTGGCGTGGTGG 2177
OY 2042 GTCAGAGTTTGGCTGCTTTTGAATCTTATGCTGCTGATGAGATGATTTGAAC 2101
DB 2178 CCTGGGCTTGGCTTCACTGAGAGCTTACGAGGCGGAGAGCCACCATGATGAAG 2237
OY 2102 ACCTTAATGAGCAAGTTGAGGCTATGAGAAAGTCAATTAAGTGAATTTCAAC 2161

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RESULT 14
AAS14363
ID AAS14363 standard; CDNA; 3868 BP.
XX
XX AAS14363;
XX
XX 12-MAR-2002 (first entry)
XX
XX CDNA encoding human p110delta isoform of PI3-kinase.
XX
XX Human: phosphatidylinositol 3-kinase; PI3K; p110delta isoform;
XX Lasp-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
XX autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
XX Type I diabetes mellitus; cytosolic; immunosuppressive; 95.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 197..3331
XX CDS /*tag= a
XX FT /product= "p110delta isoform of PI3-kinase"
XX
XX MO2C0185986-A2.
XX

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Db      2238 TCCTGATGAAAGCGGGAGACCTGAGCAAACTGAAAGGCTTGAATGACTTCCTCAAGC 2237
QY      2162 AAGAGAAAGAGATGAAACAACAAAGGTAACAGATGAATTTTATGAGCAAAATGCGGC 2221
Db      2298 TGAAGCTCAGAAAGACCCCAAGGCCCAAGACCAAGAGCTGATGACTTGTGATGCGGC 2357
QY      2222 GACCAAGATTTTCATGATGCTCTCCAGGGCTTTCTGTCTCTTAAACCTGCTCATGAGC 2281
Db      2358 AGGAGGCTTACCTAGAGGCCCTCTCCACCTGACGTCCCACTGACCCCAAGCACTGCG 2417
QY      2282 TGGGAATCTCAGGCTTGAAGAGTGTGAAATTAATGCTTTCTGCAAAAAGGCACTGTGT 2341
Db      2418 TGGCTGAAGTCTGCTGAGAGAGTGCACCTTCAAGCACTCCAAAGTAAAGCCCTGTGGA 2477
QY      2342 TGAATTGGAGAAACCCAGACATCATGTCAAGATTACTCTTTCAGACAAATGAGATCATCT 2401
Db      2478 TCATGTACAGCAAGAGAGAG-----GAGGACAGCGCGCGCGCTGCGCATCATCT 2528
QY      2402 TTAATAATGGGAGATTTACGCGCAGATATGCTAACCTTCAAGATTATTCGATTAATGG 2461
Db      2529 TTAAGAAACGGGAGTACCTCCGGCAGAGATGCTGACCTTGCAAGATGATCCAGCTCATGG 2588
QY      2462 AAAATATCTGGCAAAATCAAGGCTTATCTTGAATGTTAATCTTATGATGCTGTCAA 2521
Db      2589 ACCTCTGTGAAAGCAGAGAGGGGCTGACCTGAGGATGACCCCTATGCGCTGCCCA 2648
QY      2522 TCGGTGACTGTGGGACTTATGAGGCTGTTGAGAAATTTCCACATATATAGAGATTC 2581
Db      2649 CCGGGAGCGCACAGGCTTATGAGTGTATCTCCCTTCAAGACATGCCAACAATTC 2708
QY      2582 A---GTGTAAGAGAGGCTGAAAAGTGCATGCACTGAGTTTAAACGACACACTCCATAGT 2638
Db      2709 AACTCAACAGAGCAACATGAGCAGCCACAGCCGCTTCAACAGATGCTCCTGCTCACT 2768
QY      2639 GGGTCAAGACAGAACAGAGGGGAAATATATGATGCGGCAATGCTGTTTAAACGAT 2698
Db      2769 GGGTGAAGTCCAAAGAACCCGGGGAGGCGCTGATGAGCATATGAGGATTCACCTCT 2828
QY      2699 CATGCTGGAATTTGTTGTTGCCACCTTCATTTTGGGAATTTGACAAATATGTA 2758
Db      2829 CCTGCTGCTATTTGTTGCGCAATATGCTGCGCATTTGGCGAATGGCAAGCGAC 2888
QY      2759 ATATCATGTTAAAGATGATGACAACCTTTTCATATAGATTTTGCACATTTTGGATC 2818
Db      2889 ACATCATGATCCGAGAGAGTGGGAGCTGTTCCACATTTGATTTTGGCACTTTCTGGGA 2948
QY      2819 ACAAGAAAGAAAAATTTGTTATPAAAGAGAGCGCGTGGCTTTGTTGACAAAGATT 2878
Db      2949 ATTTCAGACCAAGTTTGAAATCAACCGGAGCGTGCATTCATCTCACTACGACT 3008
QY      2879 TCTTATAGTATTAATTAAGAGCCCAAGATATGCAACAAAGAAAGAAATTTGAAGGT 2938
Db      3009 TTGTCATGATGATTCAGCAGG-----GAAAGCTATATATATGTAATTTGAACGGT 3062
QY      2939 TTCAGAGATGTTGTTCAAGGCTTATCTATCTATTCGCGCAGATGCAATCTTTCATTA 2998
Db      3063 TCCGGGCTACTGTGAAAGGCTTACACATCTGCGGCGCCACCGGCTTCTTTCTCC 3122
QY      2999 ATCTTTTTCATGATGCTTGTGCTGGAATGCGCAAACTGCAATCTTTTGTGATATTG 3058
Db      3123 ACCTCTTTCCCTGATGCGGCGGAGCGCTGCTGAGCTCACTCTCCAAAGCATCC 3182
QY      3059 CATACATTGGAAGACCTAGCTTATGATPAAACGAGCAAGAGGCTTTGAGTATTTC 3118
Db      3183 AGTATTCMAAGHCTCCCTGGACCTGGGAAACAGAGAGGAGGACATGAACATTC 3242
QY      3119 TGAACAAATGATATGCAACACATGCTGCTGCAACAAATATGATTTGATCTTC 3178
Db      3243 GAGTGAAGTTTAAAGAGCCCTCGTGAAGCTGGAACCAAGATGAACTGCTGCGCC 3302
QY      3179 ACA 3181

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Db      3303 ACA 3305
RESULT 15
AAV31340
ID AAV31340 standard; cDNA; 5220 BP.
XX
AC AAV31340;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human phosphatidylinositol 3-kinase p110 delta subunit cDNA.
XX
KM Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 196..330
FT /+tag= a
XX
PN W09823760-A1.
XX
PD 04-JUN-1998.
XX
PE 25-NOV-1997; 97MO-US21655.
XX
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Chanrity DH, Hoekstra MF, Holtzman DA.
XX
DR MPI; 1998-322736/28.
XX
DR P-PSDB; AAM58570.
XX
PT New phosphatidylinositol 3-kinase catalytic subunit - used to
PT develop products for modulating kinase activity in immune system
PT signalling and in carcinogenesis
XX
PS Claim 4; Page 27-33; 53pp; English.
XX
XX
XX This full-length composite cDNA encodes the p110 delta catalytic
XX subunit (see AAM58570) of human phosphatidylinositol 3-kinase. It
XX was assembled from clone #249 obtained by PCR amplification (see
XX AAV31341-44) of human peripheral blood mononuclear cell cDNA, clone
XX #4928 obtained by screening a human macrophage cDNA library, and
XX further clones obtained by RACE and PCR (see AAV31345-50). The
XX following are claimed: (1) a purified and isolated polynucleotide
XX (PN) encoding p110 delta; (2) a vector comprising a DNA as in (1);
XX (3) a host cell stably transformed or transfected with a DNA as in
XX (1); (4) PN encoding a lipid kinase, and hybridizing to PN having
XX the 5220 bp sequence; (5) a purified and isolated p110 delta
XX polypeptide as in (4); (6) an antibody specifically immunoreactive
XX with p110 delta; (7) a hybridoma cell line (especially 208F
XX (HB 12200) producing a monoclonal antibody as in (6); and (8) a
XX humanized antibody as in (6). p110 delta has kinase activity and
XX may play a role in PI 3-kinase mediated signalling in the immune
XX system and in carcinogenesis. The products can be used to develop
XX agents that modulating p110 delta kinase activity and to develop
XX diagnostic reagents (claimed). They may also be used for detection
XX and diagnosis of p110 delta in a biological sample.
XX
SQ Sequence 5220 BP; 1120 A; 1525 C; 1483 G; 1092 T; 0 other;
Query Match 10.5%; Score 336.2; DB 19; Length 5220;
Best Local Similarity 53.5%; Pred No. 176-82;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;
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 QY 1862 AATATTTAAGATGAACAATTTCTCACTACCTAATTCAGCTAGTACAGTACTAAAT 1921
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 DB 2357 AGGAGGCTTACTAGAGGCTCTTCCACCTGAGTCCCACTGAGCCCAAGCCCTGC 2416
 QY 2282 TGGGAAATCTCAGGCTTGAAGTGTCAATATATCTTCTGCAAAAAGGCACTGTGT 2341
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 QY 2342 TGAATTTGGAGAACCCACATCATGTGAAATTAATCTCTTTCAGAAATGAGATCT 2401
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 Job time : 556.733 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:09:02 ; Search time 7715.41 Seconds

(without alignments)
17004.573 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207

Sequence: 1 ATGCTTCACAGACCATCATC.....AGCAGCATGCTTGAACCTGA 3207

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb_om:*

5: gb_ov:*

6: gb_pat:*

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8: gb_pl:*

9: gb_pr:*

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	3207	100.0	3207	6 AR064288	AR064288 Sequence
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7	3024.6	94.3	3207	6 HSU79143	U79143 Human phosp
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18	2528	78.4	225277	2 AC129863	AC129863 Rattus no
19	2512.8	78.4	225277	2 AC127178	AC127178 Rattus no
20	2459.8	76.7	3452	5 AF001076	AF001076 Gallus ga
21	2419.2	75.4	3389	14 AF001075	AF001075 Avian sar
22	1660.6	51.8	2556	5 AF204924	AF204924 Xenopus 1
23	827.2	25.8	250250	2 AC097304	AC097304 Rattus no
24	703.4	21.9	873	10 AF395897	AF395897 Rattus no
25	448.2	14.0	3213	6 AR116356	AR116356 Sequence
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37	336.2	10.5	5220	6 AR281257	AR281257 Sequence
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ALIGNMENTS

RESULT 1

BOVPHOS3KN 3207 bp mRNA linear MAM 27-APR-1993

LOCUS Bovine phosphatidylinositol 3-kinase 110 kDa subunit mRNA, complete cds

DEFINITION

ACCESSION M93252

VERSION M93252.1 GI:163519

KEYWORDS phosphatidylinositol 3-kinase.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.

REFERENCE 1 (bases 1 to 3207)

Hilles,I.D., Otau,M., Volintu,S., Fry,M.J., Gout,I., Dhan,R.,

Parayotou, G., Ruiz-Iarrea, F., Thompson, A. S., Totty, N. F.,
Hsuan, J. J., Courtnedge, S. A., Parker, P. J. and Waterfield, M. D.
Phosphatidylinositol 3-kinase: structure and expression of the 110
kd catalytic subunit
JOURNAL
Cell 70 (3), 419-429 (1992)
MEDLINE
92354059
PubMed
1322797
Original source text: Bos laurus cDNA to mRNA.
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CDS

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 36 from Patent WO93121328.
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 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCES
 1. (bases 1 to 3207)
 Hiles J.D. and Fry M.J.
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 VERSION AR048987.1 GI:6005026
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 AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J., Otsu, M., Panayotou, G., Volinia, S. and Gout, I.,
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 JOURNAL Patent: US 5824492-A 35 20-0CT-1998;
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RESULT 4
AR064288
LOCUS AR064288 3207 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 35 from patent US 5846824.
ACCESSION AR064288
VERSION AR064288.1 GI:5993596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3207)
AUTHORS Hlee,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,
Oleu,M., Parayotou,G., Volinia,S. and Gout,I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5846824-A 35 08-DBC-1998;
FEATURES
Source 1. 3207
/organism="unknown"
BASE COUNT 1028 a 581 c 680 g 918 t
ORIGIN

Query Match 100.0%; Score 3207; DB 6; Length 3207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
ARI64681
LOCUS ARI64681 3207 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 35 from patent US 6274327.
ACCESSION ARI64681
VERSION ARI64681.1 GI:16237792
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3207)
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J., Otsu, M., Panayotou, G., Volinia, S. and Gout, I.,
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 6274327-A 35 14-AUG-2001;
FEATURES
 source
 1..3207
 location/Qualifiers
BASE COUNT 1028 a 581 c 680 g 918 t
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Query Match 100.0%; Score 3207; DB 6; Length 3207;
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LOCUS Sequence 1 from Patent WO9403609.
DEFINITION A37232
ACCESSION A37232
VERSION A37232.1 GI:2294345
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3498)
AUTHORS Parker, P.J., Goode, N.T., Nurse, P.M. and Waterfield, M.D.
TITLE EUCARYOTIC CELLS TRANSFORMED WITH A MAMMALIAN PHOSPHOLIPID KINASE
OR PROTEIN KINASE AND ASSAYS USING THEM
PATENT: WO 9403609-A, 17-FEB-1994;
IMP CANCER RES. TECH. (GB)
JOURNAL Other publication JP 8503124T 960409.
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BASE COUNT

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Query Match

100.0%; Score 3205.4; DB 6; Length 3498;

Best Local Similarity

100.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 3206; Conservative

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 ACCESSION U79143

VERSION U79143.1 GI:1763625
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 REFERENCE 1 (bases 1 to 3207)
 Oliff, A. and Heimbrock, D.C.
 Cloning and mutagenesis of the p110 alpha subunit of human phosphoinositide 3'-hydroxylase
 Bioorg. Med. Chem. 5 (1), 65-74 (1997)
 JOURNAL 9718658
 MEDLINE 9043658
 PUBMED 2 (bases 1 to 3207)
 Stidivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledder, L.M., Oliff, A. and Heimbrock, D.C.
 REFERENCES
 Oliff, A. and Heimbrock, D.C.
 Direct Submission
 Submitted (21-NOV-1996) Cancer Research, Merck Research Labs, Summeytown Pike, West Point, PA 19486, USA
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QY	1681	ATCCCCGAAATTTCTACCCCAATTGCTTCTGTCTGTAAATGGAACCTAGAGATGAAGTA	1740
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QY	1981	CAAGGATCGGCTCTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGT	2040
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QY	2281	CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTTTGCAAAAAAGGCCACTGTGG	2340
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LOCUS AR048986
DEFINITION AR048986
ACCESSION AR048986
VERSION AR048986.1 GI:6005025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3240)
AUTHORS Hiles, I. D., Fry, M. J., Dhand, R., Warefield, M. D., Parker, P. J.,
Osun, M., Panayotou, G., Volinia, S. and Gout, I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5824492-A 34 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..3240

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Db      61 CTAGTGAATGTTTACTTACCAATGGAGATAGTACTTTAGATGATGCTCCGTAGGCT 120
Qy      121 ACCTTATATACGATTAAGACATGATATTTAAAGACAAAGAAATACCTCTCCATCA 180
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Qy      181 CTTCTTCAAGATGAATCTTCTTACATTTTCTTAAGTGTACCCAGAGAGAGAGGAA 240
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Qy      421 AGAAATTTTCAATGTTTGTAAAGAGCTGTGGATCTTGAAGATCTTAATTCACCTCAT 480
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 LOCUS AR164680
 DEFINITION Sequence 34 from patent US 6274327.
 ACCESSION AR164680
 VERSION AR164680.1 GI:16237790
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3240)
 Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
 Otsu, M., Panayotou, G., Voljina, S. and Gout, I.
 Polypeptides having kinase activity, their preparation and use
 Patent: US 6274327-A 34 14-AUG-2001;
 FEATURES
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 BASE COUNT 1057 a 582 c 682 g 919 t
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ACCESSION AR048985
VERSION AR048985.1 GI:6005024
KEYWORDS

SOURCE

ORGANISM

Unknown.
Unclassified.

1 (bases 1 to 3412)

REFERENCE Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
Otsu, M., Panayotou, G., Volinia, S. and Gout, I.
Polypeptides having kinase activity, their preparation and use
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QY 181 CTTCTTCAAGATGATCTTTTCAATTTTGTAGTGTATCCCAAGAGCAAGAAAGGAA 240
Db 181 CTTCTTCAAGATGATCTTTTCAATTTTGTAGTGTATCCCAAGAGCAAGAAAGGAA 240
QY 241 GAATTTTGAATGAACAAAGCACTTTGACCTTGGCTTTTCAACCTTTTAAAA 300
Db 241 GAATTTTGAATGAACAAAGCACTTTGACCTTGGCTTTTCAACCTTTTAAAA 300

QY 301 GTAATTGAACGATAGGCAACCGTAGAAGAAAAGATCCTCAATCGAATAATGGTTTGGT 360
Db 301 GTAATTGAACGATAGGCAACCGTAGAAGAAAAGATCCTCAATCGAATAATGGTTTGGT 360
QY 361 ATCGGCATGCCAGTGTGTGAATTCGATATGCTTAAAGATCCAGAAAGTACAGACTTCCGA 420
Db 361 ATCGGCATGCCAGTGTGTGAATTCGATATGCTTAAAGATCCAGAAAGTACAGACTTCCGA 420
QY 421 AGAATATTTCTCAATGTTTGTAAAGACGTGTGATCTTTAGGATCTTAATTCACCTCAT 480
Db 421 AGAATATTTCTCAATGTTTGTAAAGACGTGTGATCTTTAGGATCTTAATTCACCTCAT 480
QY 481 AGTAGCAATGATATGTTATCTCCCAATGTAGATCTTCAACGAACCTGCCAAAGAC 540
Db 481 AGTAGCAATGATATGTTATCTCCCAATGTAGATCTTCAACGAACCTGCCAAAGAC 540
QY 541 ATATATTAATAATTGATTAAGAGCAATATATAGTGTGATTTGGGTATATGTTCTCCA 600
Db 541 ATATATTAATAATTGATTAAGAGCAATATATAGTGTGATTTGGGTATATGTTCTCCA 600
QY 601 AATAATGCAAAACAGAGTATATCTGTAAATCAACATGACTGTGCCAAGCAAGTA 660
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QY 661 ATTGCTGAAGCAATCAGSAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAA 720
Db 661 ATTGCTGAAGCAATCAGSAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAA 720
QY 721 CTCTGTGTTTGAATATCAAGGCAAGTATTTTAAAGTGTGTGATGATGATATAC 780
Db 721 CTCTGTGTTTGAATATCAAGGCAAGTATTTTAAAGTGTGTGATGATGATATAC 780
QY 781 TTCTTAGAAAAATATCTCTGATGATGATATATAGATATAGAAAGCTGTATATCTTGGG 840
Db 781 TTCTTAGAAAAATATCTCTGATGATGATATATAGATATAGAAAGCTGTATATCTTGGG 840
QY 841 AGAATGCCAATTTGATGCTGATGCTGAAGAAAGCCCTATTTCTCAACCTGCCAATGAC 900
Db 841 AGAATGCCAATTTGATGCTGATGCTGAAGAAAGCCCTATTTCTCAACCTGCCAATGAC 900
QY 901 TGTATTCAATATGCAATCATATTTCCAGACGATCTCCACAGCTACGCAATATATGATGGA 960
Db 901 TGTATTCAATATGCAATCATATTTCCAGACGATCTCCACAGCTACGCAATATATGATGGA 960
QY 961 GAAACATCTCAAAATCCCTTGGGTTATTAATATGTCAGATCTCAAGATTAATAATCTTTGT 1020
Db 961 GAAACATCTCAAAATCCCTTGGGTTATTAATATGTCAGATCTCAAGATTAATAATCTTTGT 1020
QY 1021 GCAACCTATGATGATTAATATTTCCAGACATTTGACAGATTTGATGATGATGATGATG 1080
Db 1021 GCAACCTATGATGATTAATATTTCCAGACATTTGACAGATTTGATGATGATGATGATG 1080
QY 1081 TACCATGAGAGAAACCTTATGATATGTAATGTAAGCTCAAAAGAGTATGTTTCAAT 1140
Db 1081 TACCATGAGAGAAACCTTATGATATGTAATGTAAGCTCAAAAGAGTATGTTTCAAT 1140
QY 1141 CCAAGGTGATATGATGCTGAATTAAGATATTAACATTCCTGATCTTCTGCTGCT 1200
Db 1141 CCAAGGTGATATGATGCTGAATTAAGATATTAACATTCCTGATCTTCTGCTGCT 1200
QY 1201 CGACTTTGCTTTCCATTTGCTTCTGTTAAAGCCGAAAGGCTCTAAAGGAACTGT 1260
Db 1201 CGACTTTGCTTTCCATTTGCTTCTGTTAAAGCCGAAAGGCTCTAAAGGAACTGT 1260
QY 1261 CCATTGGCCTGGGAAATATAAATCTGTTGATTAACAGATCTCTAGATATCGGAAAA 1320
Db 1261 CCATTGGCAGGGGAAATATAAATCTGTTGATTAACAGACACTCTAGATATCGGAAAA 1320
QY 1321 ATGCTTTGATATTTTGGCAGTACTCATGACATGAAATTTGCTGAACCTATTTGGT 1380
Db 1321 ATGCTTTGATATTTTGGCAGTACTCATGACATGAAATTTGCTGAACCTATTTGGT 1380
QY 1381 GTTACTGATCAAAATCAATAAAGAACTCCATGTTTGAAGTTTGAAGTTTGA 1440
Db 1381 GTTACTGATCAAAATCAATAAAGAACTCCATGTTTGAAGTTTGAAGTTTGA 1440


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Db      1381  |||||GTTACTGATCAATCCAAATTAAGAACTCATGCTTAGAGTTGAGTTGACTGTTCTC 1440
Qy      1441  |||||AGCAGTGTGTAAGTTCAGATATGTCAGTATGTAAGACATGCGCAATGGTCTGTA 1500
Db      1441  |||||AGCAGTGTGTAAGTTCAGATATGTCAGTATGTAAGACATGCGCAATGGTCTGTA 1500
Qy      1501  |||||TCCCGTAAGCAGATTTAGTTATTCCTCAGCAGATGAGTAACAGACTAGTAGAGAC 1560
Db      1501  |||||TCCCGTAAGCAGATTTAGTTATTCCTCAGCAGATGAGTAACAGACTAGTAGAGAC 1560
Qy      1501  |||||TCCCGTAAGCAGATTTAGTTATTCCTCAGCAGATGAGTAACAGACTAGTAGAGAC 1560
Db      1561  |||||AATGAATTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACAGAGATCTCTA 1620
Qy      1561  |||||AATGAATTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACAGAGATCTCTC 1620
Db      1621  |||||TCTGMAATCAGTACGACAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTACT 1680
Qy      1621  |||||TCTGMAATCAGTACGACAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTACT 1680
Db      1681  |||||ATCCCGAAATTTAACCAGATTTGCTGTCTGTCTTAATGAGACTAGAGATGAGTA 1740
Qy      1681  |||||ATCCCGAAATTTAACCAGATTTGCTGTCTGTCTTAATGAGACTAGAGATGAGTA 1740
Db      1741  |||||GCTCAGATCTACTGCTGTGTAAGAAAGTTGAGCTCCAGTCCAGCTGAAAGAGCTATGAG 1800
Qy      1741  |||||GCTCAGATCTACTGCTGTGTAAGAAAGTTGAGCTCCAGTCCAGCTGAAAGAGCTATGAG 1800
Db      1801  |||||GCTCAGATCTACTGCTGTGTAAGAAAGTTGAGCTCCAGTCCAGCTGAAAGAGCTATGAG 1800
Qy      1801  |||||GCTCAGATCTACTGCTGTGTAAGAAAGTTGAGCTCCAGTCCAGCTGAAAGAGCTATGAG 1800
Db      1801  |||||CTTCTGAGTGCATTAACCCAGATTCCTATGTTGAGGTTTGTCTGTGCTTCTAGAA 1860
Qy      1801  |||||CTTCTGAGTGCATTAACCCAGATTCCTATGTTGAGGTTTGTCTGTGCTTCTAGAA 1860
Db      1861  |||||AAATATTTAAGATGACAAATCTTCTCAGTACTTAATGAGCTAGTACAGTCTTAA 1920
Qy      1861  |||||AAATATTTAAGATGACAAATCTTCTCAGTACTTAATGAGCTAGTACAGTCTTAA 1920
Db      1921  |||||TATGAACAGATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAGCGTTAACTAAT 1980
Qy      1921  |||||TATGAACAGATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAGCGTTAACTAAT 1980
Db      1981  |||||TATGAACAGATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAGCGTTAACTAAT 1980
Qy      1981  |||||TATGAACAGATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAGCGTTAACTAAT 1980
Db      2041  |||||AGTCAGAGTTTGGCTGCTTTTGAAGTCTTATGCGGTGATGAGATGATCTGAG 2100
Qy      2041  |||||AGTCAGAGTTTGGCTGCTTTTGAAGTCTTATGCGGTGATGAGATGATCTGAG 2100
Db      2041  |||||AGTCAGAGTTTGGCTGCTTTTGAAGTCTTATGCGGTGATGAGATGATCTGAG 2100
Qy      2041  |||||AGTCAGAGTTTGGCTGCTTTTGAAGTCTTATGCGGTGATGAGATGATCTGAG 2100
Db      2101  |||||CACCTTAATAGCAAGTTGAGGCTATGAGAAAGCTCATTAACCTGACTGACTTCA 2160
Qy      2101  |||||CACCTTAATAGCAAGTTGAGGCTATGAGAAAGCTCATTAACCTGACTGACTTCA 2160
Db      2101  |||||CACCTTAATAGCAAGTTGAGGCTATGAGAAAGCTCATTAACCTGACTGACTTCA 2160
Qy      2101  |||||CACCTTAATAGCAAGTTGAGGCTATGAGAAAGCTCATTAACCTGACTGACTTCA 2160
Db      2161  |||||CAAGAGAGAGATGAGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGCGG 2220
Qy      2161  |||||CAAGAGAGAGATGAGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGCGG 2220
Db      2161  |||||CAAGAGAGAGATGAGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGCGG 2220
Qy      2161  |||||CAAGAGAGAGATGAGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGCGG 2220
Db      2221  |||||CGACAGATTTGATGATGCTCCACAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280
Qy      2221  |||||CGACAGATTTGATGATGCTCCACAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280
Db      2221  |||||CGACAGATTTGATGATGCTCCACAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280
Qy      2221  |||||CGACAGATTTGATGATGCTCCACAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280
Db      2281  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2340
Qy      2281  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2340
Db      2281  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2340
Qy      2281  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2340
Db      2341  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2400
Qy      2341  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2400
Db      2341  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2400
Qy      2341  |||||CTGGGAAATCTCAGGCTTGAAGAGTTCGATATGCTTCTGCAAAAAGCGCATGAG 2400
Db      2401  |||||TTTAAATATGAGGATGATTTACGCGCAAGATATGTAACCTTGAATATGATG 2460
Qy      2401  |||||TTTAAATATGAGGATGATTTACGCGCAAGATATGTAACCTTGAATATGATG 2460
Db      2461  |||||GAAATATCTGCGAAATCAAGGCTTGATCTGCAATGTTACCTTATGATGATG 2520
Qy      2461  |||||GAAATATCTGCGAAATCAAGGCTTGATCTGCAATGTTACCTTATGATGATG 2520

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Db      2461  |||||GAAATATCTGCGAAATCAAGGCTTGATCTGCAATGTTACCTTATGATGATG 2520
Qy      2521  |||||ATCGGATCTGCTGCGGACTTATTCAGAGTGTGAGAAATTTCAACACTTATGAGAT 2580
Db      2521  |||||ATCGGATCTGCTGCGGACTTATTCAGAGTGTGAGAAATTTCAACACTTATGAGAT 2580
Qy      2581  |||||CAGTGTAAAGAGGCTGAAAGGTGACATGCGATTTAAACAGCAGACATCTCAGTGG 2640
Db      2581  |||||CAGTGTAAAGAGGCTGAAAGGTGACATGCGATTTAAACAGCAGACATCTCAGTGG 2640
Qy      2641  |||||CTCAAGACAAAGAAACAAAGGAGGAAATATATGATGCGGCTCAGTATTTTACAGATCA 2700
Db      2641  |||||CTCAAGACAAAGAAACAAAGGAGGAAATATATGATGCGGCTCAGTATTTTACAGATCA 2700
Qy      2701  |||||TGTGCTGATATGTTGTTGTCACCTTCAATTTTGGGAAATTTGGAATGCTCAATAGTAAT 2760
Db      2701  |||||TGTGCTGATATGTTGTTGTCACCTTCAATTTTGGGAAATTTGGAATGCTCAATAGTAAT 2760
Qy      2761  |||||ATCATGCTTAAAGATGATGACAACTGTTTCAATATTTTGGACACTTTTGGATCAC 2820
Db      2761  |||||ATCATGCTTAAAGATGATGACAACTGTTTCAATATTTTGGACACTTTTGGATCAC 2820
Qy      2821  |||||AAGAGAAATTTTGTGTTATTAACAGAGCGCGCTTGTGTTGACACAGATTTTC 2880
Db      2821  |||||AAGAGAAATTTTGTGTTATTAACAGAGCGCGCTTGTGTTGACACAGATTTTC 2880
Qy      2881  |||||TTAATAGTATGATTAAGAGAGAGCCAGAAATGACAAAGACAGAAATTTGAGAGGTT 2940
Db      2881  |||||TTAATAGTATGATTAAGAGAGAGCCAGAAATGACAAAGACAGAAATTTGAGAGGTT 2940
Qy      2941  |||||CAGAGATGTTTACAGGCTTATCTAGCTATTTGCGAGCAGATGCAATCTTTGATGATGCA 3000
Db      2941  |||||CAGAGATGTTTACAGGCTTATCTAGCTATTTGCGAGCAGATGCAATCTTTGATGATGCA 3000
Qy      3001  |||||CTTTTCTCATGATGTTGCTGCTGAGATGCGGAGATGCAATCTTTGATGATGCA 3060
Db      3001  |||||CTTTTCTCATGATGTTGCTGCTGAGATGCGGAGATGCAATCTTTGATGATGCA 3060
Qy      3061  |||||TACATTCGAAAGAGCTTACCTTATGATTAACCTGAGCAAGAGCTTTGAGATTTCA 3120
Db      3061  |||||TACATTCGAAAGAGCTTACCTTATGATTAACCTGAGCAAGAGCTTTGAGATTTCA 3120
Qy      3121  |||||AAACAAATGATGATGACACATGCTGCTGAGCAACAAATGATGATGATCTTCA 3180
Db      3121  |||||AAACAAATGATGATGACACATGCTGCTGAGCAACAAATGATGATGATCTTCA 3180
Qy      3181  |||||ACAATTTAAGCAGATGCTTTGAACTGA 3207
Db      3181  |||||ACAATTTAAGCAGATGCTTTGAACTGA 3207

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RESULT 13

AR064286

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

Sequence 32 from patent US 5846824.
 AR064286
 AR064286.1 GI:5993594

Unknown.
 Unclassified.
 1 (bases 1 to 3412)
 Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
 Otsu, M., Penayoutou, G., Volinia, S. and Gout, I.
 Polypeptides having kinase activity, their preparation and use
 Patent: US 5846824-A 32 08-DEC-1998;
 Location/Qualifiers
 1..3412
 /organism="unknown"

BASE COUNT 1129 a 616 c 706 g 961 t
 ORIGIN 93.8%; Score 3008.6; DB 6; Length 3412;

Best Local Similarity		96.1%;	Pred. No. 0;	Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;	
Qy	1	ATGCTCCAAAGACCATCATCAGGTGAACCTGGGGGATCACTTGATGCCCCAAGAATC	60		
Db	1	ATGCTCCAAAGACCATCATCAGGTGAACCTGGGGGATCACTTGATGCCCCAAGAATC	60		
Qy	61	CTAGTAGAATGTTTACTACCAATGGATGATAGTACCTTAAAGTCCCTGGAGGCT	120		
Db	61	CTAGTAGAATGTTTACTACCAATGGATGATAGTACCTTAAAGTCCCTGGAGGCT	120		
Qy	121	ACGTAAATACGATAAGATGACATTTTAAAGACAGAAATACCTCTCCATCAA	180		
Db	121	ACATTAATACGATAAGATGACATTTTAAAGACAGAAATACCTCTCCATCAA	180		
Qy	181	CTTCTCAAGATGATCTTCTACATTTTCTAGGTGATACCAAGAGACAGAAAGGGA	240		
Db	181	CTTCTCAAGATGATCTTCTACATTTTCTAGGTGATACCAAGAGACAGAAAGGGA	240		
Qy	241	GAATTTTGTATGAAACAAAGACACTTGTGACCTTGGCTTTTCAACCTTTTAAAA	300		
Db	241	GAATTTTGTATGAAACAAAGACACTTGTGACCTTGGCTTTTCAACCTTTTAAAA	300		
Qy	301	GTAATTTGAACCGTAGGCAACCGTAGAAGAAATCTCAATCGAATAATGGTTTGT	360		
Db	301	GTAATTTGAACCGTAGGCAACCGTAGAAGAAATCTCAATCGAATAATGGTTTGT	360		
Qy	361	ATCGGATGCGAGTGTGATTCGATATGTTTAAAGATCCAGAGTACAGACCTTCGA	420		
Db	361	ATCGGATGCGAGTGTGATTCGATATGTTTAAAGATCCGAAATCCGAAATCCAGACCTTCGA	420		
Qy	421	AGAAATATTCATGATGTTTGTAAAGAGCTGATCTTAGGGATCTTAATTCACCTCA	480		
Db	421	AGAAATATTCATGATGTTTGTAAAGAGCTGATCTTAGGGATCTTAATTCACCTCA	480		
Qy	481	AGTAGAGCAATGTATGTTTATCTCCAAATGTGAATCTTCACAGAACTGCGAAAGAC	540		
Db	481	AGTAGAGCAATGTATGTTTATCTCCAAATGTGAATCTTCACAGAACTGCGAAAGAC	540		
Qy	541	ATATTAATTAATTTGGATTAAGGGCAATTAATAGTGTGATTTGGTAAATAGTTCTCA	600		
Db	541	ATATTAATTAATTTGGATTAAGGGCAATTAATAGTGTGATTTGGTAAATAGTTCTCA	600		
Qy	601	AATAATGACAAACAGAAATATCTCGAAATCAACCAATGATGTGTGCGACAGACAGTA	660		
Db	601	AATAATGACAAACAGAAATATCTCGAAATCAACCAATGATGTGTGCGACAGACAGTA	660		
Qy	661	ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACACTAAAA	720		
Db	661	ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACACTAAAA	720		
Qy	721	CTCTGTGTTTAAATATCAGGGCAAGTATTTTAAAGTGTGATGTGATTAATAC	780		
Db	721	CTCTGTGTTTAAATATCAGGGCAAGTATTTTAAAGTGTGATGTGATTAATAC	780		
Qy	781	TTCTAGAAAAATATCTCTGAGTCAGTATAGTATTAAGAAAGCTGATATATGCTGGG	840		
Db	781	TTCTAGAAAAATATCTCTGAGTCAGTATAGTATTAAGAAAGCTGATATATGCTGGG	840		
Qy	841	AGGATGCCCAATTTGATGCTGATGCTTAAGAAAGCTTTATTTTCACCTGCAATGAC	900		
Db	841	AGGATGCCCAATTTGATGCTGATGCTTAAGAAAGCTTTATTTTCACCTGCAATGAC	900		
Qy	901	TGTTTCAATATGTCATATTTCCAGAGCATTTCCACAGCTACCCATATATGATGGA	960		
Db	901	TGTTTCAATATGTCATATTTCCAGAGCATTTCCACAGCTACCCATATATGATGGA	960		
Qy	961	GAACATCTCAAAATCCCTTGGGTTTAAATAGTGAACCTCAGAATTAATTTCTTGT	1020		
Db	961	GAACATCTCAAAATCCCTTGGGTTTAAATAGTGAACCTCAGAATTAATTTCTTGT	1020		
Qy	1021	GCAACCTATGTAATGTAATATTTGAGACATTTGACAAAGATTTATTTTGAACAGTATC	1080		
Db	1021	GCAACCTATGTAATGTAATATTTGAGACATTTGACAAAGATTTATTTTGAACAGTATC	1080		
Qy	1081	TACCATGAGAGGAAACCTTATGATATGGAACATCCAAAGAGTACTGTTCCAT	1140		
Db	1081	TACCATGAGAGGAAACCTTATGATATGGAACATCCAAAGAGTACTGTTCCAT	1140		
Qy	1141	CCAGGTGGAATGATGCTGAATTAAGATATATCATCTCGATCTTCTGCTGCT	1200		
Db	1141	CCAGGTGGAATGATGCTGAATTAAGATATATCATCTCGATCTTCTGCTGCT	1200		
Qy	1201	CGACTTGGCTTTCCATTTGTTCTGTAAAGGCGGAAAGGCTGTAAGAGGAAACCTG	1260		
Db	1201	CGACTTGGCTTTCCATTTGTTCTGTAAAGGCGGAAAGGCTGTAAGAGGAAACCTG	1260		
Qy	1261	CCATTGGCTGGGAAATTAATTAACCTGTTGATTAACAGATACCTATCTGAGAAA	1320		
Db	1261	CCATTGGCTGGGAAATTAATTAACCTGTTGATTAACAGATACCTATCTGAGAAA	1320		
Qy	1321	ATGCTTTGAATCTTTGGCAGATACCTCATGACTAGAAAGATTTGCTGAACCTATTGGT	1380		
Db	1321	ATGCTTTGAATCTTTGGCAGATACCTCATGACTAGAAAGATTTGCTGAACCTATTGGT	1380		
Qy	1381	GTTACTGATCAATCCAAATTAAGAAACCTCATGTTTAAAGATTTGATGATGCTGTC	1440		
Db	1381	GTTACTGATCAATCCAAATTAAGAAACCTCATGTTTAAAGATTTGATGATGCTGTC	1440		
Qy	1441	AGCATGTGTAAAGTTTCCAGATATGTCAGTATGTAAGAGCATGCCAATTTGCTGTA	1500		
Db	1441	AGCATGTGTAAAGTTTCCAGATATGTCAGTATGTAAGAGCATGCCAATTTGCTGTA	1500		
Qy	1501	TCCGTAAGAGGATTTAGTTATTCCTCATGAGGACGAGTAACAGACTAGCTAGAGAC	1560		
Db	1501	TCCGTAAGAGGATTTAGTTATTCCTCATGAGGACGAGTAACAGACTAGCTAGAGAC	1560		
Qy	1561	AATGAATTAAGAGAAATGATTAAGAAACAGCTCCAGCAATTTGTATACAGAGATCTCTA	1620		
Db	1561	AATGAATTAAGAGAAATGATTAAGAAACAGCTCCAGCAATTTGTATACAGAGATCTCTA	1620		
Qy	1621	TCTGAATACACTGACAGAGAAAGATTTTCAATGAGTCAACAGCAATTTGTAACT	1680		
Db	1621	TCTGAATACACTGACAGAGAAAGATTTTCAATGAGTCAACAGCAATTTGTAACT	1680		
Qy	1681	ATCCCGAAATTTTACCCAAATTTGCTCTGTGTTAAATGGAACCTAGAGATGAAGTA	1740		
Db	1681	ATCCCGAAATTTTACCCAAATTTGCTCTGTGTTAAATGGAACCTAGAGATGAAGTA	1740		
Qy	1741	GCTCAGATGTAAGTCTGTTGTAAGAGTGTGCTCCATCAAGCTGAAACAGGCTATGAG	1800		
Db	1741	GCTCAGATGTAAGTCTGTTGTAAGAGTGTGCTCCATCAAGCTGAAACAGGCTATGAG	1800		
Qy	1801	CTTCTGGAATGCAATTAACCAAGATCTATGCTTGAAGTGTGCTGCTGCTTGAAGA	1860		
Db	1801	CTTCTGGAATGCAATTAACCAAGATCTATGCTTGAAGTGTGCTGCTGCTTGAAGA	1860		
Qy	1861	AAATATTTAAAGATGCAAACTTTCTCAGTACCTAATTAAGCTATGATCAGTACTAAA	1920		
Db	1861	AAATATTTAAAGATGCAAACTTTCTCAGTACCTAATTAAGCTATGATCAGTACTAAA	1920		
Qy	1921	TATGAAGATATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAAGCTTAATAT	1980		
Db	1921	TATGAAGATATTTGATTAACCTGCTGTGAGATTTTACTCAAAAAAGCTTAATAT	1980		
Qy	1981	CAAGGATGCTGCTTTTCTTTTGGCATTTTAAATCTGAGAGCAATATTAACAGTT	2040		
Db	1981	CAAGGATGCTGCTTTTCTTTTGGCATTTTAAATCTGAGAGCAATATTAACAGTT	2040		
Qy	2041	AGTCAGAGTTTGGCTGCTTTTGGAGTCTATGCTGCTGCTGCTGCTGCTGCTGCTG	2100		
Db	2041	AGTCAGAGTTTGGCTGCTTTTGGAGTCTATGCTGCTGCTGCTGCTGCTGCTGCTG	2100		
Qy	2101	CACCTTAATAGGCAAGTGAAGCTATGAAAGCTCAATTAACCTTGAATCTGCAAT	2160		
Db	2101	CACCTTAATAGGCAAGTGAAGCTATGAAAGCTCAATTAACCTTGAATCTGCAAT	2160		

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LOCUS AR164679 3412 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 32 from patent US 6274327.
VERSION AR164679.1 GI:16237788
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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BASE COUNT 1129 a 616 c 706 g 961 t
ORIGIN
Query Match 93.8%; Score 3008.6; DB 6; Length 3412;
Best Local Similarity 96.1%; Pred. No. 0;
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LOCUS Sequence 5 from Patent WO0185986.
DEFINITION AX327651
ACCESSION AX327651
VERSION AX327651.1 GI:18097981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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JOURNAL ICOS CORPORATION (US)
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QY 2521 ATCGGTGATGTTGTGGATTTATCGAGTGTGTGAGAAATTTCTCACTATATGCAAT 2580
DB 2533 ATCGGTGATGTTGTGGATTTATGAGTGTGTGAGAAATTTCTCACTATATGCAAT 2592
QY 2581 CAGTGTAAAGGAGGCTGAAAGTGCATGCACTGAGTTTAAACGACACACTCCATCATGTCG 2640
DB 2593 CAGTGTAAAGGAGGCTGAAAGTGCATGCACTGAGTTTAAACGACACACTCCATCATGTCG 2652
QY 2641 CTCAAGAACAGAACAGGAGGAGAAATATATGATGAGGAGCATGATTTGTTTACAGATCA 2700
DB 2653 CTCAAGAACAGAACAGGAGGAGAAATATATGATGAGATTTGATGATGATGATGATGAT 2712
QY 2701 TGTGCTGATATTTGTGTTGCCACTTTCAATTTGGAAATTTGAGATGCTCAATATGTAAT 2760
DB 2713 TGTGCTGATATTTGTGTTGCCACTTTCAATTTGGAAATTTGAGATGCTCAATATGTAAT 2772
QY 2761 ATCATGTTAAAGATGATGGAACAATGTTTCAATATGATTTTGGACACTTTTGAATGAC 2820
DB 2773 ATCATGTTAAAGATGATGGAACAATGTTTCAATATGATTTTGGACACTTTTGAATGAC 2832
QY 2821 AAGAAGAAAAATTTGTTATTAACGAGAGCCGTGCGTTGTGTTGACACAAGATTTT 2880
DB 2833 AAGAAGAAAAATTTGTTATTAACGAGAGCCGTGCGTTGTGTTGACACAAGATTTT 2892
QY 2881 TTAATATGATTTAGTAAGAGAGCCCAAGAAATGCAAAAGACAAAGAAATTTGAGAGGTT 2940
DB 2893 TTAATATGATTTAGTAAGAGAGCCCAAGAAATGCAAAAGACAAAGAAATTTGAGAGGTT 2952
QY 2941 CAGAGATGTTTAAAGGCTTATCTAGCTATTTGGGAGGATCCAAATCTCTTCAATAT 3000
DB 2953 CAGAGATGTTTAAAGGCTTATCTAGCTATTTGGGAGGATCCAAATCTCTTCAATAT 3012
QY 3001 CTTTTCTCAATGATGCTTGGCTGTTGATGTCAGAACTGCAATCTTTGATGATATTTGCA 3060
DB 3013 CTTTTCTCAATGATGCTTGGCTGTTGATGTCAGAACTGCAATCTTTGATGATATTTGCA 3072
QY 3061 TACATTTCAAAAGACCTTACCTTATGATTAACCTGAGCAAGAGGCTTTGAGATTTTCAATG 3120
DB 3073 TACATTTCAAAAGACCTTACCTTATGATTAACCTGAGCAAGAGGCTTTGAGATTTTCAATG 3132
QY 3121 AAACCAATGATGATGCAACCAATGCTGAGCAAGCAAAAGGATTTGATGATCTTCAAC 3180
DB 3133 AAACCAATGATGATGCAACCAATGCTGAGCAAGCAAAAGGATTTGATGATCTTCAAC 3192
QY 3181 ACAATTAAGCAGATGCTTTGAACTGA 3207
DB 3193 ACAATTAAGCAGATGCTTTGAACTGA 3219

Wed Nov 12 14:55:42 2003

us-09-325-095-35.rge

Search completed: November 7, 2003, 10:44:03
Job time : 7725.91 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2003, 14:40:25 ; Search time 45 Seconds

(without alignments)
6130.183 million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709

Sequence: 1 MPRSSSGELMGHLMPPRI.....GWTTKMDIPIHTKQHALNX 1069

Scoring table: BLAST62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mhc:*
9: sp_organella:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	5545	97.1	1068	13	042391	042391 gallus gall
2	5443	95.3	1083	15	039483	039483 avian saeco
3	4104	71.9	852	13	09PTES	09PTES xenopus lae
4	1974	34.6	1064	11	08BT19	08BT19 mus musculu
5	1966	34.4	1043	11	08CU28	08CU28 mus musculu
6	1964.5	34.4	1037	11	08CI98	08CI98 mus musculu
7	1963	34.4	1047	11	08BS14	08BS14 mus musculu
8	1903.5	33.3	1068	4	000034	000034 mus musculu
9	1677.5	29.4	1088	5	P91634	P91634 homo sapien
10	1527	26.7	291	11	Q91XL6	Q91XL6 ractus norv
11	1472.5	25.8	1102	4	Q9BEC8	Q9BEC8 homo sapien
12	1472.5	25.8	1102	4	Q81V23	Q81V23 homo sapien
13	1467	25.7	1113	11	Q9EOL1	Q9EOL1 mus musculu
14	1049.5	18.4	1658	11	Q61182	Q61182 mus musculu
15	1038.5	18.2	1509	11	Q61194	Q61194 mus musculu
16	1014.5	17.8	1686	4	000443	000443 homo sapien

17	859.5	15.1	318	11	Q9CTK7	Q9CTK7 mus musculu
18	859	15.0	1876	5	Q9VTN5	Q9VTN5 drosophila
19	804.5	14.1	286	4	Q9BFS4	Q9BFS4 homo sapien
20	751	13.2	1607	5	Q20187	Q20187 caenorhabdi
21	718	12.6	887	11	Q88763	Q88763 ractus norv
22	714	12.5	887	4	Q8NEB9	Q8NEB9 homo sapien
23	685	12.0	887	4	Q15134	Q15134 homo sapien
24	680.5	11.9	847	11	Q8R3S8	Q8R3S8 mus musculu
25	660	11.6	260	11	Q8CSQ7	Q8CSQ7 mus musculu
26	660	11.6	949	5	P91635	P91635 drosophila
27	657	11.5	949	5	Q9W1M7	Q9W1M7 drosophila
28	649	11.4	808	10	Q8GUA6	Q8GUA6 medicago tr
29	631.5	11.1	901	5	Q9TX17	Q9TX17 caenorhabdi
30	625.5	11.0	897	5	Q9XZRO	Q9XZRO caenorhabdi
31	624.5	10.9	813	10	Q8H1S8	Q8H1S8 brassica na
32	600	10.5	650	5	Q9TX16	Q9TX16 caenorhabdi
33	578.5	10.1	1016	3	Q9Y8E4	Q9Y8E4 pictia angu
34	554	9.7	499	10	Q8RXR0	Q8RXR0 arabidopsis
35	513	9.0	409	11	Q8CFP1	Q8CFP1 mus musculu
36	491.5	8.6	732	10	Q04269	Q04269 chlamydomon
37	478.5	8.4	1889	10	Q94H07	Q94H07 oryza sativ
38	477.5	8.4	273	5	Q9BLU5	Q9BLU5 leishmania
39	474	8.3	2051	10	Q9SCX1	Q9SCX1 arabidopsis
40	473	8.3	1208	10	Q81129	Q81129 arabidopsis
41	465	8.1	1308	5	Q8MYR7	Q8MYR7 drosophila
42	465	8.1	2160	5	Q9UIK8	Q9UIK8 drosophila
43	465	8.1	2178	5	Q9W4X4	Q9W4X4 drosophila
44	459.5	8.0	608	10	Q8LSD9	Q8LSD9 oryza sativ
45	442	7.7	1466	6	Q28925	Q28925 bos laurus

ALIGNMENTS

RESULT 1
042391 PRELIMINARY; PRT; 1068 AA.
ID 042391
AC 042391;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Phosphoinositide 3-kinase catalytic subunit.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97334438; PubMed=9188528;
RA Chang H.W., Aoki M., Fuman D., Auger K.R., Bellacosa A.,
RA Tsichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
RT "Transformation of chicken cells by the gene encoding the catalytic
RT subunit of PI 3-kinase.";
RL Science 276:1848-1850(1997).
DR EMBL: AF001076; AB82534.1; -
DR InterPro: IPR000008; C2.
DR InterPro: IPR001263; PI3Ka.
DR InterPro: IPR002420; PI3K_C2.
DR InterPro: IPR003113; PI3K_p85B.
DR InterPro: IPR000341; PI3K_ras bind.
DR InterPro: IPR000403; PI3_P14_Kinase.
DR Pfam: PF00613; PI3Ka; 1.
DR Pfam: PF00792; PI3K_C2; 1.
DR Pfam: PF02192; PI3K_p85B; 1.
DR Pfam: PF00794; PI3K_Pbd; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00145; PI3Ka; 1.
DR SMART: SM00146; PI3K; 1.
DR SMART: SM00142; PI3K_C2; 1.
DR SMART: SM00143; PI3K_p85B; 1.

DR SMART; SM00144; PI3K_tbd; 1.
 DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
 DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
 DR PROSITE; PS00917; PI3_4_KINASE_3; 1.
 DR KINASE.
 SQ SEQUENCE 1068 AA; 124287 MW; 9912A96B3397735E CRC64;

Query Match 97.1%; Score 5545; DB 13; Length 1068;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 1030; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPPRPSGGLMGTHLMPRLIVLCLPNSMTVTECLREATLTITIKHELFKARKYPLHIO 60
 DB 1 MPPRPSGGLMGTHLMPRLIVLCLPNSMTVTECLREATLTITIKHELFKARKYPLHIO 60
 QY 61 LLODESSYIFSVYQEAAREEFPEDETRRLCDLRFOPFLKYIEPVGNREKILNREIGFA 120
 DB 61 LLODESSYIFSVYQEAAREEFPEDETRRLCDLRFOPFLKYIEPVGNREKILNREIGFA 120
 QY 121 IGMPVCEFDWVCKDEVDFFRNIIIVCKEAVDLRDLSPHSRAMVYVPPNVSSPELPKH 180
 DB 121 IGMPVCEFDWVCKDEVDFFRNIIIVCKEAVDLRDLSPHSRAMVYVPPNVSSPELPKH 180
 QY 181 IYNKLDKQIIVYVWVISPNDKOKYTKLNHDCVPEQVIAEIRKKTREMLSSBOLK 240
 DB 181 IYNKLDKQIIVYVWVISPNDKOKYTKLNHDCVPEQVIAEIRKKTREMLSSBOLK 240
 QY 241 LCVLEYOGKYLTKVCGDEYELKYPLOSQYKIRSCIMLGMPNLMMAKESLYSOLPMD 300
 DB 241 LCVLEYOGKYLTKVCGDEYELKYPLOSQYKIRSCIMLGMPNLMMAKESLYSOLPMD 300
 QY 301 CETMPSYRRISTATPYMNGESTKSLVWINSALRIKILCATYVNVNIRIDKIYRTGI 360
 DB 301 TPTMPSYRRISTATPYMNGEATKSLMTINSALRIKILCATYVNVNIRIDKIYRTGI 360
 QY 361 YHGGEPFLCDNVNTQRPVPCSNPRNMENLYDYIPLPRAARLCISGVKRGKAKKEHC 420
 DB 361 YHGGEPFLCDNVNTQRPVPCSNPRNMENLYDYIPLPRAARLCISGVKRGKAKKEHC 420
 QY 421 PLAMGNINLPDYTDPLVSGKALNMPVPHGLEDLNIGVTSNPKEPCLLEDFDMF 480
 DB 421 PLAMGNINLPDYTDPLVSGKALNMPVPHGLEDLNIGVTSNPKEPCLLEDFDMF 480
 QY 481 SSVVYKPDMSYIEEHANNSVSREAGFSYSHAGLSNRLARDNDELRENDYQOLRAITRPL 540
 DB 481 SSVVYKPDMSYIEEHANNSVSREAGFSYSHAGLSNRLARDNDELRENDYQOLRAITRPL 540
 QY 541 SEITEQEKDFLMSHHYCVNTPELIPKLLSVKMSRDEVAQMYCLVQDWPPIKEQAME 600
 DB 541 SEITEQEKDFLMSHHYCVNTPELIPKLLSVKMSRDEVAQMYCLVQDWPPIKEQAME 600
 QY 601 LLDGNYPPMVGAFVRCLEKYLTDKLSQYLIQVQVLYKQYQYDNLVREFLKKAALT 660
 DB 601 LLDGNYPPMVGAFVRCLEKYLTDKLSQYLIQVQVLYKQYQYDNLVREFLKKAALT 660
 QY 661 QRIQGFPMHLKSEMHNTKVSQRFGLLESYCRACGMYLKHLNROVEAMEKILNTDILK 720
 DB 661 QRIQGFPMHLKSEMHNTKVSQRFGLLESYCRACGMYLKHLNROVEAMEKILNTDILK 720
 QY 721 OEKKETQKQVQKFLVEQKRRDPMDALOGFISPLNPAHQNLLEECRINSSAKRPLM 780
 DB 721 OEKKETQKQVQKFLVEQKRRDPMDALOGFISPLNPAHQNLLEECRINSSAKRPLM 780
 QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRODMTLQIIRIMENIMQNGSLDMLPEYGLS 840
 DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRODMTLQIIRIMENIMQNGSLDMLPEYGLS 840
 QY 841 IGDGVLLEVNNSHTIMQIQCKGKGLAQLQNSHTLQWLKDKNGEITYDAIDIFTS 900
 DB 841 IGDGVLLEVNNSHTIMQIQCKGKGLAQLQNSHTLQWLKDKNGEITYDAIDIFTS 900
 QY 901 CAGCYATITLIGIDRHNINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960
 DB 901 CAGCYATITLIGIDRHNINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960

DB 901 CAGCYATITLIGIDRHNINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960
 QY 961 LVIISGAECECTREPEREPOECYAYLAIRQNALFINLPSMNGSGMPELOSFDIA 1020
 DB 961 LVIISGAECECTREPEREPOECYAYLAIRQNALFINLPSMNGSGMPELOSFDIA 1020
 QY 1021 YIRKTLALDKTEQEALEYFMKQNDAHGGWTTKMDIFHTIKOHALN 1068
 DB 1021 YIRKTLALDKTEQEALEYFMKQNDAHGGWTTKMDIFHTIKOHALN 1068

RESULT 2
 ID 039483 PRELIMINARY; PRT: 1083 AA.
 AC 039483;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Gag-V-phosphoinositide 3-kinase catalytic subunit fusion protein (fragment).
 GN Gag-V-p3K.
 OS Avian sarcoma virus 16.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_Taxid=60629;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9733438; PubMed=9188528;
 RA Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,
 RA Tsichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
 RT "Transformation of chicken cells by the gene encoding the catalytic
 RT subunit of p13-kinase."
 RL Science 276:1848-1850(1997).
 DR EMBL; AF001075; AAB62532.1;
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001263; PI3K.
 DR InterPro; IPR002420; PI3K_C2.
 DR InterPro; IPR003113; PI3K_p85B.
 DR InterPro; IPR000341; PI3K_ras_bind.
 DR InterPro; IPR000403; PI3_P14_kinase.
 DR Pfam; PF00613; PI3Ka; 1.
 DR Pfam; PF00792; PI3K_C2; 1.
 DR Pfam; PF02192; PI3K_p85B; 1.
 DR Pfam; PF00794; PI3K_tbd; 1.
 DR Pfam; PF00454; PI3_P14_kinase; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00145; PI3Ka; 1.
 DR SMART; SM00146; PI3K; 1.
 DR SMART; SM00142; PI3K_C2; 1.
 DR SMART; SM00143; PI3K_p85B; 1.
 DR SMART; SM00144; PI3K_tbd; 1.
 DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
 DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
 DR PROSITE; PS00917; PI3_4_KINASE_3; 1.
 DR KINASE.
 FT NON TER
 SQ SEQUENCE 1083 AA; 125869 MW; 371EF705A78AC8 CRC64;

Query Match 95.3%; Score 5443; DB 15; Length 1083;
 Best Local Similarity 95.9%; Pred. No. 0;
 Matches 1012; Conservative 27; Mismatches 16; Indels 0; Gaps 0;

QY 14 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLHIOLEDESSYIFSV 73
 DB 29 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLHIOLEDESSYIFSV 88
 QY 74 TOEAREEFPEDETRRLCDLRFOPFLKYIEPVGNREKILNREIGFAIGMPVCEFDWYD 133
 DB 89 TOEAREEFPEDETRRLCDLRFOPFLKYIEPVGNREKILNREIGFAIGMPVCEFDWYD 148
 QY 134 PEVQDFRNIIIVCKEAVDLRDLSPHSRAMVYVPPNVSSPELPKHLYNKLKQIIVV 193
 DB 149 PEVQDFRNIIIVCKEAVDLRDLSPHSRAMVYVPPNVSSPELPKHLYNKLKQIIVV 208

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OY 194 IMVIVSPNDKOKYTLKINHCVPEQVIAEAIIRKKTSMILSSQOLKCVLEPYGKXITLK 253
DB 209 IMVIVSPNDKOKYTLKINHCVPEQVIAEAIIRKKTSMILSSQOLKCVLEPYGKXITLK 268
OY 254 VCGDSEYFLEKYPLOYKYIRSCIMLGMPMLMAKESYLSOLPMDCFMPSYRST 313
DB 269 VCGDSEYFLEKYPLOYKYIRSCIMLGMPMLMAKESYLSOLPMDCFMPSYRST 328
OY 314 ATPYNGESTSKIMVINSALRIKILCATYVNVNIRIDKIYVGTGIYHGSEPLCDNVNT 373
DB 329 ATPYNGEATKSLMTINSALRIKILCATYVNVNIRIDKIYVGTGIYHGSEPLCDNVNT 386
OY 374 QRPVCSNPRNEMNTIYITPDLPRARLCLSTCSVGRKGAKEHCPLANGINLPDYT 433
DB 389 QRPVCSNPRNEMNTIYITPDLPRARLCLSTCSVGRKGAKEHCPLANGINLPDYT 448
OY 434 DTLVSGMALNLMPVPHGEDLNPICVGTGSPNKETPCLELEEDWSSVYKPFDMVIE 493
DB 449 DTLVSGMALNLMPVPHGEDLNPICVGTGSPNKETPCLELEEDWSSVYKPFDMVIE 508
OY 494 EHAMVSVRBEAGPSYSHAGLSNRLARDNELRENDKEOLRAICTRDPLEITEDEKDFLMS 553
DB 509 EHAMVTSIRBELGFNYSYAGLSNRLARDNELRENDKEOLRAICTRDPLEITEDEKDFLMS 566
OY 554 HRHVCVTIPILPKLLSVKNSRDEVAOMYCLVKNMPPIKPEQAMELLDGVPDMVRG 613
DB 569 HRHVCVTIPILPKLLSVKNSRDEVAOMYCLVKNMPPIKPEQAMELLDGVPDMVRG 628
OY 614 FAVRCLEKYLTDPLKLSQYLOLVOLKYEOYLDNLVRLPKLKLTLNORIGHFFMHLKS 673
DB 629 FAVRCLEKYLTDPLKLSQYLOLVOLKYEOYLDNLVRLPKLKLTLNORIGHFFMHLKS 688
OY 674 EMNKTVSQRFGLLESYCRACGYLKLHROYVAMEKLINLTDLKOEKDEFOKYOMK 733
DB 689 EMNKTVSQRFGLLESYCRACGYLKLHROYVAMEKLINLTDLKOEKDEFOKYOMK 748
OY 734 FLYEONRPRPMDALOGFISPLNPAHOLGMLREBCKRINSAGKPLMNMENPDINSELL 793
DB 749 FLYEONRPRPMDALOGFISPLNPAHOLGMLREBCKRINSAGKPLMNMENPDINSELL 808
OY 794 FOUNNEIFKRGDDLRQMLTLOIRIMENIMONOGDLNMLPVGCLSTGCVGLIETVRN 853
DB 809 FOUNNEIFKRGDDLRQMLTLOIRIMENIMONOGDLNMLPVGCLSTGCVGLIETVRN 868
OY 854 SHTIMOJQCKGKLGALQFNSHTLHOWLKDKNKEIYDAIDLPTRSCAGYCATFLLGI 913
DB 869 SHTIMOJQCKGKLGALQFNSHTLHOWLKDKNKEIYDAIDLPTRSCAGYCATFLLGI 928
OY 914 GDBRNSNIMWKDQGLFHIDFGHFLDHKKKFGYKREBVPFVLTODELIYISKAQDECTK 973
DB 929 GDBRNSNIMWKDQGLFHIDFGHFLDHKKKFGYKREBVPFVLTODELIYISKAQDECTK 988
OY 974 TRFEFERQEMCYAYLAIRQHANLFTLBSMTGSGMPELOSPDIAIYIKTLALDTEQ 1033
DB 989 TRFEFERQEMCYAYLAIRQHANLFTLBSMTGSGMPELOSPDIAIYIKTLALDTEQ 1048
OY 1034 EALEYFMKONDAHGGMTTKMDMIFETIKOHALN 1068
DB 1049 EALEYFMKONDAHGGMTTKMDMIFETIKOHALN 1083

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RESULT 3

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O9PTES PRELIMINARY; PRT; 852 AA.
AC O9PTES;
DT 01-MAY-2000 (TEMBUREJ. 13, Created)
DT 01-MAY-2000 (TEMBUREJ. 13, Last sequence update)
DE Phosphoinositide 3 kinase catalytic subunit (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=distal nephron;
RA Al-Khalili O.K., Tran T., Eaton D.C.;
RT "Molecular cloning of Xenopus laevis phosphoinositide 3 kinase
  catalytic subunit mRNA."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=distal nephron;
RA Al-Khalili O.K., Eaton D.C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF049424; AAF15300.1;
DR InterPro: IPR000008; C2.
DR InterPro: IPR001263; P13Ka.
DR InterPro: IPR002420; P13K_C2.
DR InterPro: IPR003113; P13K_p85B.
DR InterPro: IPR000341; P13_rac bind.
DR InterPro: IPR000403; P13_P14_kinase.
DR Pfam: PF00613; P13Ka; 1.
DR Pfam: PF00792; P13K_C2; 1.
DR Pfam: PF02182; P13K_p85B; 1.
DR Pfam: PF00794; P13K_rtd; 1.
DR Pfam: PF00454; P13_P14_kinase; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00145; P13Ka; 1.
DR SMART: SM00146; P13Kc; 1.
DR SMART: SM00142; P13K_C2; 1.
DR SMART: SM00144; P13K_rbd; 1.
DR PROSITE: PS00915; P13_4_KINASE_1; 1.
DR PROSITE: PS00916; P13_4_KINASE_2; 1.
DR PROSITE: PS50290; P13_4_KINASE_3; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 852
SQ SEQUENCE 852 AA; 98705 MW; 15C1F3CCDDE28884 CRC64;

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Query Match 71.9%; Score 4104; DB 13; Length 852;
Best Local Similarity 89.6%; Pred. No. 3.6e-311;
Matches 763; Conservative 43; Mismatches 46; Indels 0; Gaps 0;

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OY 84 DETRRICDLRLFOPLKVLIEPVNGREBKILNREIGFALGMPVCEPDMVKOPEVODFFRN 143
DB 1 DETRRICDLRLFOPLKVLIEPVNGREBKILNREIGFALGMPVCEPDMVKOPEVODFFRN 60
OY 144 LNVCKEAVDIRDINSFHSRAMVYVPPNVSSPELPKHINYKLDKGOIIVIVIVSPND 203
DB 61 LNVCKDSVELRDANGPISRALVYVPPNVSSPELPKHIESKLDKGOIIVIVIVSPND 120
OY 204 KQVYTLKINHDCVPEQVIAEAIIRKKTSMILSSQOLKCVLEPYGKXITLKVCCDEYFLE 263
DB 121 KQVYTLKINHDCVPEQVIAEAIIRKKTSMILSSQOLKCVLEPYGKXITLKVCCDEYFLE 180
OY 264 KYPLSQYKYIRSCIMLGMPMLMAKESYLSOLPMDCFMPSYRSTATPYNGETS 323
DB 181 KYPLSQYKYIRSCIMLGMPMLMAKESYLSOLPMDCFMPSYRSTATPYNGETS 240
OY 324 TKSILWINSALRIKILCATYVNVNIRIDKIYVGTGIYHGSEPLCDNVNTORVPCSNPRV 383
DB 241 AKSLMAINSTLRIRIKILMATYVNVNIRIDKIYVGTGIYHGSEPLCDNVNTORVPCSNPRV 360
OY 384 NEWLNDIYIPDLPRARLCLSTCSVGRKGAKEHCPLANGINLPDYTDLVSGMAL 443
DB 301 NEWLNDIYIPDLPRARLCLSTCSVGRKGAKEHCPLANGINLPDYTDLVSGMAL 360
OY 444 NLMPVPHGEDLNPICVGTGSPNKETPCLELEEDWSSVYKPFDMVIEEENAMGVSRE 503
DB 361 NLMPVPHGEDLNPICVGTGSPNKETPCLELEEDWSSVYKPFDMVIEEENAMGVSRE 420
OY 504 AGFSYSHAGLSNRLARDNELRENDKEOLRAICTRDPLEITEDEKDFLMSHRHYCVTIE 563
DB 421 LGYNSHSGLSNRLARDNELRENDKEOLRAICTRDPLEITEDEKDFLMSHRHYCVTIE 480

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QY 564 ILPKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMBLDNCYDPDPMVGRPAVFCLEKYL 623
DB 481 VLSKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMBLDNCYDPDPMVGRPAVFCLEKYL 540
QY 624 TDDKLSQVLLQVQVVKYEOYLDNLVRLFKKALTNRQIGHFFPMHLKSPMHNKTYSOR 683
DB 541 TDDKLSQVLLQVQVVKYEOYLDNLVRLFKKALTNRQIGHFFPMHLKSPMHNKTYSOR 600
QY 684 FGLLSEYCRACGMYLKHNLNROVEAMEKLINLTILQOEKDETOYQOMKELYEOMERPD 743
DB 601 FGLLSEYCRACGMYLKHNLNROVEAMEKLINLTILQOEKDETOYQOMKELYEOMERPD 660
QY 744 FMDALQGLSPNPAHQIGNRLRECRIMASAKRPLMLSMENPDIMSEMLFLNNEIIFKN 803
DB 661 FMDALQGLSPNPAHQIGNRLRECRIMASAKRPLMLSMENPDIMSEMLFLNNEIIFKN 720
QY 804 GDDLROMLTLQIIRIMENIWONOGDLRMLPYGLSIGDCVGLIEVVRNSHTIMOIQCK 863
DB 721 GDDLROMLTLQIIRIMENIWONOGDLRMLPYGLSIGDCVGLIEVVRNSHTIMOIQCK 780
QY 864 GGLKALQFNSHTLHQLKDKNKGSIYDAIDLFTSCAGYCVATFLLIGDRHNSIMV 923
DB 781 GGLKALQFNSHTLHQLKDKNKGSIYDAIDLFTSCAGYCVATFLLIGDRHNSIMV 840
QY 924 KDGOLFPHIDFG 935
DB 841 KDGOLFPHIDFG 852

RESULT 4
Q8BT9 PRELIMINARY; PRT: 1064 AA.
ID Q8BT9 AC Q8BT9;
AC Q8BT9;
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DB Phosphatidylinositol 3-kinase catalytic subunit.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT The Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK090116; BAC41102.1;
SQ SEQUENCE 1064 AA; 121753 MW; 3E96729B25C52D1C CRC64;

Query Match 34.6%; Score 1974; DB 11; Length 1064;
Best Local Similarity 39.4%; Pred. No. 6,8e-145;
Matches 440; Conservative 196; Mismatches 371; Indels 110; Gaps 23;

QY 1 MPPRRSSG-ELMGH---LMPRIIVECLLPNGMYTTECLREATLITIKHELFEKARY 56
DB 1 MPPRRSSG-ELMGH---LMPRIIVECLLPNGMYTTECLREATLITIKHELFEKARY 60
QY 57 PLHQLLDESSYIFVSVTOEAREBEFFDETRRLCDLRLFOPLKYIEPVGNREKILNRE 116
DB 61 PMFNLLMDSDSYFACVNOTAVYELLEDTRRLCDVRPLVPLKVCATRSCEPAEK-LDSK 119
QY 117 IGFALGPVCEFDVNVKDFVQFRKNILAVCKEAVDLRLNBSHSAFMYVPPNVASSSE 176
DB 120 IGVRLGKGLHEDFALQDPENEFRRKRFSEAKIOSLVGLSWIDWLKHTYBP--EHEPS 177
QY 177 LKXHTNKLDKGOIIVIVIVIVISPNNDKOKYTLKINHDCVPEGVIAEAIKKTRSMILSS 236
DB 178 VLENEDDKLYGKLVVAVHP---ENSQVFSFOVSPNINPLIKINLAIQKR----- 225

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QY 237 EQLKLCVLEYQK-----YILKVGCGDEYELKXPYLSQYKIRSCIMLGRMPLIML 288
DB 226 -----LITRGEDASPCDYLQVSGRVEYFGHPLIQFYINCMNRLPLPHILY 278
QY 289 AKESLYSOLPMDCFTPSYRRISTATPYMNGESTIK---SLWVINSALRIKILCATYVN 345
DB 279 ECKIKKMBQEMIALAEMINRSSNMLPLPLPKTRVISHIWDNNNPQITLVKGN--K 336
QY 346 VNIRIDKIVRGYIHGGPPLCDNVTQGVPCSNR--KHEMLNVIYIPLDPRARICL 404
DB 337 LNTIEYTKVHVRAGLPHGTIELCKTVASSEISGRKHIMEQLEPDIINICDLPFRMLCF 396
QY 405 SICS---VGRGAK-----EEHCPLAMGNINFDYTDLVSGKMLNLM 446
DB 397 AVTAVALDKVTKSTKTINRSKYQTRKAKGVYPAWNTVTFDRGQLRSDVILHSW 456
QY 447 -PYPHGLELLNPIGVTSNP-----NKEIPCLELFDWFSSVVKFPDMGV 491
DB 457 SSFPELEMLNLMGTQVTPYAEANATLHITPENKQPCYPPFD-----KI 505
QY 492 IEHAWKSVSRERAGFSYSHAGLSNRLARDNELBNDKEQALCTDPLSEITEQEKFL 551
DB 506 IERAAEIASGDSA--NVSSRGKKFLA-----VLRKELDRPILSQCGENEMDLI 552
QY 552 WSHRHVC-VTIPILPKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMBLDNCYDPDM 610
DB 553 WTLRQDCRENPPQSLPKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMBLDNCYDPDM 612
QY 611 VRGFAVRCLEKYLTDKLSQYLLQVQVVKYEOYLDNLVRLFKKALTNRQIGHFFPMH 670
DB 613 VREYAVGCL--RQMSDELSQYLLQVQVVKYEOYLDNLVRLFKKALTNRQIGHFFPMH 671
QY 671 LKSEMNKTVSQRGGLLESTYCRACGMYLKHNLNROVEAMEKLINLTILQOEKDETOY 730
DB 672 LRSEVHTPAVSQGVILAEYCRGSGVMKVLRSQYBALNKLKTLSLILNNAVKLSRAK 731
QY 731 QMKRLVQMRPDMDALQGLSPNPAHQIGNRLRECRIMASAKRPLMLSMENPDIMS 790
DB 732 GKEAMHTCLQSAVRELSLQSPNPAHQIGNRLRECRIMASAKRPLMLSMENPDIMS 790
QY 791 ELLEPQNE--IIFKNGDLRQMLTLQIIRIMENIWONOGDLRMLPYGLSIGDCVGLI 848
DB 786 SRATGEDSVGIFKNGGDLRQMLTLQIIRIMENIWONOGDLRMLPYGLSIGDCVGLI 845
QY 849 EVVRNSHTIMOQC-KGGLKALQFNSHTLHQLKDKNKGSIYDAIDLFTSCAGYCV 907
DB 846 EVVSTSETIADIQNSSNVATAFAFNKDALNMLKEVNSGDDLRALIEFTLSCAGYCV 905
QY 908 TTEIIGDRHNSIMVQDDQGLPHIDFGHFLDHKKKFGYKREVPVLTQDFLIVISKG 967
DB 906 SYVLGIGDRHNSIMVQDDQGLPHIDFGHFLDHKKKFGYKREVPVLTQDFLIVISKG 965
QY 968 AOECKTEPERFQEMCYKAVLAIRQANLEFINLSMNLGSGMDELQSPDDIAYIRKTLA 1027
DB 966 --KGNTEKFERPFOCCDAVLILRRGNLEFTLFAIMLTGRLBELTSVKDIOYKLQSLA 1023
QY 1028 LDKTQEALEYFMKQMDAHHGWTTKMDYLFHTIKQ 1064
DB 1024 LKSEEBALQKQKFDALRESWTTKYVMMAHTVRK 1060

RESULT 5
Q8CJ28 PRELIMINARY; PRT: 1043 AA.
ID Q8CJ28 AC Q8CJ28;
AC Q8CJ28;
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DB Phosphatidylinositol 3-kinase p110delta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129P2/OlaAed;
 RX MEDLINE=22160404; PubMed=12130661.
 RA Okkenhang K., Bilancio A., Parjot G., Priddle H., Sancho S.,
 RA Beskeet E., Pearce W., Week S.E., Salpekar A., Waterfield M.D.,
 RA Smith A.J., Vanheesbroeck B.,
 RT "Impaired B and T cell antigen receptor signaling in pl1delta p1 3-
 RT kinase mutant mice";
 RL Science 297:1031-1034(2002).
 DR EMBL, AF532989; AA05615.1; --
 KM Kinase.
 SQ SEQUENCE 1043 AA; 119712 MW; AD8DE07D8F847795 CRC64;
 Query Match 34.4%; Score 1966; DB 11; Length 1043;
 Best Local Similarity 39.8%; Pred. No. 2.8e-144;
 Matches 430; Conservative 188; Mismatches 389; Indels 74; Gaps 19;
 QY 16 MP-----RIVECLPNCMTVTECLREATLITIKHELFKEARKYPLHQ 60
 Db 1 MPGVDCMFMFTKEBSQSVVDFLLPTGVILNFPVSNANLSTIKOYLHRAQYEPFLH 60
 QY 61 LLOESSYIFVSVTOEARREBPFBETRRLCDLRLFOPLKYIEPVGNREKILNREIGFA 120
 Db 61 MLSDEPARYVFTCVNQTAEQDELEORLDCIOFLPLRLVAREGDVKILNSQISL 120
 QY 121 IGMVCEPDMVKDEVDQFRNIIINVCKEAVDLRLDINSPHRAMVVPVNVESPELPK- 179
 Db 121 ICKLHFEDSLRDEVANDFTYKROFCCEAAHROQLGWEMLYSFLQLEPARGWRA 180
 QY 180 ---HIYNKLDKQIIVIVIVSVSPNDKQKTYTLKINHCEVEQYIAEARIKTKSMILSS 236
 Db 181 GLKVSNR-----ALVVVVKFEGSESESTFPQVSTDMPLAMACLRK-----A 225
 QY 237 EQLKLCVLEYQGYIKLYKCCDEYFLEKYPISQYKTRSCITLGRMPLMLAKESLYSQ 296
 Db 226 TVFQPIVEQPEEYALQVNGRHEYLGNYPICHFOYICSLHSGILPLTWVHSSILAM 285
 QY 297 LPMOCFTMPSRSRISTATPRYMGSETSKSLMVINSALRIKILCATYVNVIRIDIKIV 356
 Db 286 RDEQSNAPVOYOKPRAPRPPIPAKPPSSVSLMSLEQPFSEILIGRKVNADER--MKLVV 343
 QY 357 RTGIYHGEPLCDVNTQRY-PCSNPRNEMWNLIDYIPDLRAARLCTISV----- 409
 Db 344 QAGGFHGNEMLCKTVSSSEVAVVCSFPWKQLEFDISVCDLPRARLCEFAIYAVEAKK 403
 QY 410 -KGRKAKEHCHPLANGNINLPDYDTLVSGKALMLMP-VPRGLEDLNPIGVTSNP 466
 Db 404 ARSTFKKSKADCCPIAWANMLLPYKQDLKGERCLVWMPSPVPEKGBLLNPAQTVAGNP 463
 QY 467 NKETPCLEBERDMSSVYKPPDMGVIEBHANMSVSRGFSYAGLSNRLARNEIREN 526
 Db 464 NTESAA-----ALVIYLP-----VAHPYFPALKEILIGHNGRGRT--EEEL--- 508
 QY 527 DKEOIRAITRDLPLSEITEQKDFLWNGHRYCVT-IEEILPKLTSVMNNSRDVAQNYC 585
 Db 509 ---QIRBILRRGGELIYEHKXDLVWKMREHVQHFEBALARLELVTKMNKHEVADOLY 565
 QY 586 LVMDMPRIKPEQAMLLDCNYRDMVYGFVAVRCLKLYLTDKLSQYLIVOLVLYKVOYL 645
 Db 566 LLSGMPFLPYLSALELDFSPDCYVSPAIKSLRK-LTDELFQYLLQVLYKVSYL 624
 QY 646 DNLIVRLTKKALTNQIIGFFFWHLKSEWANKTVSOFGILLSEYCRACCMYIKHLNRQ 705
 Db 625 DCEITKFLGRALANRRIIGHFLFWHLRSEWNVPSVALRFGILMEAYCRGSTHNNKVLKQ 684
 QY 706 VEAMEKLTINLTDIKQEKDETOKVOKFLVQV-NRRPDPMDALQGFSPLNPAHOLGNL 764
 Db 685 GEALSKKALNDYKVSQ-QTKTPQTKEMNMHGMROETIWEALSHSQSPDSELTLEEV 743
 QY 765 RLEBCRISSAKRPLMLNWPNDIMSELFPONNEIFKNGDDLQDMLTLOIIRIMENTW 824

Db 744 CVEOCTPMDSKMKPLMTWYSSEBAGSA---GNVGILIFKNGDDLQDMLTLOIMDYLM 800
 QY 825 QNOGLDIRMLPYGLSLGDCWGLEEVNRSTIWOIQ-KGGLGALQFNSHTLHWKLD 883
 Db 801 KOBGLDIRMTPYGLPLGDRGTGLIEVWHSITIANIQUNSNMAYATAFNADALLNMLKS 860
 QY 884 KMKGEIYDAIDLFTRSACAGCVATFLLIGDRHNSIMVWDQQLPHIDGFLDHKK 943
 Db 861 KNPBEALDRAIEFTLTSACGCVATVYLGIDRHSNIMRESQULPHIDGFLHGNKT 920
 QY 944 KEFYKRRVPFVLTPDPLVYISKAGQECTYREERFOEMCYKALIROHANIPLNFS 1003
 Db 921 KFGINRRVFFILTYDEVVHYIQG--KTNNSKEFERFGYCERAYTILRRGLFLHLFA 978
 QY 1004 MMLGSGMPELQSFDDIAYIKRTIADLTKTEQALAEYFKOMNDAHNGMTTMDKIFHTIK 1063
 Db 979 LMRAGLPELSCSKDIDQYLDKSLGKTEBEALKHFRVKTENLRESWKTQVNLHNVS 1038
 QY 1064 Q 1064
 Db 1039 K 1039

RESULT 6
 ID Q8CI98 PRELIMINARY; PRT; 1037 AA.
 AC Q8CI98;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Phosphatidylinositol 3-kinase catalytic delta polypeptide.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC035203; AA035203.1; --
 KM Kinase.
 SQ SEQUENCE 1037 AA; 119130 MW; 4446B78B5F37A0E2 CRC64;
 Query Match 34.4%; Score 1964.5; DB 11; Length 1037;
 Best Local Similarity 40.1%; Pred. No. 3.6e-144;
 Matches 426; Conservative 189; Mismatches 389; Indels 59; Gaps 18;
 QY 20 ILVBCILPNCMTVTECLREATLITIKHELFKEARKYPLHQILOESSYIFVSVTOEAR 79
 Db 12 VVDFELIPTGVILNFPVSNANLSTIKOYLHRAQYEPFLHMSDPEAYFTCVNQTABQ 71
 QY 80 EEFDETRRLCDLRLFOPLKYIEPVGNREKILNREIGFAIGMPVCEPDMVXDEVD 139
 Db 72 QLEDEQRRLCDIQFLPVRLVAREGDRYKXILNSQISLILKGLHFEPSLDPEVND 121
 QY 140 RNILNVCKAVDLRLDINSPHRAMVVPVNVESPELPK-----HIYNKLDKQIIVIV 195
 Db 132 RTKMRQFCCEAAHROQLGWEMLYOVSFPLQLEPARGWAGLLRVSNR-----ALL 183
 QY 196 VIYSPNNNDKQKTYTLKINHDCVPEQVTAEARIKTRSMILSSBDKLCVLEYQGYIKVC 255
 Db 184 VNVKFGSESESTFPQVSTDMPLAMACLRK-----ATVRFQPEEYALQVN 236
 QY 256 GCDYFLEKYPISQYKTRSCITLGRMPLMLAKESLYSOLPMDFTMPSYSRRISTAT 315
 Db 237 GRHEYLGNVPLCHFOYICSLHSGILPLTWVHSSILAMRDEQSNAPVOYOKPRAPRP 286
 QY 316 PYNNGETSLNVLNINSALRIKILCATYVNVIRIDIKIVRTGIYHGEPLCDVNTQRY 375
 Db 297 PIPAKPPSSVSLMSLEQPFSEILIGRKVNADER--MKLVVQAGLPHGNEMLCKTVSSSE 354

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Oy 376 V-PCSNPRMNMELNYDIYIPDLPRARLCLISGV-----KGRKAKEHEPLAMGN 426
Db 355 VNVSEPRVKORLEBDSVCDLPRNARLCPALYAVEAKARSTKKSKAADCIAMAN 414
Oy 427 INLFYDTDTLVSGKALNLMP-VPHGLEDLNPIGVTSNPNKETPCLLEBDFWSSVVK 485
Db 415 LMLDYDQDLKTGERCLVMPVSVPDEKCELLNPAQTAVGNNTSAA-----ALVIY 466
Oy 486 FPDMSVIEEHANMSVSEAGSYSHAGLSNPLARDNEIRENDKEQRAICTRDLSETTE 545
Db 467 LPE---VAPHPVYFPALKEKILELGNHGERGRITTEEOU-----QALREILRRSGELYE 517
Oy 546 QEXQELMHRHVCYT-IPEILPKLLSTYKNSRSDVAQMGCLVQKMPICEQAMELDDC 604
Db 518 HEKDLVWKMRHVOEHPEALRLVTKMKHEVQAQMLYLCSPELPLVLSALELDF 577
Oy 605 NYDDPMVGFARCLEKYLTDKLSQVLIQVLQVLYEQLVLDNLVPLKALKALTNORIG 664
Db 578 SFPDCYVSFAIKSLRK-LTDELFQYLLQVLQVLYESYLDCELTFLRLRANRKG 636
Oy 665 HFFPMHLKSEMNKTVSQRFGLLESYCRACGMVYLKHLNQYVAMEKILNLTDLKQEK 724
Db 637 HFLFHLHLSSEMHVSVALRFGILMEAYCRGSTHMKVLMKQGEALSKLALNDFKVSQ 696
Oy 725 DETQVQMKFLVEQ-MRRPDMDALQGFSLPINAHQGNL-RLEBGRIMSARPLMAN 782
Db 697-KTKPQTKEMMHMCROETMEALSHLOSPLDPSLTLEBVCVSQCTFMOSKMPYLIM 755
Oy 783 WENPDMSELLFONNEIFKNGDDLRQDMLTLQIRIMENIQONQGLDRLMLPYGCLSIG 842
Db 756 YSSEBAGA---GNVGIIIFKNGDDLQGMMLTQMIQLMDVLMKQGLDRLMTPYCYCLPTG 812
Oy 843 DCGVLEIVVNRSHITMQIC-KGLKALQFNSHTLHOMLKRNKGEYDAIDLFTSC 901
Db 813 DRTGLIEVLVHSDITIANIQLNKSNNAAATAPFKDALMLWLKSKNGEALDRAIEFTLSC 872
Oy 902 AGCYATATFLIGDGHNSNIMWKDGOLEPHIDFGHLDHKKKFGYKERVVFTOPL 961
Db 873 AGCYATVVLGIDGHSNDIMRESGQLPHIDFGHFGFKFKGFINERVPFILTDFV 932
Oy 962 IVISKAQOECTKTRFEFERFQEMCYAYLAIRQANLFINLFEMLSGMPLOSFDIAY 1021
Db 933 HVIOQG--KTNSEKFERFGYCEBAYITLIRHGLFLFLFALMAAGFELSCKDIOY 990
Oy 1022 IAKTLALDKTEGEALEYFNKQNDAAHHGWTTKMDWITFIHQ 1064
Db 991 LKDSLALGKTEBEALKHFRVKFNEALRESWTKVWMLAHNVSK 1033

RESULT 7
OBS14 PRELIMINARY; PRT; 1047 AA.
ID OBS14;
AC OBS14;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Phosphatidylinositol 3-kinase catalytic delta polypeptide.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=2354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK040867; BAC30725.1;
SQ SEQUENCE 1047 AA; 120186 MW; 73654D27449A30B2 CRC64;

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Query Match 34.4%; Score 1963; DB 11; Length 1047;
Best local Similarity 39.6%; Pred. No. 4,8e-144;
Matches 429; Conservative 189; Mismatches 390; Indels 76; Gaps 19;

Oy 16 MPP-----RIVBCLLPNGMTVTLBCLRENTVLTTHKELFKERKRYPLHQ 60
Db 1 MPPGVDCPMEFWTKESQSVVVDVFLPTGYLNFVPSRNNLSTIKQVLMHRAQYELFLH 60
Oy 61 LLDDESSYIVSVTAQEAEREFEDETRLCDLRFQFELKVIIPVGNREKILNREIGFA 120
Db 61 MLDSPBAIVFTCNQOTLEQOELEDEORRLCDIQFPLVLRVAREGDRVKKLINSQSL 120
Oy 121 IGMPVCEFDVWKPEVDFRRNLIANCKEAVDLRDLNSPBRAMYVPPVNESSPELPK- 179
Db 121 IGKHLHFDSLRODEVNDFRTKORQCEBAARQQGWEMLOYSPFMOLPSARGMRA 180
Oy 180 ---HIYKLDKQGLIVIVITVYSPNDKQKTYTLKINHDCYPEQVIAAIRKTRSM LSS 236
Db 181 GLRVSNR-----ALIVVKEGSEBSFTPOVSTKMPFLMALMALKRK-----A 225
Oy 237 EQLKLCVLEYQKYLKAVCGDEYFELEKYPLSOYKYIRSGIMGRMNLMLAKESLYSQ 296
Db 226 TVFRQPLVEQPEEYALVNGRHEYLGNYPCLCFQYICSLHSGLTFLHVMHSSSLAM 285
Oy 297 LPMDCFTMPSYSRRISTATPYMNGETSTKSLWVINSALRIKICATYVNVNIRDIXY 356
Db 286 RDEQSNAPQQRKRAPRPPIPAKKPSVSLSMEQFSEILBGRVYNDER--MKLVV 343
Oy 357 RTGIYHGEPLCDNVNTQRY-PCSNPRMNMELNYDIYIPDLPRARLCLISGV----- 409
Db 344 QAGLPHGNEMLCIKTVSSSEVAVVCSBPWKORLEBDSVCDLPRNARLCPALYAVEAKK 403
Oy 410 ---KGRKAKEHECHPLANGNINLPYDTDLVSGKALNLMP-VPHGLEDLNPIGVTSNP 466
Db 404 ARSTKSKSKADCCIAANMLFPHYKQDLKTGERCLTMHRSVPDEKCELLNPAQTAVGNP 463
Oy 467 NKETPCLLEBDFWSSVVKFPDMSVIEEHANMSVSEAGSYSHAGLSNPLARDNEIREN 526
Db 464 NTEBAA-----ALVIYPE---VAPHPVYFPALKEKILELGNHGERGRITTEEOU--- 509
Oy 527 DKEQIRALCTRDPLSETTEQKDFLMGHRHCYT-IPEILPKLLSTYKNSRDEVA---Q 582
Db 510 ---QALREILRRSGELYEHEKDLVWKMRHVOEHPEALRLVTKMKHEVQAQLSQ 566
Oy 583 MYCLVMPPIKRPQAMELDQNYPPDMVGFARCLEKYLTDKLSQVLIQVLQVLYE 642
Db 567 MLYLCSMPPELPVLSAELDPSPDCYVSFAIKSLRK-LTDELFQYLLQVLQVLYE 625
Oy 643 QYLDNLVRFLLKXALTNRIGHFEFWMHLKSEMNKTVSQRFGLLESYCRACGMVYLKHL 702
Db 626 SYLDCELTKFLGRLANRKHGFLFHLRSEMHVPVVALRFGILMEAYCRGSTHMKVL 685
Oy 703 NROYEAMEKILNLTDLKQEKDETQKQKFLVEQ-MRRPDMDALQGFSLPINAQOL 761
Db 686 MKQGEALSKLALNDFVAVSQ-KTKPQTKEMMHMCROETMEALSHLOSPLDPSLT 744
Oy 762 GNLRLEBORINSSAKRPLMLWBNPDIMSELLFONNEIFKNGDDLRODMLTLQIRIME 821
Db 745 EEVCEQCTFENDSKKPLMIMYSSEBAGA---GNVGIIIFKNGDDLRODMLTLQIMQMD 801
Oy 822 NIMQNGIDLMLPYGCLSIGDCVGLIEVENSHTIMQIC-KGLKALQFNSHTLHOW 880
Db 802 VLMKQEGDLNMTPTGCLPTGDRGLIEVLVHSDITIANIQLNKSNNAAATAPFNKQALN 861
Oy 881 LKDKKGEIYDAIDLFRSCAGYCVATFIIIGIDRNSNIMWKDQGLPHIDGHEFDH 940
Db 862 LKSKNPGALRAIBEFTLSQAGYCVATYVIGIDRHSNDIMRESGQLFIHDFHFIGN 921
Oy 941 KKKKGYRERVPFULTQDPLIVISKAQOECTKTRFEFERFQEMCYAYLAIRQANLFIN 1000
Db 922 FTKTGFIRERVPFILTDFVHVIQOQ--KTNNSKFERFGYCEBAYITLIRHGLFLH 979
Oy 1001 LFSMMLSGMPLOSFDIAIYIRKTLALDKTEGEALEYFNKQNDAAHHGWTTKMDWIFH 1060

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Db      980 LFLALMRAAGLPELSCSKDIQYLKOSLALGKTEEBALKHFRVKNFALRESKTKTYNMLAH 1039
Qy      1061 TIKQ 1064
Db      1040 NVSK 1043

RESULT 8
000334 PRELIMINARY; PRT; 1068 AA.
ID 000334
AC 000334
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Phosphatidylinositol 3-kinase delta catalytic subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mahlum C.E., Becker K.P., Morris A.J.
RT "H. sapiens mRNA for phosphoinositide 3-kinase delta catalytic
RT subunit."
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U57843; AAB53966.1; -.
DR InterPro; IPR001263; PI3Ka.
DR InterPro; IPR002420; PI3K_C2.
DR InterPro; IPR003113; PI3K_p85B.
DR InterPro; IPR000401; PI3K_ras_bind.
DR InterPro; IPR000403; PI3_P14_kinase.
DR Pfam; PF00613; PI3Ka; 1.
DR Pfam; PF02192; PI3K_C2; 1.
DR Pfam; PF02193; PI3K_p85B; 1.
DR Pfam; PF00794; PI3K_rbd; 1.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3Kc; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00143; PI3K_p85B; 1.
DR SMART; SM00144; PI3K_rbd; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
KM Kinase.
SQ
SEQUENCE 1068 AA; 121879 MW; 2B342FDA445C9A31 CRC64;

Query Match 33.3%; Score 1903.5; DB 4; Length 1068;
Best Local Similarity 38.3%; Pred. No. 2.2e-139;
Matches 434; Conservative 179; Mismatches 367; Indels 153; Gaps 23;

Qy      16 MPP-----RIIVECLLRNGMTVTIECLREALTITIKELPFEAKRYPLHQ 60
Db      1 MPPGVDCPMEEFMTKENORVVVDLLPLPGVYLVNPPVSNNALSTIKQLMIRADYEPFLH 60

Qy      61 LLODESSYIFVSVQEAEREFEFPDETRRLCDLRFQFLKITEBVGNREKILNREIGFA 120
Db      61 MLSAPKAVYFTCTICOTHAEGQLEDEQRRLCDVQFPFLPKIRVAEGSDVKVLINSQISL 120

Qy      121 IGMVFCEFDVWKDEVDVDFRNILNVCKEAVDLRLDLSNPHSRAMVYVPNVESSEPE---- 176
Db      121 IKGKLFHFDSDLCDEVDNDFRAKMCQCFEAAARQIQGWEAMLDYSPFLDLEPSAQWGP 180

Qy      177 -----LPHGIYTKLKDQGIIVIVIVYVSPNDKQYTKLKNIDCVPEBOVIAAIAIKTKRSM 232
Db      181 GTLRLPFR-----ALLNVNFKEGSESEFTQVSTKVDVFLMLMACALRK----- 224

Qy      233 LLSSEQKLCVLEQGYKYLKVCSCDEFELEKYLPSQYKTYRSCIMLGMPNMLMAKES 292
Db      225 ---ATVRRQPLVEGREDYTLGVNGBHELYLGSYPLCGFQV----- 261

Qy      293 LYSQLEPMDCTFMPYSRRISTATPYMNGESTKGLMWINSLARTKIICATVYVNVNIDID 352

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Db      262 ---OKPR-----AKPPIPAKKSSVSLMSLEOPFRRIELLIQSKVNADER--M 304
Qy      353 KIYVRIGIYHGGEIACDNVANTORVP--CSNPRNEMLVYDIYIDLPAPRAALCTISCSV-- 409
Db      305 KLVYQAGLPHGNEMLCCTVSSSEVSCEPVMQKRLFPDINICDLPMAALCFPLVAVIE 364
Qy      410 -----KGRGAKEEHCPYLAAGNINLFDYTDTLVSGMALNLMP-VPHGLEDLINPIGVT 462
Db      365 KAKKARSTKKSKKADCPRIAMNIMLFDYKQCKTGRCGLYMPSPVDEKELLNIPGTV 424
Qy      463 GSNPKET-----PCLF-----LEDFMSSVYKPFDMSVIEHA 496
Db      425 RSNNTDSAAALLICLPEVAPHPYVYALRKLPGMLLASREW-----PELLMMLHA 478
Qy      497 NWSY-SRGAQFSYSHAGL-----SNRLARDNEL-----RENDKQGRAI 534
Db      479 EDSAPSRMIGVAPNGLVPLGVQAPDADACSRLLQILEGRSSECVNHTBEEOQLQREI 538
Qy      535 CTRDPLSEITEOEKDFLMSHRHVCVT-IPILPRLLSVKNRSDVEVAQWYCLWKDWPPI 593
Db      539 LERRSGELYEHKEDLVWKLRIHEVQEHFPAALARILLVTGMKHEDVAPALPAVSNPEL 598
Qy      594 KPEQAMLELCCNTPEDPMVGRPAVRCLEKYLITDQLSYLLQLYQVLYKEQTLNMLVPL 653
Db      599 PVLSALRLDPSFPDCHVGSFAIKSLRK-LTDELFQYLLQIVQVLYKESYLLDCELTKFL 657
Qy      654 LKKALTNQRIQHFEFMHLKSEBMNKTVSOREGSLTSGACAGVYLGLHRYOYAMEKLI 713
Db      658 LERLANRKLGHFLFMHLRSEBMHVPVALRFGLLTLEAYICGSGTHMKVYLMKQGEALSKL 717
Qy      714 NLTDILKQEKDETOXVOMKFLVEO--NRPDFDALOGFSLPYNPAHQLGNRLRECRIM 772
Db      718 ALNDFVLTSSQ-KTPKQQTKEMLHLCWRGEAYLEASHLSQSPDPSFLAAVECEQCTFM 776
Qy      773 SSARPLMLMENDPDIINSELLFQNNELIFKNGDDLRODMKTLQIRIMENIKQNGCIDLR 832
Db      777 DSKKKPLMIWYSNEBASG---GTVGIIFFKNGDLRDMTLTLMQIDMLMKOEGIDL 833
Qy      833 MLPYGCISIDDCVGLIEVENSHTIMQIQK-KGSLKALCPNSHTHQMLKDKNKGRIYD 891
Db      834 MTPYGCLEPTDRTGLLEVLRSDTIANIQNKSMAATAFENDALNMLKSKNPGALD 893
Qy      892 AAIDLFTSCAGCVATFLLIGIDGRHNSNTMVXDQGLFHIIDFGFLDHKKKFGYRRER 951
Db      894 RAIEEFTLSCAGCVAAIYVVGIGDRHSDNIMIESGGLFHIIDFGFLGNKTKFGINRER 953
Qy      952 VPFVLTODFLIVISKGAQECTKREPERFQEMCYKAYLAIRQANLFINPSMMLSGMP 1011
Db      954 VPFILTYDLVHVIQOG--KTNNSEKFERFPGYCERATYILRRHGLFLHLFALMRAAGLP 1011
Qy      1012 ELQSFDDIAYIKRTIALDKTEQALIEFMKQNDADHNGGTTTKMDYFHIKQ 1064
Db      1012 ELSCSKDIQYLKOSLALGKTEEBALKHFRKFNALREGKTYNMLAHNVSK 1064

RESULT 9
001634 PRELIMINARY; PRT; 1068 AA.
ID 001634
AC 001634
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Phosphatidylinositol 3-kinase catalytic subunit (EC 2.7.1.137)
DE (PI3K2E protein) (CG4141 protein).
GN PI3K2E OR CG4141.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97133288; PubMed=8978685;

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Db 1013 KHGLILSLPSMISTGTGLPEISSEKDLVLAETLVLDYTEKARSHFPAKSEALANSWK 1072
QY 1053 TRKDMIFPTIKOH 1065
Db 1073 TSLMASHNFSKN 1085

RESULT 10
Q91XL6 PRELIMINARY; PRT; 291 AA.
ID 091XL6
AC 091XL6
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Phosphatidylinositol 3-kinase alpha catalytic subunit (EC 2.7.1.137)
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RA Schaefer M., Plum C., Albrecht N., Reusch P.;
RT "Expression of phosphatidylinositol 3-kinases in rat vascular smooth
RT muscle cells."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF395897; AA83379.1; -
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00454; P13_P14_kinase.1.
DR SMART; SM00146; P13Kc.1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
KW Kinase; Transferase.
FT NON_TER 1
FT TER 291
SQ SEQUENCE 291 AA; 33934 MW; CF0B1EA450F8B78E CRC64;

Query Match 26.7%; Score 1527; DB 11; Length 291;
Best Local Similarity 99.3%; Pred. No. 8e-111;
Matches 289; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 705 QVEAMEKLINTLDLKEKDEKDEKQVQMKFLVEQRRRDEPDALQGFSLPMPAHLQNL 764
Db 1 QVEAMEKLINTLDLKEKDEKDEKQVQMKFLVEQRRRDEPDALQGFSLPMPAHLQNL 60
QY 765 RLEBCRINSASAKRPLMLNWPDIIMSELLFONNEIIFKNGDDLQDMITLQIIRIMENIW 824
Db 61 RLEBCRINSASAKRPLMLNWPDIIMSELLFONNEIIFKNGDDLQDMITLQIIRIMENIW 120
QY 825 QNOGLDRLMLPYGLSLGDCVGLIEVVRNSHTIMOIOCKGLKCALQNSHTLHOMLKDK 884
Db 121 QNOGLDRLMLPYGLSLGDCVGLIEVVRNSHTIMOIOCKGLKCALQNSHTLHOMLKDK 180
QY 885 NKGEIYDAIDLFTKSCAGYCVATFIIGIDRNSNIMVKKDGLFHDGFLDHHKKK 944
Db 181 NKGEIYDAIDLFTKSCAGYCVATFIIGIDRNSNIMVKKDGLFHDGFLDHHKKK 240
QY 945 FGYYRERVPLVTDPLIVISKAQECTKTFERFQEMCYKALAIRQHA 995
Db 241 FGYYRERVPLVTDPLIVISKAQECTKTFERFQEMCYKALAIRQHA 291

RESULT 11
Q9BZC8 PRELIMINARY; PRT; 1102 AA.
ID 09BZC8
AC 09BZC8
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phosphoinositide-3-kinase gamma catalytic subunit (EC 2.7.1.137).
GN P13G.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350661; PubMed=7624799;
RA Stoyanov B., Volinia S., Hancock T., Rubio I., Loubchenkov M.,
RA Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nurnberg B.,
RA Gierschik P., Seedorf K., Hansen J.D., Waterfield M.D., Wetzker R.;
RT "Cloning and characterization of a G protein-activated human
RT phosphoinositide-3 kinase."
RL Science 269:690-693 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Michael M., Schaefer M., Stoyanov B., Wetzker R., Nurnberg B.;
RT "Regulation of a G-protein-activated phosphoinositide-3-kinase."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF377656; AAG6115.1; -
DR InterPro; IPR001263; P13K.
DR InterPro; IPR002420; P13K_C2.
DR InterPro; IPR000341; P13K_ras_bind.
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00613; P13Ka.1.
DR Pfam; PF00792; P13K_C2.1.
DR Pfam; PF00794; P13K_rbd.1.
DR Pfam; PF00454; P13_P14_kinase.1.
DR SMART; SM00145; P13Ka.1.
DR SMART; SM00146; P13Kc.1.
DR SMART; SM00142; P13K_C2.1.
DR SMART; SM00144; P13K_rbd.1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
KW Kinase; Transferase.
SQ SEQUENCE 1102 AA; 126481 MW; 402B867EBDD2191A CRC64;

Query Match 25.8%; Score 1472.5; DB 4; Length 1102;
Best Local Similarity 33.4%; Pred. No. 9.4e-106;
Matches 385; Conservative 192; Mismatches 402; Indels 173; Gaps 40;

QY 1 MPPRSSGELMGHILMPRLVLECLP-----NGMI-----VTLEC 36
Db 23 MKPSAASLSSMELIP-----IEFVLPISQKCKSPETALLHVAGHNVEQMKQAVLRA 78
QY 37 LREATLITIGELFKERKRYPLHQL-----QDESSYIVSVTQEMEREFEFETRL 89
Db 79 LRTSVADAFYHRL-----GRHFLLLYOKKGQWYEIYDYQVYQVTLCLRYWKATHRSP 132
QY 90 CDRLPQPLKVIIEPVGNREKILNREIGFAIGPVCEFPVWQDEYQDPRRNLIVCKE 149
Db 133 GQIHLVQ-----RHPSSESQAQFQRLTALIGIDVAVNSHDBLEFTRRGIVTRMA 186
QY 150 AYDLRLDINSBHRAMVYVPPNVSSPELPKHIYKRLDKQIIVYIWIIVASPNNDKQRYTL 209
Db 187 EVASRD-----PLVYMHVWVTSKP-LPEYLMWKILANNCFIYI-----HSTTSQT 233
QY 210 KINHDCVPEVOYIAEAIK--KTRSMILSSBQLKLVIEFGKTIKAKCGDEYFLEKPYL 267
Db 234 KVSPPDDTPGAILLOSFFTKYAKKKSAMDIPES-----QSBQDPVLRVCGDBEYLVGTP 287
QY 268 SOYKIRSCAMLGMPVLM-----MAKESLYSOLPM--DCEFTMPSYSRISATPYMN 319
Db 288 KNFQWVRHCLKNGEELHIVLDTPEPDALDVRKEBMLVDCTGVGYHQLT-----IH 342
QY 320 GE-----TSKSLWVINSALRIKILCATYVNVNIRID-----KIYRTGIYHGE 365
Db 343 GXQHSVFTVSLWDCDCKRFXV-----IRGIDIPVLPHNTDLTFVVEANIQHGOQ 392
QY 366 PLCDNVNTQVPCSNPRMNMWLVYDIYIPLPAAKLCLISGVK-----GRKAKEHCP 421
Db 393 VLCQRRTPKPTPEVLMVWLEFISIKIKDLPKALMLNLIQYCGKAPALSSKASAPSS 452

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QY 422 LAMGNINLFDYTDLV-----SGKALNLMVPVPHGLD--LNLPIGVT-GSNPNKE- 469
DB 453 ESKGVRLLYYNNLLIDHRELLRGEVYLHMWQISGKGDDGSPNADKLISATIPDEN 512
QY 470 TPCLELEFDWSSVVKFPDMSVIEEHANWVSREAGFSYSHAGLSNRLARDNELRENDKE 529
DB 513 SMSISILLDNVCHPIALPHQPTPDPEGDRV-----RAEMPNQRL-----K 553
QY 530 QLRALCTRDPLSEITEOEKDFLWSHRHYCVTIPILRPLLSVKNNSDEVAQWYCL--- 586
DB 554 QLEAIIADPLNPLTAEDKELLMHFRYESLKHKPKAYPKLFSSVKKGQOEIYAKTYQLLAR 613
QY 587 --VKDMPRIKPEQAMELLDCNYPDPVGRFAVRCLEKYLTDKLSQYILQVLYKBOY 644
DB 614 REVWQSLADVGLTMQLDNCNFDENVRALAVQKLES--LEDDVLYHLLQVLYQAKFEPY 672
QY 645 LDNLVRLFLKALTNORIGHFFFWHLKSEM--HNKTVSQRFGLLLESYCRACGYLKH-L 702
DB 673 HDSALARFLKRGKLNKRIGHFLFWFLRSEIASHYQORFAVILBAYLRGCGTAMLHDF 732
QY 703 NROYVAMEKLINLT-DI--LKOEKDETOKV--QMKFLVEQMRRRDPMDALOGFLSPINP 757
DB 733 TOQVQVIEMLQKVTLDIKSLSAEKYDVSSQVTSQKQKLENLQNSQLPES--FRVPYDP 789
QY 758 AHQGLNLRLEBGRIMSSAKRPLMLNME--NPDIMSELLFONNE--IIFKNGDDLRQDML 812
DB 790 GLKAGALAIKCKWASKKKRPLMLERKCADPTALS-----NETGIIIFKHDDLRQDML 843
QY 813 TLQIIRIMENIMONOGDLRLMPLPGCLSIGDCVGLIEVVRNSHTIMOJ-OCKGGLKGLAQ 871
DB 844 ILQIIRIMESIWETESLDLCLLPYGCISGTGKIGMIEIWKADYTIKIQOSTVGTGTA-- 901
QY 872 FNSHTLHQLMKDKN-KGEIYDAIDLFTSCAGYCVATFIIGIDRHNNSNIMVKDQGLF 930
DB 902 FKDEVLANMLKRSKPTSEKFOAAVERFYVSCAGYCVATFVLGIDGRHNDNIMITETGMLF 961
QY 931 HIDFGHFLDHKKKKFGYKREVRPVLTODPLIVISKAQOECTKREFEFOEMKAYLA 990
DB 962 HIDFGHILGNYSFLGINKERVPVLTDFPLFMGTSGKKTSP--HFQKFODICYKATILA 1019
QY 991 IROHANLFINLFSMMLGSGMPELQSPFDIAYIRKTLALDKTBOALEYFMKQONDAHHGG 1050
DB 1020 LRHNHTNLILFLSMMLMTGMPQLTSEKEDIYIRDALTVGNKEDAKKFFLDQIEVCRDKG 1079
QY 1051 WTTKXDWIYFHTI 1062
DB 1080 WTVQFNWFLHLV 1091

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RESULT 12

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ID Q81V23 PRELIMINARY; PRT, 1102 AA.
AC Q81V23;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Phosphoinositide-3-kinase, catalytic, gamma polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pancreas;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC035683; AAH35683.1;
KW kinase
SQ SEQUENCE 1102 AA; 126453 MW; 87281A0E1CBEFF406 CRC64;

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Query Match 25.8%; Score 1472.5; DB 4; Length 1102;
 Best Local Similarity 33.4%; Pred. No. 9.4e-106;
 Matches 385; Conservative 192; Mismatches 402; Indels 173; Gaps 40;

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QY 1 MPPRSSGELGWLHMPRLIVECLLP-----NGMI-----VTLLEC 36
DB 23 MKPRSAASLSSMLIP-----IEFVLPISQKCKSPETALLHVAGHNVMQKQWILRA 78
QY 37 LREATLITIKELFEKARKYPLHQL-----QDESSYIFVSVTQAEAREEFDETERL- 89
DB 79 LETSVAADFYHRL-----GPHHFLLYQKKGQWYIEYDKQVQVQLDLCRYWKAHTRSP 132
QY 90 CDLLFPQFLKVIPEVGNREKILNREIGALIGMPVEFPMVQKPEVODPPRNLINVCKE 149
DB 133 GQIHLYQ-----RHPSSESOAFORQLTALIGVDVDSNVHDELEFTRRGLVTRPMA 186
QY 150 AVDLRLDINSPRAMYYVPPVWESSPELPHIYKRLDKGQIIVVIVVIVSPNDKQYTL 209
DB 187 EVASRD-----PLVAMHPVWTSKP-LPELWMLKIANNCIFVI-----HRETSQTI 233
QY 210 KINHDCVPEQVIADAIRK--XTRSMLLSSEQLKLVLEYGQYILKVGCCDEYFLKRYPL 267
DB 234 KVPSPDTPFGAILQGFTRKMAKKSLMDIPES-----QSEODFVLRYCGRDEYLVGETPI 287
QY 268 SQYKTIISCTMLGKMPNML-----MAKESYQLPM--DCFTMPYSRRISTATYMN 319
DB 288 KNFQWVRHCKLNGEELHIVVLDTPPDPALDEVKKEWELVDDCTGVTSYHEQLT-----IH 342
QY 320 GE-----TSTKSLAVINSALRIKILCATYVNVNIRID-----KIYVRTGIYHGE 365
DB 343 GKDHESVPTVSLMDCDKRFYK-----IRGIDILPVLPRTDVLTVFEANIQHGOQ 392
QY 366 PLCDNVNTPRVPCSNPRNENLNYDIYIPDLPRARLCLSIGSVK---GKGAKEEHCP 421
DB 393 VLCQRTSPKPFTEBEVLMNVLEFSIKIKDLPKALLNLQYCGKAPALSKAESPS 452
QY 422 LAMGNINLFDYTDLV-----SGKALNLMVPVPHGLD--LNLPIGVT-GSNPNKE- 469
DB 453 ESKGVRLLYYNNLLIDHRELLRGEVYLHMWQISGKGDDGSPNADKLISATIPDEN 512
QY 470 TPCLELEFDWSSVVKFPDMSVIEEHANWVSREAGFSYSHAGLSNRLARDNELRENDKE 529
DB 513 SMSISILLDNVCHPIALPHQPTPDPEGDRV-----RAEMPNQRL-----K 553
QY 530 QLRALCTRDPLSEITEOEKDFLWSHRHYCVTIPILRPLLSVKNNSDEVAQWYCL--- 586
DB 554 QLEAIIADPLNPLTAEDKELLMHFRYESLKHKPKAYPKLFSSVKKGQOEIYAKTYQLLAR 613
QY 587 --VKDMPRIKPEQAMELLDCNYPDPVGRFAVRCLEKYLTDKLSQYILQVLYKBOY 644
DB 614 REVWQSLADVGLTMQLDNCNFDENVRALAVQKLES--LEDDVLYHLLQVLYQAKFEPY 672
QY 645 LDNLVRLFLKALTNORIGHFFFWHLKSEM--HNKTVSQRFGLLLESYCRACGYLKH-L 702
DB 673 HDSALARFLKRGKLNKRIGHFLFWFLRSEIASHYQORFAVILBAYLRGCGTAMLHDF 732
QY 703 NROYVAMEKLINLT-DI--LKOEKDETOKV--QMKFLVEQMRRRDPMDALOGFLSPINP 757
DB 733 TOQVQVIEMLQKVTLDIKSLSAEKYDVSSQVTSQKQKLENLQNSQLPES--FRVPYDP 789
QY 758 AHQGLNLRLEBGRIMSSAKRPLMLNME--NPDIMSELLFONNE--IIFKNGDDLRQDML 812
DB 790 GLKAGALAIKCKWASKKKRPLMLERKCADPTALS-----NETGIIIFKHDDLRQDML 843
QY 813 TLQIIRIMENIMONOGDLRLMPLPGCLSIGDCVGLIEVVRNSHTIMOJ-OCKGGLKGLAQ 871
DB 844 ILQIIRIMESIWETESLDLCLLPYGCISGTGKIGMIEIWKADYTIKIQOSTVGTGTA-- 901
QY 872 FNSHTLHQLMKDKN-KGEIYDAIDLFTSCAGYCVATFIIGIDRHNNSNIMVKDQGLF 930
DB 902 FKDEVLANMLKRSKPTSEKFOAAVERFYVSCAGYCVATFVLGIDGRHNDNIMITETGMLF 961
QY 931 HIDFGHFLDHKKKKFGYKREVRPVLTODPLIVISKAQOECTKREFEFOEMKAYLA 990
DB 962 HIDFGHILGNYSFLGINKERVPVLTDFPLFMGTSGKKTSP--HFQKFODICYKATILA 1019

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Qy 991 IROHANLFINLFSMMLSGMPELOSFDIATIRKTLALDCKTEQALEYFMKQNDAAHGG 1050
Db 1020 LRRHTNLLIILFSMMLTGMQTLSTKEDIEYIRDALTVGKNEBDKAKKYLDOIIEVCRDGG 1079
Qy 1051 WTRKDWIFHTI 1062
Db 1080 WTVQFNWFLHLV 1091

RESULT 13
Q9EQL1 PRELIMINARY; PRT; 1113 AA.
ID Q9EQL1
AC Q9EQL1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Phosphatidylinositol 3-kinase gamma isoform.
GN PI3KCG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chakravarti S., Mccoll S.R.;
RT "Cloning of a murine ortholog of PI 3-kinase gamma.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF208345; AACG1122.1;
DR MGD; MGI:1353576; P13K3CG.
DR InterPro; IPR001263; P13Ka.
DR InterPro; IPR002420; P13K_C2.
DR InterPro; IPR000341; P13K_tas_bind.
DR InterPro; IPR000403; P13_P14_Kinase.
DR Pfam; PF00613; P13Ka; 1.
DR Pfam; PF00792; P13K_C2; 1.
DR Pfam; PF00794; P13K_Tbd; 1.
DR Pfam; PF00454; P13_P14_Kinase; 1.
DR SMART; SM00145; P13Ka; 1.
DR SMART; SM00146; P13K; 1.
DR SMART; SM00142; P13K_C2; 1.
DR SMART; SM00144; P13K_Tbd; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS02090; P13_4_KINASE_3; 1.
KM Kinase.
SQ SEQUENCE 1113 AA; 127538 MW; 6729FBE8ASD35691 CRC64;

Query Match 25.7%; Score 1467; DB 11; Length 1113;
Best Local Similarity 33.1%; Pred. No. 2,6e-105;
Matches 381; Conservative 199; Mismatches 411; Indels 160; Gaps 38;

Qy 1 MPPRSSGELGMLHMPRIIVECLTNGMIVT-----LECLREATLTITIKELKEA 53
Db 23 MKPPSAAGSLSSMELIP-----IEFVLPTSORISKIPETALHVAHGNGVEOMKQVWLRA 78
Qy 54 RXYPL-----HQLLDSESYIFVSVTQEAERESEPFDETRRLCDRLPQPLK-----V 101
Db 79 LRTSVAAEFHRLRDPDQFLLYQKKGQWYELIDRYQVAVTLDCLHYMKLHMKSGCOLHVV 138
Qy 102 IEPVGNFEKILNLEIGFAIGMPVCEFDWVDEPEVDFRRNIIAIVCKEAVDLRLDLSNPS 161
Db 139 ORHVPSEETLAFQKQLTSLIGYDVTDISNVHDELEFRRRLVYPRMAEVAGRDAK----- 194
Qy 162 RAMVVPVNPVSESELKRHLYNKLDKQQLIVIVIVIVISPNNDKKYTLKINHDCVPEQVI 221
Db 195 --LVAMHPWYSK-LPDYLSKTIANNCFIVI-----HNGTISQTIKVSADDTPTGIL 245
Qy 222 AEAIRK--KTRSMILSESQLKLVLEYGKYLKVCQDGFLEKYPPLSGYKYSICML 279
Db 246 QSFPTTAKKSKSLMNISES-----QSEQDFVLAVCGDELYVETPLKFNQVWRQCLKN 299
Qy 280 GRMENML-----MAKESLYSLPM--DQFTMPSYSRISTATAPVMNGE---TSTKSL 327

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Db 300 GDEIHLVLDPPDPALDEVERKEEWPVDDCTGVYGHQULT-----IHGKHESVFTVSL 354
Qy 328 WIVNSALRIKILCATYNNVNRID-----KIVYTGIVHGGEPLCDNNVNTQVRP 377
Db 355 WDCRRKFRVK-----IRGIDIPVLPRNDLIVFEANIQGQVLQQRRTSRPF 404
Qy 378 CSNPRNENMLNYDIYIPDLPPAARLCU--CSYVGRKGAKKEHCP-----LAWG 425
Db 405 AEEVLNKNVWLEFGKIKIDLPKGAALNQTIVCCKPTLSKASAPTPSESGKQALYYV 464
Qy 426 NINLPDYTDILVSGKALNMPVPHLED--LNPICVT-GSNPNK-TPCLELEPFMS 481
Db 465 NLLIIDHRFILRHGDYVLHWMQISGKAEQGSFNAADLTATNPDKENSISILLNVC 524
Qy 482 SVVFPMSVIEEHNAMSVERAGFSYSHGLSRLARDNELRNDDEORAIOTRPLS 541
Db 525 HPILPFRHPTPPDEGCRV-----RAEMVQLR--KOLEAIIATDPLN 565
Qy 542 EITEQKDFLMSHRHYCVTIPILPKLLSVKNNSDEVAQWYCL-----VKDWPIKPE 596
Db 566 PLTAEDEKELMHFRYESLKHPRKAVPKLFSSVKNQCGEIVAKTYQLLARREIWDQALDVG 625
Qy 597 QAMELIDCNYPDPNVRGFAVRCLEKYTFDPKLSQYLIQLVQLKYEGYLDNLVRLPKK 656
Db 626 LTMQLDLCNFSDEVNRAIAVQKLES--LEDDVLYHLLQLVQAVKFEFPHSALRPLKR 684
Qy 657 ALTNQRIQHFFPFLKEM-HNKTVSORPGLLLESYRACG-MYKHLNANQVEMETLIN 714
Db 685 GLRNKRIGHFLPWLRESLAQSHYQRFVILAEAVRGGGTAMLQFTQVHIEMLQK 744
Qy 715 LT-DI--LKOEKDETKV--QMKFLVEOMRRPDMALQGLSPILPAHOLGNRLREEC 769
Db 745 VTIDIKLSAEKDVSSQVLSQKLESQNSLPS---FRVYPYGLKAGTLVIEKC 801
Qy 770 RINSASRPLMLNWE--NPDIMSELLFQNN-----IIFKQDDLRQDMLTLOIRIMENIW 824
Db 802 KVAASKKPLMERKCADPTVLS-----NETGIIFKHDDLRQDMLTIQIRIMESIW 855
Qy 825 QNGCLDRLMPLPYGLSLGDCVGLIEVVRNSHTTMOI-QCKGGLKALQFNSHTLHQLKD 883
Db 856 ETSLLDLCILPYGISGDKIGMIEIKDATTIAQIQOSTVGATGA--FDEVLNHWLKE 913
Qy 884 KNK-GEIYDAIDLFETSCAGYCAATFILGIGRHSNINWMDQGLFIHDFGFLHKK 942
Db 914 KCPLEKFPAAVERFVYSCAGYCAATFVLGIGRANNDINISETGNLFHIDFGHILGNK 973
Qy 992 IROHANLFINLFSMMLSGMPELOSFDIATIRKTLALDCKTEQALEYFMKQNDAAHGG 1051
Db 1032 RHHTNLLIILFSMMLTGMQTLSTKEDIEYIRDALTVGKSEBDKAKKYLDOIIEVCRDGG 1091
Qy 1052 WTRKDWIFHTI 1062
Db 1092 WTVQFNWFLHLV 1102

RESULT 14
Q61182 PRELIMINARY; PRT; 1658 AA.
ID Q61182
AC Q61182;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Phosphoinositide 3-kinase.
GN PI3KCA OR CPK-M.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=baib C; PubMed=8662856;
RX MEDLINE=9627830; Williams L.T.;
RA Molz L., Chen Y.W., Hirono M.,
RT "Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
  domain.";
RL J. Biol. Chem. 271:13892-13899(1996).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; U52193; AAC52604.1; -.
DR HSSP; P21707; IBYN.
DR MGD; MGI:1203729; P1K3C2a.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002420; P1K3a.
DR InterPro; IPR000341; P1K3a_bind.
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00613; P1K3a; 1.
DR Pfam; PF00792; P1K3_C2; 1.
DR Pfam; PF00794; P1K3_rbd; 1.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00787; P13_P14_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00145; P1K3a; 1.
DR SMART; SM00146; P1K3C; 1.
DR SMART; SM00142; P1K3_C2; 1.
DR SMART; SM00144; P1K3_rbd; 1.
DR SMART; SM00312; P13_P14_kinase; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00915; P13_4_KINASE 1; 1.
DR PROSITE; PS00916; P13_4_KINASE 2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
DR PROSITE; PS0195; P13_4_KINASE_3; 1.
DR KINASE.
SQ SEQUENCE 1658 AA; 187439 MW; BBC8E81DE20F20 CRC64;

Query Match 18.4%; Score 1049.5; DB 11; Length 1658;
Best Local Similarity 33.1%; Pred. No. 1.7e-72;
Matches 270; Conservative 141; Mismatches 297; Indels 107; Gaps 24;

OY 296 QLPMDCFPMSPY-----SRISTATPYMNGSTSTSLWYNSALRIKILICATYVAVN 347
DB 614 QVSMHDLTAIYDLRLANSSRCSTGCP--RGSNITKEMATATQLOFTYAAAGISISN 671
OY 348 -IRIDIKIYVRTGIYHGEPLCDVNVTVORVPCSNP-----RNVENLVNDIYIPDLPRAR 401
DB 672 WVSNEYKYLLICSLSHNGKDLFPKIQSKVGTYNKFYLIKWDLLIPPIQISQLPLESV 731
OY 402 LCLSLCSV-----KRRKAKKEHCHLANGNIN--LPDYDTLVLSKALNIMP 447
DB 732 LHLTLFGVLNOSGGSSPDNNKQKRG-----PEALGKSLTLFDKRFITCGTKLLYIMT 785
OY 448 VPHGLDLNLPFGVGNPNK-----ETPCLLELPWFSSVVFPPMSVIBEHANVSRE 503
DB 786 SSH-----TNSIGALPKSKYMERIYLOVDF-----PSAPDII----- 820
OY 504 AGFSYSHAGLSNRLARDNELR--END-KEOLRAICTRDPLESLTEOEKDFLMSHRHYCVT 560
DB 821 ----YTSQIDRNIIQQDKLETLFESDIKGLDDIHRDSSFSLSKEDKVFLENNRYCJLK 876
OY 561 IPELIPKULLLV---KANSRDEVAOMYCLVADMPFKPEQAMELLDCNVPDPVNGRFAVR 617
DB 877 HPNCLPKILASAPNKMWAN---LATTYSLHWPPLCPILAELLDARFADQVGSILANS 933
OY 618 CLEKLTLDKLSQYLIQVQVLYKQYLDNLLVRFLLKALTNORIGHFFHNLSEMIN 677
DB 934 WMEA-ISDELDLIPQVQALKYEIYANSSIVRELSALNIOIASHLYLLDALHD 992
OY 678 KTVSGRFGILLSEYCRACGMVLR-HINROVEAMEKILNLTDLIOEKDEKDETQVOMKFLV 736
DB 993 THFGSRVHEVIVGALLSVGKGLRELSKQMKLVOLLGVAEKVQAGSSTRQVVLQK--- 1049

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OY 737 EOMRRPDMALOGFL-----SPINAHQGLRLBCECRINSSAKRPLMNNENPDIMS 790
DB 1050 -----SMERVGSFLLRNKCRPLPKRSYANXELNITKSCSFSSNAPLVTWVMDPLG 1102
OY 791 ELLEFONNEIIFKNGDDLRQMDLTLQIIRIMENIWOGLDLRLMPLYCCLISGDCVGLIEV 850
DB 1103 EEI-----NVMFKVGEDIRQMDLALQWIKIMDKITLWKEGLDLRWVIFPCLISTGDRGVVEL 1158
OY 851 VRNSHTIMQIQCKGLGALQFNSHTLQWLKQKNKQ-EIYDAIDLFSTSCAGYCATF 909
DB 1159 VPASDTRLRKIQVEGVVGS--FKDKPLAEWLKRYNPEEYERKASENFITYSCAGCCVATY 1216
OY 910 ILIGDRHNSNINWKKDGGQLFHIDFGHFLDHKKKXFGYKKEERVVFLTQDFLLIVISKAQ 969
DB 1217 VLGIQDRHNDINIMLRSGHMFHIDFGKFLGHAQMGFSFKDRAPFVLTSMAYVINGEK 1276
OY 970 ECTYTRFEFRPOENCYAVYLAIRQHANLFTNLFSSMLGSCMPBLOSFDDIAYIRKTLALD 1029
DB 1277 ---FTIRFOQFVDFDCCOAVMLIRKQTNLFNLSTLMIPLSGLPBELTISQDLKYVRDALQ 1333
OY 1030 KTEOBALSYFMKONNDAHGQWTTKMDMIFHTIKQ 1064
DB 1334 TTDAEATIFPTR-LIESLSIATKFNPFHNLAQ 1367

RESULT 15
AC O61194 PRELIMINARY; PRT: 1509 AA.
ID O61194
AD O61194
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE P170 phosphatidylinositol 3-kinase.
GN P1K3C2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10990;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96278746; PubMed=8663140;
RA Vrbasius J.V., Gultherme A., Czech M.P.;
RT "Mouse p170 is a novel phosphatidylinositol 3-kinase containing a C2
  domain.";
RL J. Biol. Chem. 271:13304-13307(1996).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; U55772; AAB07682.1; -.
DR HSSP; P21707; IBYN.
DR MGD; MGI:1203729; P1K3C2a.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001263; P1K3a.
DR InterPro; IPR002420; P1K3_C2.
DR InterPro; IPR000341; P1K3a_bind.
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00613; P1K3a; 1.
DR Pfam; PF00792; P1K3_C2; 1.
DR Pfam; PF00794; P1K3_rbd; 1.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00787; P13_P14_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00145; P1K3a; 1.
DR SMART; SM00146; P1K3C; 1.
DR SMART; SM00142; P1K3_C2; 1.
DR SMART; SM00144; P1K3_rbd; 1.
DR SMART; SM00312; P13_P14_kinase; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00915; P13_4_KINASE 1; 1.
DR PROSITE; PS00916; P13_4_KINASE 2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
DR PROSITE; PS0195; P13_4_KINASE_3; 1.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:37:15 ; Search time :8 Seconds
(without alignments)
2792.864 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709
Sequence: 1 MPRPSSGELWGHIMLPRI.....GWTTKMDWIFHTIKOHALNX 1069

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	5709	100.0	1068	P11A_BOVIN	P32871 bos taurus
2	5657	99.1	1068	P11A_HUMAN	P42336 homo sapien
3	5645	98.9	1068	P11A_MOUSE	P42337 mus musculu
4	1976.5	34.6	1044	P11D_HUMAN	O00329 homo sapien
5	1966	34.5	1070	P11B_RAT	O92110 rattus norv
6	1966	34.4	1070	P11B_HUMAN	P42338 homo sapien
7	1958	34.3	1043	P11D_MOUSE	O35904 mus musculu
8	1477.5	25.9	1102	P11G_MOUSE	O91597 mus musculu
9	1467	25.7	1101	P11G_HUMAN	P48736 homo sapien
10	1465.5	25.7	1102	P11G_PIG	O02697 sus scrofa
11	1370	24.0	1570	P3K1_DICDI	P54673 dictyostell
12	1262.5	22.1	1858	P3K2_DICDI	P54674 dictyostell
13	1109	19.4	1585	P3K3_DICDI	O94125 caenorhabd
14	1096	19.2	1146	AGEL_CAEEL	O94125 caenorhabd
15	1064.5	18.6	1634	PK3B_HUMAN	O00750 homo sapien
16	923	16.2	1506	PK3G_MOUSE	O00167 mus musculu
17	881.5	15.4	1448	PK3G_HUMAN	O75747 homo sapien
18	875	15.3	1505	PK3G_RAT	O70113 rattus norv
19	685	12.0	801	VP34_SCHPO	P50520 schizosacch
20	661.5	11.6	876	P3K4_YEAST	P54676 dictyostell
21	648.5	11.4	875	VP34_YEAST	P22543 saccharomyc
22	645	11.3	814	P3K1_SOYBN	P42347 glycine max
23	635	11.1	814	P3K1_ARATH	P42339 arabidopsi
24	629	11.0	812	P3K2_SOYBN	P42348 glycine max
25	602	10.5	1020	VP34_CANAL	O92213 candida alb
26	442	7.7	854	P14K_HUMAN	P42336 homo sapien
27	442	7.7	1900	ST14_YEAST	P39104 saccharomyc
28	297	5.2	1066	P1K1_YEAST	P39104 saccharomyc
29	268.5	4.7	1093	P14K_DICDI	P54677 dictyostell
30	242.5	4.2	851	YDBG_SCHPO	O10366 schizosacch
31	205.5	3.6	2787	TELI_YEAST	P38110 saccharomyc
32	202.5	3.5	2549	FRA1_RAT	P42346 rattus norv
33	196.5	3.4	2549	FRA1_HUMAN	P42345 homo sapien

34	195.5	3.4	2549	1	FRA1_MOUSE	O9119 mus musculu
35	192	3.4	4128	1	PRKD_HUMAN	P78527 homo sapien
36	184	3.2	2470	1	TOR1_YEAST	P3169 saccharomyc
37	180.5	3.2	4128	1	PRKD_MOUSE	P97313 mus musculu
38	173.5	3.0	2335	1	TOR1_SCHPO	O14356 schizosacch
39	172	3.0	2473	1	TOR2_YEAST	P32600 saccharomyc
40	166.5	2.9	2366	1	RAD3_SCHPO	O02099 schizosacch
41	157.5	2.8	2368	1	ESR1_YEAST	P38111 saccharomyc
42	143.5	2.5	3056	1	ATM_HUMAN	O13315 homo sapien
43	141	2.5	3066	1	ATM_MOUSE	O62388 mus musculu
44	140	2.5	2337	1	TOR2_SCHPO	O91782 schizosacch
45	138	2.4	4540	1	DYHC_PARTE	O27171 parametium

ALIGNMENTS

RESULT 1
P11A_BOVIN
ID: P11A_BOVIN STANDARD; PRT; 1068 AA.
AC P32871;
DT 01-OCT-1993 (Rel. 27, Last Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE alpha isoform (EC 2.7.1.153) (P13-kinase p110 subunit alpha) (Ptdins-
DE 3-kinase p110) (P13K).
GN P13KA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92354059; Pubmed=1322797;
RA Hiles I.D., Otau M., Volinia S., Fry M.J., Gout I., Dhand R.,
RA Panayotou G., Ruiz-Larrea F., Thompson A., Totty N.F., Hsuan J.J.,
RA Courtneidge S.A., Parker P.D., Waterfield M.D.;
RT "Phosphatidylinositol 3-kinase: structure and expression of the 110
RT kd catalytic subunit.";
RL Cell 70:419-429 (1992).
CC -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC -!- PREFERENCE FOR PTDINS(4,5)P2.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC triphosphate.
CC -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M93252; AAA30698.1; -
DR PIR: A43322; A43322.
DR InterPro: IPR000008; C2.
DR InterPro: IPR000403; P13_P14_kinase.
DR InterPro: IPR002420; P13K_C2.
DR InterPro: IPR003141; P13K_P85B.
DR InterPro: IPR000341; P13K_P85B.
DR InterPro: IPR001263; P13K_P85B.
DR InterPro: IPR001263; P13K_P85B.
DR Pfam: PF00454; P13_P14_kinase; 1.
DR Pfam: PF00792; P13K_C2; 1.
DR Pfam: PF02192; P13K_P85B; 1.
DR Pfam: PF00794; P13K_P85B; 1.

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DR Pfam; PF00613; P13Ka; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; P13K_C2; 1.
DR SMART; SM00143; P13K_P85B; 1.
DR SMART; SM00144; P13K_Cbd; 1.
DR SMART; SM00145; P13K; 1.
DR SMART; SM00146; P13K; 1.
DR PROSITE; PS5004; C2 DOMAIN_2; FALSE_NEG.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
DR Transferrase; Kinase; Multigene_family.
KM DOMAIN 319 428 C2 DOMAIN.
FT DOMAIN 797 1068 P13K/P14K.
SQ SEQUENCE 1068 AA; 124327 MW; C753DC2CF39FD0F0 CRC64;

Query March 100.0%; Score 5708; DB 1; Length 1068;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPPRPSGELWGIHMPRIIVECLIPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60
DB 1 MPPRPSGELWGIHMPRIIVECLIPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60
OY 61 LLDDESSYIFVSVTQEARREPFDETRRLCDLRFQPLKATIEVGNREKILNREIGFA 120
DB 61 LLDDESSYIFVSVTQEARREPFDETRRLCDLRFQPLKATIEVGNREKILNREIGFA 120
OY 121 IGMVVCEDMWKDEVDVDFRRNIIIVCKEAVDLRLNPHBRAMVYVYVNVSSPELPKH 180
DB 121 IGMVVCEDMWKDEVDVDFRRNIIIVCKEAVDLRLNPHBRAMVYVYVNVSSPELPKH 180
OY 121 IGMVVCEDMWKDEVDVDFRRNIIIVCKEAVDLRLNPHBRAMVYVYVNVSSPELPKH 180
DB 121 IGMVVCEDMWKDEVDVDFRRNIIIVCKEAVDLRLNPHBRAMVYVYVNVSSPELPKH 180
OY 181 IYNKLDKQIIVIVWIVSPNNDKQYTKIKINHDCVPEQVIAEAIKRTKRSMLSSSEQLK 240
DB 181 IYNKLDKQIIVIVWIVSPNNDKQYTKIKINHDCVPEQVIAEAIKRTKRSMLSSSEQLK 240
OY 241 LCVLEYQGRYILKVCCEDEYFLEKYPISQYKIRSCIMLGKRPNIMLAKSLVSQLPMD 300
DB 241 LCVLEYQGRYILKVCCEDEYFLEKYPISQYKIRSCIMLGKRPNIMLAKSLVSQLPMD 300
OY 301 CPTMVSRRISTATAPYNNGETSTSLWVINGALIKILCATYVWVNRIDDKIYVITGI 360
DB 301 CPTMVSRRISTATAPYNNGETSTSLWVINGALIKILCATYVWVNRIDDKIYVITGI 360
OY 361 YHGEPLCDNVNTQRPVCSNPRNEMLNVDIYIPDLPRARLCLISCSYKGRKAKSEHC 420
DB 361 YHGEPLCDNVNTQRPVCSNPRNEMLNVDIYIPDLPRARLCLISCSYKGRKAKSEHC 420
OY 421 PLAMGNINLFDYDTLTVSGKALNIMPVPHGLEDLNPIGVGVSNNKETPCLLELFPWF 480
DB 421 PLAMGNINLFDYDTLTVSGKALNIMPVPHGLEDLNPIGVGVSNNKETPCLLELFPWF 480
OY 481 SSVNFPNMSVTEEHANMSVSREAGFSYSHAGLSNRILADNLEFRENDEKQALICTRDL 540
DB 481 SSVNFPNMSVTEEHANMSVSREAGFSYSHAGLSNRILADNLEFRENDEKQALICTRDL 540
OY 541 SEITEQEKQFLSHSHHYCVTIEIPILKLLSVKMSRDEVAQVYCLVQWPIKEQANE 600
DB 541 SEITEQEKQFLSHSHHYCVTIEIPILKLLSVKMSRDEVAQVYCLVQWPIKEQANE 600
OY 601 LLDENVPDENVGFAVRCLKYLTDKLSQYLIQVQVILKQYQYDNLVRFLLKALTN 660
DB 601 LLDENVPDENVGFAVRCLKYLTDKLSQYLIQVQVILKQYQYDNLVRFLLKALTN 660
OY 661 QIGHFFHMLKSEHNKTVSQRFGLLESYCRACGMVKHINROVEAMEKILNLTDLK 720
DB 661 QIGHFFHMLKSEHNKTVSQRFGLLESYCRACGMVKHINROVEAMEKILNLTDLK 720
OY 721 QEKKDETKYOMKFLVEONRRPDMFALOGFLSPLNPAHOGNLRLSECRINSASKRPLM 780
DB 721 QEKKDETKYOMKFLVEONRRPDMFALOGFLSPLNPAHOGNLRLSECRINSASKRPLM 780
OY 781 LAMWNPDIWSELFPONNEIIFKNGDDLRODMTLQIIRIMENIWOQGLDRLMYPGCL 840
DB 781 LAMWNPDIWSELFPONNEIIFKNGDDLRODMTLQIIRIMENIWOQGLDRLMYPGCL 840

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DB 781 LAMWNPDIWSELFPONNEIIFKNGDDLRODMTLQIIRIMENIWOQGLDRLMYPGCL 840
OY 841 IGDCVGLIEVYNSHTIMQIOCKGGLKALQPSNHTLHOMLWLDKNGGELYDAIDFTPS 900
DB 841 IGDCVGLIEVYNSHTIMQIOCKGGLKALQPSNHTLHOMLWLDKNGGELYDAIDFTPS 900
OY 901 CAGYCAATFLLGIDRHNSINWYKDDGOLFHDGFLDHHKKKPKYKEERVVFLTDPF 960
DB 901 CAGYCAATFLLGIDRHNSINWYKDDGOLFHDGFLDHHKKKPKYKEERVVFLTDPF 960
OY 961 LIVISKAQECTRTREPERFOEMCYKAYLAIROHANLFINLFSMVLGSGMPELQSFDDIA 1020
DB 961 LIVISKAQECTRTREPERFOEMCYKAYLAIROHANLFINLFSMVLGSGMPELQSFDDIA 1020
OY 1021 YIRKTLALDTQEDALEYFMKQNDNAHNGWTTKMDMIFHTIKOHALN 1068
DB 1021 YIRKTLALDTQEDALEYFMKQNDNAHNGWTTKMDMIFHTIKOHALN 1068

RESULT 2
ID P13A_HUMAN STANDARD; PRT; 1068 AA.
AC PA2336; Q99762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE alpha isoform (EC 2.7.1.153) (P13-kinase p110 subunit alpha) (PtdIns-
DE 3-kinase p110) (P13K).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9529146; PubMed=7713498;
RA Volinia S., Hiles I., Ormondroyd E., Nizetic D., Antonacci R.,
RA Rocchi M., Waterfield M.;
RT "Molecular cloning, cDNA sequence, and chromosomal localization of
RT the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene."
RL Genomics 24:472-477(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97196568; PubMed=9043658;
RA Strdiyvan S.M., Aherm J., Controy R.R., Barnett S.F., Ledder L.M.,
RA Oliff A., Heimbrock D.C.;
RT "Cloning and mutagenesis of the p110 alpha subunit of human
RT phosphoinositide 3'-hydroxylase."
RL Bioorg. Med. Chem. 5:65-74(1997).
CC -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC PREFERENCE FOR PTDINS(4,5)P2.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-D-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidy1-D-myo-inositol 3,4,5-
CC triphosphate.
CC -!- SUBUNIT: HETEROIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC
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CC
CC -----
CC EMBL; Z29090; CAA82333.1; -
CC EMBL; U79143; AAB39753.1; -
CC PIR; I38110; I38110.
CC Genew; HGNC:8975; P13KA.

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DR   MIM, 171834; -.
DR   GO; GO:007048; P:oncogenesis; TAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_P14_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_tas_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_P14_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SMO0239; C2; 1.
DR   SMART; SMO0142; PI3K_C2; 1.
DR   SMART; SMO0143; PI3K_p85B; 1.
DR   SMART; SMO0144; PI3K_rbd; 1.
DR   SMART; SMO0145; PI3Ka; 1.
DR   SMART; SMO0146; PI3Kc; 1.
DR   PROSITE; PS00004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00815; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   KW      Transferrase; Kinase; Multigene family.
FT   DOMAIN          319       428             C2 DOMAIN.
FT           797       1068            PI3K/PIAK.
FT   CONFLICT        43         43             V -> I (IN REF. 2).
FT   CONFLICT        170        170            H -> N (IN REF. 2).
FT   CONFLICT        187        187            R -> K (IN REF. 2).
FT   CONFLICT        286        287            K -> ML (IN REF. 2).
FT   CONFLICT        332        332            R -> S (IN REF. 2).
FT   CONFLICT        346        346            L -> V (IN REF. 2).
FT   CONFLICT        723        723            R -> K (IN REF. 2).
FT   CONFLICT        751        751            L -> F (IN REF. 2).
FT   CONFLICT        767        767            K -> E (IN REF. 2).
FO   SEQUENCE        1068 AA;  124412 MW;  9E16BA7401A87B57 CRC64;

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Query Match	99.1%	Score 5657	DB 1	Length 1068
Best Local Similarity	98.9%	Pred. No. 0		
Matches 1056; Conservative	8	Mismatches	4	Indels 0; Gaps 0;

Qy	1	MPBRSSSELMGHIHMPRIILVCELLPNGMIVTLECEABEATITITIKHLPFKARXYPLHQ	60
Dp	1	MPBRSSSELMGHIHMPRIILVCELLPNGMIVTLECEABEATITIKHLPFKARXYPLHQ	60
Qy	61	LLOOBESSYIFWSVTOAEAREEFPFDETRRLCDLRLFOPLKATIEPVGNEBEKILNREIGPA	120
Dp	61	LLOOBESSYIFWSVTOAEAREEFPFDETRRLCDLRLFOPLKATIEPVGNEBEKILNREIGPA	120
Qy	121	IGMPVCEFDWVKDPEVODFRRNILNVCKEAYDLRLNSPHSRAMVYYPNVNESSPELEKH	180
Dp	121	IGMPVCEFDWVKDPEVODFRRNILNVCKEAYDLRLNSPHSRAMVYYPNVNESSPELEKH	180
Qy	181	IYNKLDKSOIIVLIMVIVISPNNDKOKXYTLKINHCVPSOVLAEALRKTRSMILSSBOLK	240
Dp	181	IYNKLDKSOIIVLIMVIVISPNNDKOKXYTLKINHCVPSOVLAEALRKTRSMILSSBOLK	240
Qy	241	LCVLEYGQXYLLKVCGCDEYFLEKXPLBSQYXYIRSCIMLGMSPNMLMAKESLYSOLPMD	300
Dp	241	LCVLEYGQXYLLKVCGCDEYFLEKXPLBSQYXYIRSCIMLGMSPNMLMAKESLYSOLPMD	300
Qy	301	CFPMPSYSRRISTATPYMNGESTSTSLMWINSALRIKILCATYUVVNIRIDIDKIYVRTGI	360
Dp	301	CFPMPSYSRRISTATPYMNGESTSTSLMWINSALRIKILCATYUVVNIRIDIDKIYVRTGI	360
Qy	361	YHGGEPLCDNNVORVPCSNPRMNEMLVYDIYPLPRAARLCISICSVKRGKAXEHC	420
Dp	361	YHGGEPLCDNNVORVPCSNPRMNEMLVYDIYPLPRAARLCISICSVKRGKAXEHC	420
Qy	421	PLANGINILFDYDTVLVSGKALNIMPVPHGEDILNIPIGVTSNPNKTEPCLLEBDFWF	480
Dp	421	PLANGINILFDYDTVLVSGKALNIMPVPHGEDILNIPIGVTSNPNKTEPCLLEBDFWF	480

QY	481	SSVKEPDMSVIEEHANNSVSRREAGFSYSHAGLSNRLARDNELENDXEQOLRAICTRDEPL	540
Db	481	SSVVEFPDMSVIEEHANNSVSRREAGFSYSHAGLSNRLARDNELENDXEQOLRAICTRDEPL	540
QY	541	SEITEOEKDFLMSHHYCVTTIPELLKLLSVKNMSRBEVAMCVLJVDMPRIKREQAME	600
Db	541	SEITEOEKDFLMSHHYCVTTIPELLKLLSVKNMSRBEVAMCVLJVDMPRIKREQAME	600
QY	601	LDDCNYBPBMVARGFAVRCLEKYLTDKLSQYLIQVQVLYKRYEQYDNLVRFELKKALTN	660
Db	601	LDDCNYBPBMVARGFAVRCLEKYLTDKLSQYLIQVQVLYKRYEQYDNLVRFELKKALTN	660
QY	661	ORIGHFFFWHLKSEMHKNTVSQRFGLLLESYCRACGMYPKHLNROVEAMEKLIINTDLIK	720
Db	661	ORIGHFFFWHLKSEMHKNTVSQRFGLLLESYCRACGMYPKHLNROVEAMEKLIINTDLIK	720
QY	721	OEKDETOXVOMKFLVEQMRPDPFDALOGFLSPINPAHOLGNPLBECRIMSSAKRPLM	780
Db	721	OEKDETOXVOMKFLVEQMRPDPFDALOGFLSPINPAHOLGNPLBECRIMSSAKRPLM	780
QY	781	LNWENPDIMSLELFPONNEIIFKNGDDELQOMLTLOIIRIMENIMONOGJDLRMLPYGCLS	840
Db	781	LNWENPDIMSLELFPONNEIIFKNGDDELQOMLTLOIIRIMENIMONOGJDLRMLPYGCLS	840
QY	841	IGDCVGLIEVVNRSHHTIMOIOCKGGLKGCALOPNSHTTHQWLKDKNKGSIYDAIDLFTRS	900
Db	841	IGDCVGLIEVVNRSHHTIMOIOCKGGLKGCALOPNSHTTHQWLKDKNKGSIYDAIDLFTRS	900
QY	901	CAGICVAFIILIGIDRHNNSIMVXDDGLFHIIDRGHFLDKKKKRGYRERYPFLTODF	960
Db	901	CAGICVAFIILIGIDRHNNSIMVXDDGLFHIIDRGHFLDKKKKRGYRERYPFLTODF	960
QY	961	LIVISKGAOECTREFERFQEMCYKATLAROHAHLFINLFSMMLSGSMBELQSFDDIA	1020
Db	961	LIVISKGAOECTREFERFQEMCYKATLAROHAHLFINLFSMMLSGSMBELQSFDDIA	1020
QY	1021	YIRKTLALDKTEOEALVEYFMKONDDAHHGWTYKMDIEMHTIKOHALN	1068
Db	1021	YIRKTLALDKTEOEALVEYFMKONDDAHHGWTYKMDIEMHTIKOHALN	1068

RESULT 3	PI1A_MOUSE	STANDARD:	PRT: 1068 AA.
ID	PI1A_MOUSE		
AC	P42337:		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,		
DE	alpha isoform (EC 2.7.1.153) (P13-kinase p110 subunit alpha) (Ptdins-		
DE	3-kinase p110) (PI3K).		
GN	PIK3CA.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c;		
RA	MEDLINE=94187738; PubMed=8139567;		
RA	Klippel A., Escobedo J.A., Hirano M., Williams L.T.;		
RT	"The interaction of small domains between the subunits of		
RT	phosphatidylinositol 3-kinase determines enzyme activity.";		
RL	Mol. Cell. Biol. 14:2675-2685(1994).		
CC	-1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A		
CC	PREFERENCE FOR PTDINS(4,5)P2.		
CC	-1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-		
CC	bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-		
CC	triphosphate.		
CC	-1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)		
CC	SUBUNIT.		
CC	-1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.		
CC	-1- SIMILARITY: Contains 1 C2 domain.		

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CC -----
DR EMBL; U03279; AAA1834.1; -.
DR MGI; MGI:1206581; P13Ka.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000403; P13_P14_kinase.
DR InterPro; IPR003420; P13K_C2.
DR InterPro; IPR003113; P13K_P85B.
DR InterPro; IPR000341; P13K_rae_bind.
DR InterPro; IPR01263; P13Ka.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF02192; P13K_C2; 1.
DR Pfam; PF00794; P13K_P85B; 1.
DR Pfam; PF00613; P13K_P85B; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; P13K_C2; 1.
DR SMART; SM00143; P13K_P85B; 1.
DR SMART; SM00144; P13K_P85B; 1.
DR SMART; SM00145; P13Ka; 1.
DR SMART; SM00146; P13Ka; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; FALSE_NEG.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
DR Transferrase; Kinase; Multigene family.
KW DOMAIN 319 428 C2 DOMAIN.
FT DOMAIN 797 1068 P13K/P14K.
SQ SEQUENCE 1068 AA; 124453 MW; 67F54FCF8747FE1C CRC64;

Query Match 98.9%; Score 5645; DB 1; Length 1068;
Beet Local Similarity 98.8%; Pred. No. 0;
Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MPPRSSGELMGHILMPRIIVLVECLPFGMITVTECLREATLITIKHELFKARKYPLHQ 60
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QY 61 LLQDESSYIFVSVTQEAEREERFDETRRLCDLRLFOPLKVIIEPVNGEEKILNREIGFA 120
DB 61 LLQDESSYIFVSVTQEAEREERFDETRRLCDLRLFOPLKVIIEPVNGEEKILNREIGFA 120
QY 121 IGMPCVCEPMKVDPEVQDFRRRIILNVCEAVDLRLNPHSRAMVVPYVNESSPELPEKH 180
DB 121 IGMPCVCEPMKVDPEVQDFRRRIILNVCEAVDLRLNPHSRAMVVPYVNESSPELPEKH 180
QY 181 IYNNKLDKQOIIIVIVIVIVISPNNDKQYTLKINHDCVPRQVIAEAIRKKTREMLSSSEQLK 240
DB 181 IYNNKLDKQOIIIVIVIVIVISPNNDKQYTLKINHDCVPRQVIAEAIRKKTREMLSSSEQLK 240
QY 241 LCVLEYQKQYILKYVCGDEYFLKXPYLSQYKXIRSCIMLGRPMNIMLAKESLYSQLEPMD 300
DB 241 LCVLEYQKQYILKYVCGDEYFLKXPYLSQYKXIRSCIMLGRPMNIMLAKESLYSQLEPMD 300
QY 301 CFYMSYSRRISTATAPYNGESTKSLWVINSALRIKILCAVYVAVNRDIDKIYVRGI 360
DB 301 CFYMSYSRRISTATAPYNGESTKSLWVINSALRIKILCAVYVAVNRDIDKIYVRGI 360
QY 361 YHGGPPLCDNVVTVQVPCSNPRMNMVLYDIYIPLPRAARCLISICVYGRKAKEBHC 420
DB 361 YHGGPPLCDNVVTVQVPCSNPRMNMVLYDIYIPLPRAARCLISICVYGRKAKEBHC 420
QY 421 PLAMGNINLFDYTDITLVSGKALNLMVPVHGLELIDLPNIGVTSNPNNKTEPCLELEPWF 480
DB 421 PLAMGNINLFDYTDITLVSGKALNLMVPVHGLELIDLPNIGVTSNPNNKTEPCLELEPWF 480

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QY 481 SSVYKPPDMSVIREHANWSYREAGFSYSHAGLSNRLARNDLRENDKQALAICTRPDL 540
DB 481 SSVYKPPDMSVIREHANWSYREAGFSYSHAGLSNRLARNDLRENDKQALAICTRPDL 540
QY 541 SETTEQKDFLMSHRIYCTTPEILKLLISVKNRSDEVAQWYCLVKMPPIKPEQAME 600
DB 541 SETTEQKDFLMSHRIYCTTPEILKLLISVKNRSDEVAQWYCLVKMPPIKPEQAME 600
QY 601 LLQCNYPDPWVRGPAVRCLEKYLTDDELKSOYLQLQVQLKYBEQYLDNLVRFLLKXALYN 660
DB 601 LLQCNYPDPWVRGPAVRCLEKYLTDDELKSOYLQLQVQLKYBEQYLDNLVRFLLKXALYN 660
QY 661 QRIHGFPEFMHLSKSENNKTYSORFGLLBSYCRACGYLKHILNROYAMEKILNLTDLK 720
DB 661 QRIHGFPEFMHLSKSENNKTYSORFGLLBSYCRACGYLKHILNROYAMEKILNLTDLK 720
QY 721 QEKKDEFTQYKMFVLEQMRPPFMDALQFLSPNPAHOGULRIECCIMSSAKRPLW 780
DB 721 QEKKDEFTQYKMFVLEQMRPPFMDALQFLSPNPAHOGULRIECCIMSSAKRPLW 780
QY 781 LNMENPDMSELLFONNEIIFKNGDDLRODMLTLQIRIMENIMONOGDLRLMYPGCLS 840
DB 781 LNMENPDMSELLFONNEIIFKNGDDLRODMLTLQIRIMENIMONOGDLRLMYPGCLS 840
QY 841 IGDVGLIEVVRNSHTIMQICKGGLKALQFNSHTLHQLKDKNKEIYDAAIDLETRS 900
DB 841 IGDVGLIEVVRNSHTIMQICKGGLKALQFNSHTLHQLKDKNKEIYDAAIDLETRS 900
QY 901 CAGYCVATFLIGIDRHNNSIMWKDQQLPHIDFGHLDHKKKFGYKRRVPPVLTQDF 960
DB 901 CAGYCVATFLIGIDRHNNSIMWKDQQLPHIDFGHLDHKKKFGYKRRVPPVLTQDF 960
QY 961 LIVSKAOCCTTRERFERQEMCYKAYLAIRQHANFIMLFSMILSGSMBELSPDIA 1020
DB 961 LIVSKAOCCTTRERFERQEMCYKAYLAIRQHANFIMLFSMILSGSMBELSPDIA 1020
QY 1021 YIRKTLADLTQEGALEYFMKQWMDAHGWTTKMDWIFHTIRQHALN 1068
DB 1021 YIRKTLADLTQEGALEYFMKQWMDAHGWTTKMDWIFHTIRQHALN 1068

RESULT 4
P1ID_HUMAN STANDARD; PRT; 1044 AA.
AC 000329; 015445;
ID 15-JUN-1998 (Rel. 36, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE delta isoform (EC 2.7.1.153) (P13-kinase p110 subunit delta) (PtdIns-
DE 3-kinase p110) (P13K) (p110delta).
GN P13CD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9727223; PubMed=9113989;
RA Vanhaesebroeck B.A.M., Welham M.J., Kotani K., Stein R., Warne P.H.,
RA Zvelebil M.J., Higashi K., Voljani S., Dowward J., Waterfield M.D.,
RA "p110delta, a novel phosphoinositide 3-kinase in leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4330-4335(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97382246; PubMed=9235916;
RA Chantry D., Vojtek A., Kashishian A., Holtzman D.A., Wood C.,
RA Gray P.W., Cooper J.A., Hoekstra M.F.,
RA "p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit
RA that associates with p85 and is expressed predominantly in
RA leukocytes.";
RL J. Biol. Chem. 272:19236-19241(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-ID-myo-inositol 4,5-

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RA Mulder H., Stenson Holat L., Degerman E.;
 RT "phosphatidylinositol-3 kinase and activation of phosphodiesterase 3B
 in adipocytes." 1998 to the EMBL/GenBank/DBJ databases.
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS(4,5)P2 WITH A
 CC REFERENCE FOR PTDINS(4,5)P2 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
 CC triphosphate.
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
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 CC
 CC -----
 CC EMBL; AJ012482; CAA10046.1; .
 CC InterPro; IPR000403; P13_P14_kinase.
 CC InterPro; IPR002420; P13K_C2.
 CC InterPro; IPR003113; P13K_P85B.
 CC InterPro; IPR000341; P13K_P85B_bind.
 CC InterPro; IPR001263; P13Ka.
 CC Pfam; PF00454; P13_P14_kinase; 1.
 CC Pfam; PF00792; P13K_C2; 1.
 CC Pfam; PF00794; P13K_P85B; 1.
 CC Pfam; PF00794; P13K_P85B; 1.
 CC Pfam; PF00613; P13Ka; 1.
 CC SMART; SM00142; P13K_C2; 1.
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 CC SMART; SM00146; P13K_P85B; 1.
 CC PROSITE; PS00915; P13_4_KINASE_1; 1.
 CC PROSITE; PS00916; P13_4_KINASE_2; 1.
 CC PROSITE; PS00917; P13_4_KINASE_3; 1.
 CC TRANSFERASE; Kinase; Multigene family.
 CC DOMAIN 800 1050 P13K/P14K.
 CC SEQUENCE 1070 AA; 122607 MW; 4E8EB233396A4D5 CRC64;
 SO
 Query Match 34.5%; Score 1968; DB 1; Length 1070;
 Best Local Similarity 39.6%; Pred. No. 1.6e-126;
 Matches 438; Conservative 199; Mismatches 380; Indels 90; Gaps 22;

QY 354 IYVRTGTYHGBEPLCDNVNFORVPCNSPR-WNEMLYDIYIPDLPRARLCLISCS----- 408
 DB 351 VHYRAGLPHGTETLCKTVSSSEISGKNDHIMNBOLEEDINDICOLPRARLCPFAVAVLDK 410
 QY 409 VKGRKGAK-----EHCPLANGININLEDYTTTLVSGKALUM-PVPIGLE 453
 DB 411 VKTKKSKRTINPSKYOTIRAKGVHVAWNVWDFPKQOLSGDVIHLSMSFPELE 470
 QY 454 DLNPIGVTSNP-----NKETPCLEDFWFSVVKFPMDSVIEEHANMS 499
 DB 471 EMLNFWTQVOTNPAENATLHFKPENKQPIYYPFD-----KIIEKAEIA 519
 QY 500 VSRBAGSYSHAGLSNLRARDNELRENDKEQLPACTRDELSITTEQKDFLWNSHRHYC- 558
 DB 520 SGDSA--NVSSRGKRLA-----VLKEILDRDPLSQLCENEMDLITLRQDCR 566
 QY 559 VTIPELLPKLLSYKXNSRDEVAQMYCLVWDVPPIKEQOMELLDCYPPPMVGRFVRC 618
 DB 567 ENFPQSIPKLLSTKNMKEDVAQOLQIWPRLPERALELDFENYPOQYREYAVGC 626
 QY 619 LEXLTDDKLSOYLLOLVOLVLYKYEOYLDNLVPLFKKALTNRIGHFPMHLKSEMHNK 678
 DB 627 L-RQMSDEELSYLLQVLOLVLYKYEPPFLDCAISRFLERALDNRIGQFLMHLRSEVHTP 685
 QY 679 TVSQRFGLLESYCRACGMVYLKHLNRQVEAMEKILNLTDLKOBKDETOQKVOQKFLVEQ 738
 DB 686 AVSIQFVILEAYCRGSGVGMKVLSSQVEALNLTCTINSILKUNAMKLBRAKGEAMHTC 745
 QY 739 MRPPDFMDALQGFSPINPAHQGNLFLBECRLMSAKRLMLNWMENPDIWSELFPONNE 798
 DB 746 LKQSAVREALSDLOSPINPCVILSELVEKCRVMSKMKPLMYVSRAEGEAV--G 801
 QY 799 IIFKNGDDLRQMDTLQILIRIMENIMONOGDLRMLPYGCLSIGDCVGLIEVANSHTIM 858
 DB 802 VIFKNGDDLRQMDTLQILIRIMENIMONOGDLRMLPYGCLSIGDCVGLIEVANSHTIA 861
 QY 859 QIQG-KGGLKALQPNSTHTLQWLNKDKNKEIYDAIDLTFRSCAGYCVATFIIIGDRH 917
 DB 862 DIQNSSNVATAAFAFNNDALNLMLKEVNSGDDLRDAIEFTLSCAGYCVASYVLIGDRH 921
 QY 918 NSNINMTDQGLPFIIDGHLGDKKKKFKYKREVPVLTQDPLIYVSKAQOECTKREF 977
 DB 922 SDNINMTVKTQGLPFIIDGHLGDKKKKFKYKREVPVLTQDPLIYVSKAQOECTKREF 979
 QY 978 ERPOEMCYKAVLATIRHANLPINLFSMWLGSMPDELQSPDIAYIRKTLADTKTEQALE 1037
 DB 980 GRFQCCEDAVLIRRHGNLFTILFALMTAGLDELISVADIOYLKDSLALGKSEERALK 1039
 QY 1038 YFMKQNDIAHGGWTTQMDWIFHTIKQ 1064
 DB 1040 QFKQKPFDEALRESWTTKVNMMADHTVRK 1066

RESULT 6
 P11B HUMAN STANDARD; PRT, 1070 AA.
 ID P11B HUMAN
 AC P42338;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
 DE isoform (BC 2.7.1.153) (P13-kinase p110 subunit beta) (ptdins-3-kinase
 DE p110) (P13K) (P13Kbeta).
 GN P13KB.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94067128; PubMed=8246984;
 RA Hu P., Mondino A., Skolnik E.Y., Schlessinger J.;
 RT "Cloning of a novel, ubiquitously expressed human

DB 974 GNTKFGRCFQCEADAVLILRRHGNLFITLFAIMLTAGLPELTSVXDIOYLKDSIALGKS 1033
 QY 1032 EORALEYFMKONDAHHGGWTMDMIFPHIKQ 1064
 DB 1034 EEBALKQFKQKDEALRESWTYVWMAHTVRK 1066

RESULT 7
 P11D_MOUSE STANDARD; PRT: 1043 AA.

ID P11D_MOUSE
 AC 035904;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
 delta isoform (EC 2.7.1.153) (P13-kinase p110 subunit delta) (PtdIns-
 3-kinase p110) (P13K) (p110delta).
 GN PI3CD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=97382246; PubMed=9235916;
 RA Chanzy D., Vojtek A., Kaehlihan A., Holtzman D.A., Wood C.,
 Gray P.W., Cooper J.A., Hoeberlin M.F.;
 RT "p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit
 that associates with p85 and is expressed predominantly in
 leukocytes.";
 RT J. Biol. Chem. 272.19236-19241(1997).
 RL J. Biol. Chem. 272.19236-19241(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
 CC triphosphate.
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
 CC -----
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 CC -----
 CC EMBL, U86587; AAC25676.1; -
 CC DR PIR, T43502; T43502.
 CC DR MGI, MGI:1098211; P13cd.
 CC DR InterPro: IPR000403; P13_P14_kinase.
 CC DR InterPro: IPR002420; P13_C2.
 CC DR InterPro: IPR003113; P13K_P85B.
 CC DR InterPro: IPR000341; P13K_P85B.
 CC DR InterPro: IPR001263; P13Ka.
 CC DR Pfam, PF00454; P13_P14_kinase, 1.
 CC DR Pfam, PF00792; P13K_C2, 1.
 CC DR Pfam, PF02192; P13K_P85B, 1.
 CC DR Pfam, PF00794; P13K_P85B, 1.
 CC DR Pfam, PF0613; P13Ka, 1.
 CC DR SMART, SM00142; P13K_C2, 1.
 CC DR SMART, SM00143; P13K_P85B, 1.
 CC DR SMART, SM00144; P13K_P85B, 1.
 CC DR SMART, SM00145; P13Ka, 1.
 CC DR SMART, SM00146; P13K_C2, 1.
 CC DR PROSITE, PS000915; P13_4_KINASE_1, 1.
 CC DR PROSITE, PS000916; P13_4_KINASE_2, 1.
 CC DR PROSITE, PS00290; P13_4_KINASE_3, 1.
 CC DR Transferrase, Kinase; Multigene family.
 CC KW TRANSFERRASE; KINASE; MULTIGENE FAMILY.
 CC FT DOMAIN 775 1028 P13K/P14K.

SEQ SEQUENCE 1043 AA; 119647 MW; A998F9E092CA31D CRC64;
 Query Match 34.3%; Score 1958; DB 1; Length 1043;
 Best Local Similarity 39.7%; Pred. No. 7, 6e-126;
 Matches 429; Conservative 187; Mismatches 391; Indels 74; Gaps 19;

QY 16 MPP-----RIIVECLLPNGMVTLECLREATLITIKHELFKEARKYPLHQ 60
 DB 1 MPPGVDCPMEFMTKESQSVVDPLFLPTGVNLNFPVSRNANLSTIKOVLMMHRAQVEPLRH 60
 QY 61 LLODESSYIFVSTQPAERESEFFDETTRLCDLRFQPLKVTPEVGNREKELNBEIGA 120
 DB 61 MLSDPEAYVFTCNQVABEQELEDQBRRLCDIOPLFLVRLVARBGRVKYKLINSISLL 120
 QY 121 IGMPEVEFPMVKDPEVQDRRNILNVCKEAVDLRLDINSHSAMVYPPNVSSPELPK- 179
 DB 121 IAKGHEFSLRDPVENDFRTKROFCBAAHROQLGWEVWLOYSFLOLEPSANGMRA 180
 QY 180 ---HIYNKLDKQGLIVIVIVYSPPNDKOKYTLKINHDCVPEQVIAEAIRKKTSMILSS 236
 DB 181 GILRVENR-----ALVNVKFESESESFTFOVSTKMPALAMCALRK-----A 225
 QY 237 EQLKLCVLEYQKYLKVCOCDEYFLEKYPLSQYKTRSCIMGRNPMIMLAKESLYSQ 296
 DB 226 TVPRQPLVEQPEEYALQVNGRHELYGNVPLCHFYICSLHSGLTPLHVMHSSSILM 285
 QY 297 LPMDCFTMPSYRRISTATPPYNNGETSTSLWYNALIKILCATVYVANNIRIDIKIYV 356
 DB 286 RDEQSNPAPQVQPRKAPPEIPAKKPSVSLWLEQPFSELEGRKVNDE--MKLVY 343
 QY 357 RTGIYHGGELCGNNVNTQRY-PCSNPRMWEMLNYDIYIPDLPRARLCLSTICSV----- 409
 DB 344 QAGLPHENEMLCKTVSSSEVNVCSSEPVWKORLEFDLSVCDLPRMARLCEALYVVEKAKK 403
 QY 410 --KGRKAKEHNPPLAWGNINLFDYDTLVSGKALNLMP-VPHGLEDLNLPIGVTGSPN 466
 DB 404 ARSTKKSXKADCPAANMLLFDYKQDLKTGRCCLYMWSPVDEKELLNPAGYVAGNP 463
 QY 467 NKETPCELEPDMSSVYKPPDMSVIEBANMSVSEAGSYAHAGLSNLANDELREN 526
 DB 464 NTESSA-----ALVYLPK--VAPHPVYPALEKILELRHGRGRIT-EEEL--- 508
 QY 527 DKQDLRAICTRDLPELSELTQEQKDFLMGSHRYCVT-IPEILPKLLSVKMSRDEVAOMYC 585
 DB 509 ---QRLLEBRGGELYEHEKDLVWKRHVEQHEPEALARLLVTKMKHDEVAOMLY 565
 QY 586 LVKQMPRIKEQAMELDCYVDPMPVGFVAVRCLKLYLTDDKLSQYLQLOVYLKYEQYL 645
 DB 566 LDCGMPPELPVLSALDELDDSPDCYVGSFAIKSLRK-LTDDLEFQYLLQLOVYLKYESYL 624
 QY 646 DNILVRLKKAALTNQKIGHFFFWHLKSEMNKTVSGRGLLESYCRAGCMYLYKHLNQ 705
 DB 625 DCELTGFLGRLANRKIGHFLFWHLHSEMHVPSVALRFGLTIMAYCRGSTHMKVLMKQ 684
 QY 706 VEAMEKILNLIDIAKOEKDKDTQVOKKFLVEQ--MRBPDEMDALQGFPLNPAPHQNL 764
 DB 665 GEAUSKLAALNDPVKVSQ-KTKPKQTKEMMHMKQGETWALSHIOSPLDSPGLLEEV 743
 QY 765 RLEECRIMSAPRLMWENPDIMSBLFPONNIIIFKNGDLPQDMTLQIITIMENIW 824
 DB 744 CVEQCTFSDSKMKPLMWVSESEAGS---GNVGIIIFKNGDLPQDMTLQIIMQIMQVLM 800
 QY 825 QNQGIDLEMLPYGLSTIDCVGLIEVYRANSTIQIQ-CGKLGALQOFNHTJHOMK 883
 DB 801 KQEGDLTAMTPYGCILPTGDRGTGLEVLHSTINTIQLNKSNNMATAAFNDALINMKS 860
 QY 884 KKKGRIYAAIDLPFRSCAGYCVATFPIGIDRHSNINMVADQQLFIIDGFLDHKKK 943
 DB 861 KNPGBALRALIEFTLSAGYCVATFVIGIGRHSNDINMIESQGLFIIDGFLHGNKXT 920
 QY 944 KFGYREKRVFVLTQDFLIVISKGAOECTKTRFERPQEMCYKAYLAIRQANLEFINFS 1003
 DB 921 KFGIKREKRVFVLTQDFLIVIQG--KTNSEKKEFRFGYCEBAYTILRRGLFLHIFA 978

QY 1004 MMLGSMPELQSFDDIAYIRKTLALDTEQEALEYFNKONNDHGGWTKMDIFHTIK 1063
 Db 979 LMAAGHPELSCSKDIOYLKDSIALGKTEBEALKHFRVKNFNEALRESWTKRWMLAINVS 1038
 QY 1064 Q 1064
 Db 1039 K 1039

RESULT 8
 P13G_MOUSE STANDARD; PRT: 1102 AA.

ID P13G_MOUSE STANDARD; PRT: 1102 AA.
 AC 09UG7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
 DE gamma isoform (EC 2.7.1.153) (P13-kinase p110 subunit gamma) (Ptdins-
 DE 3-kinase p110) (P13K) (P13Kgamma).
 GN P13KCG OR P13KGI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirsch E.;
 RT "Murine P13Kgamma: cDNA cloning and gene structure description";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wymann M.P., Hirsch E.;
 RT "Murine G protein-coupled phosphoinositide 3-kinase gamma cDNA and
 RT genomic organisation.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
 CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2) (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol 4,5-
 CC bisphosphate = ADP + 1-phosphatidy1-1D-myo-inositol 3,4,5-
 CC triphosphate.
 CC -1- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
 CC G PROTEINS (BY SIMILARITY). MORMANNIN SENSITIVE IN NM RANGE.
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
 CC -1- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
 CC SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
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 CC
 DR EMBL; AJ249413; CAB89851.1; -;
 DR EMBL; AJ249414; CAB89851.1; JOINED.
 DR EMBL; AJ249415; CAB89851.1; JOINED.
 DR EMBL; AJ249416; CAB89851.1; JOINED.
 DR EMBL; AJ249417; CAB89851.1; JOINED.
 DR EMBL; AJ249418; CAB89851.1; JOINED.
 DR EMBL; AJ249419; CAB89851.1; JOINED.
 DR EMBL; AJ249420; CAB89851.1; JOINED.
 DR EMBL; AJ249420; CAB89851.1; JOINED.
 DR EMBL; AJ249420; CAB89851.1; JOINED.
 DR MGD; MGI:1353576; P13KCG.
 DR InterPro; IPR000403; P13_P14_kinase.
 DR InterPro; IPR002420; P13K_C2.
 DR InterPro; IPR000341; P13K_rae_bind.
 DR InterPro; IPR001263; P13Ka.
 DR Pfam; PF00454; P13_P14_kinase; 1.
 DR Pfam; PF00792; P13K_C2; 1.
 DR Pfam; PF00794; P13K_tbd; 1.

DR Pfam; PF00613; P13Ka; 1.
 DR SMART; SMO0142; P13K_C2; 1.
 DR SMART; SMO0144; P13K_tbd; 1.
 DR SMART; SMO0145; P13Ka; 1.
 DR SMART; SMO0146; P13KCG; 1.
 DR PROSITE; PS00915; P13_4_KINASE_1; 1.
 DR PROSITE; PS00916; P13_4_KINASE_2; 1.
 DR PROSITE; PS50290; P13_4_KINASE_3; 1.
 DR Transferrase; Kinase; Multigene family.
 FT DOMAIN 18 1073 POLY-ARG.
 FT 828 1073 P13K/P14K.
 SQ SEQUENCE 1102 AA; 126361 MW; 39594CFDD0C21D57 CRC64;

Query Match 25.9%; Score 1477.5; DB 1; Length 1102;
 Best Local Similarity 33.3%; Pred. No. 5,5e-93;
 Matches 380; Conservative 199; Mismatches 412; Indels 149; Gaps 37;

QY 1 MPFRSSGELIWIHMPRIIVCELLPENGIVT-----LECLREATLITTHIEFLKFA 53
 Db 23 MKPRSAAGSLSSWELIP---IEFVLPTSQRISKPTETALHVAHGQNVQMKAWLRA 78
 QY 54 RKYPV-----HOLLQDESSYIFVSVYQAEAREFPETRLCDRLFPPLK-----V 101
 Db 79 LETSVAAEFYHRLGPQFLLYOKGQWEIYDRYVQVTLDLHYWKLMHKSPGOIHVV 138
 QY 102 IEPVGRREKILNREIGFAIGMPVCEFDWYKQDEVDPRNINLVCKEAYDLRLNSPHS 161
 Db 133 QRHVPSBEETLAPKQULTSLGIVYDTISVHDELEFTRRLVTPRMAEVAGDAK---- 194
 QY 162 RANVYVPVNVSSPELPHKIIYNKLDKQIIVVIWIVSPNNDKQYTLKINHCVBEQVI 221
 Db 195 --LYAHMPWTSKP--LPDYLSKIANNCIPIVT-----HRCGTSQTIKVSADDTGTL 245
 QY 222 AEAIK--KTRSNLSSBQKLCVLEQGYIKVCGCBYFLKPLSGYKTRSCIML 279
 Db 246 QSEFTTKAKKSLMNI PES-----QSEODFVLRVCGREYIVGETPLKNGFQVROQLKN 299
 QY 280 GRNPNML-----MAKESLYQLPW--DCEFTMPSYRRISTATPYMNGE---TSTKSL 327
 Db 300 GDEIHLVDTPPRALDEVRKEWPLVDCTGVTHQELT-----IHGDHSSVYTVSL 354
 QY 328 WINSALRIKILCATYVNVNIRDID-----KIYRTGIYHGSEPLCDNVNTPRV 377
 Db 355 WDCDRFRVK-----IRGIDIPVLPNTDLVFPANIQHQOVLQCGRTSPKPF 404
 QY 378 CSNPRNENLVNDIYIPDLPRARLCLST--CSVKRKAKEHCP-----LAWG 425
 Db 405 ABEVLNVWLEFGIKIKIDLPKGLNLNLIQYCCKTPSLSSKASAEFGSESKGKAOILYV 464
 QY 426 NINLPYDTIVSGKALMLMPVPHGLEP--LNPIGVT--GSPNKE--TPCLELEFDWPS 481
 Db 465 NLLILHRLHRLRGDYLHWMQISGAKEGSEFNADKLTSATPDKNSGISILLDNYC 524
 QY 482 SVKFPDMSVIEBHANSVSRGAFSPYSHAGLSNRLARDNELRENDKEQRLAICTRDPUS 541
 Db 525 HPALCPKHPPTPEBEDRV-----RAEMPNQRL-----KQLEALIAIDPLN 565
 QY 542 EITQEKDPLWGRHRYCVTIPILLPLLLSVKNSDEVAQMYCL-----VKDWPPIKEB 596
 Db 566 PLTAEDKELIWMFRYSLSLGHPRAYPLPFSYVKGQOEIVAKTYOLAREIEWQSALDVG 625
 QY 597 QAMELLDCNVPDMWGFVRCLEKLTDDKLSOYLIOIYOVLKYQOYLDNLVRLKK 656
 Db 626 LTMQLDNCNPSDENVAIVQKLES--LEDDDVLYHLLQVQAVKFPYHDSALARFLLR 684
 QY 657 ALTNQRIGHFFMHLKSEM--HNKTVSQRFGLLESYCRAGC--MYLGLHROVEAMEKLI 714
 Db 685 GARNRKILGHFLWFLRSEIQAQRHYQGRFAVILEALRCCGRAMIQDFQGVHVEIMLK 744
 QY 715 LT-DI--LKQEKDELQKY--QMKFLVEQMKRPDEFDALQGLFSLPNPHQGNRLLEC 769
 Db 745 VVIDIKSLAEKYDVSSQVISOIKQLESLQNSNLPES--FRVPYDPLKAGTLVIERC 801

QY 770 RIMSSAKRPLMLNME--NPDIIMSELLFQNN---11FKNGDDLRQDMLTIQIIRIMENTW 824
DB 802 KWMAKKKKPLMLFEKADPVLVS-----NETIGILFKHGDDBRQDMLIIQIIRIMESIW 855
QY 825 QNQGDLRLMPLPGCLISGDCVGLIEVVRNSHTIMQI-QCKGSLKGLAQENSHLHQLKD 883
DB 856 ETESLIDLCPLPGCISITGDKIMIEYKQDPTTIAQIQOSTVGNTGA--FQDEVLNHMLKE 913
QY 884 KNR-GEYDAIDLFTRSGAGYCAVATPILGIDRHNNSINWKKDGLFHIDFGHLDHKK 942
DB 914 KCIIEEFQAAVERFVYSCAGYCAVATPVLGIDRHNNSINWKKDGLFHIDFGHLDHKK 973
QY 943 KKEGYKERVVFLVTDPLVIVISKAGQECTKREEFERFQENCKAYIATQHANLFLNLF 1002
DB 974 SFLGINERVPVLTPODLFVWSSGKKTSP--HFQKFOVCVAYALDRHTLTLTLF 1031
QY 1003 SMMLGSMPELQSDIDAIYRKTALDKTQEDALEYEMKQNDHNGMTTKMDWIFHTI 1062
DB 1032 SMMLMGMPLQSLKEDIEYIRDAITVGSSEDAKKYFLDQIEVGRDKGWTIVQFWPLHLV 1091

RESULT 9
ID P11G HUMAN STANDARD; PRT: 1101 AA.
AC P48736;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphatidyl-inositol-4,5-bisphosphate 3-kinase catalytic subunit,
gamma isoform (EC 2.7.1.153) (P13-kinase p110 subunit gamma) (Ptdins-
3-kinase p110) (PI3K) (PI3Kgamma).
GN PIK3CG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350661; PubMed=7624799;
RA Stoyanov B., Volinia S., Hanck T., Rubio I., Loubchenkov M.,
RA Malek D., Stoyanova S., Vannesebroeck B., Dhand R., Nuenberg B.,
RA Giersechik P., Seedorf K., Hsuan J.-J., Waterfield M.D., Metzker R.;
RT "Cloning and characterization of a G protein-activated human
RT phosphoinositide-3 kinase".
RT Science 269:690-693(1995).
RN [2]
RP REVISIONS.
RA Waterfield M.D.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBS databases.
CC -! FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC PTINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC -! CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC triphosphate.
CC -! ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC G PROTEINS.
CC -! PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -! SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC SUBUNIT (BY SIMILARITY).
CC -! TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.
CC -! SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
CC -----
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CC -----
CC EMBL; X83368; CAA58284.1; -.
DR PDB; 1EBY; 17-NOV-00.
DR PDB; 1EBZ; 17-NOV-00.

DR Genew: HGNC:8978; PIK3CG.
DR MIM; 601232; -.
DR GO; GO:0004429; F.1-phosphatidyl-inositol 3-kinase; TAS.
DR GO; GO:0007186; P;G-protein coupled receptor protein signalin...; TAS.
DR InterPro; IPR000403; P13_P14_kinase.
DR InterPro; IPR002420; PI3K_C2.
DR InterPro; IPR000341; PI3K_tas_bind.
DR InterPro; IPR001263; PI3Ka.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00792; PI3K_C2; 1.
DR Pfam; PF00794; PI3K_tbd; 1.
DR Pfam; PF00613; PI3Ka; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00144; PI3K_tbd; 1.
DR SMART; SM00145; PI3Ka; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
DR TRANSFERASE; Kinase; Multigene family; 3D-structure.
KM DOMAIN 18 22 POLY-ARG.
FT DOMAIN 827 1072 PI3K/PI4K.
SO SEQUENCE 1101 AA; 126410 MW; 266BA6495C8A39E CRC64.

Query Match 25.7%; Score 1467; DB 1; Length 1101;
Best Local Similarity 35.3%; Pred. No. 2,9e-92;
Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;

QY 107 NREKILNREIGRAIGMPVCEFDVMDPEVODFRRLINLVCKEAVLDRLNSHRSAMY 166
DB 143 SEESQARQQLTALIGVDVDSNVHDELEFRRGLVTPRMAEVSARD-----PKLYA 196
QY 167 YPPVNSSPPLPKHIVNKLDKQIIVIVIVSPNNDKQYTLKINDCVPEQVIAAIR 226
DB 197 MHPWVTSKRP-LPEYLMKRIANNCIFVLT-----HNSITQITKVSDDITPGALIOSFT 249
QY 227 K--KTRGMLSSBQDLKLVLEYGKYLKVCQDEYFLKRYPLSQYKYSICMLGMPN 284
DB 250 KMAKKKSLMDIPES-----QSEDDFVLRVCGRDEYLVGSETPIKNFWVHCLCKNGEIH 303
QY 285 LML-----MAKESLYSQLPM--DCFTMPSYSRRISTATPYNGE-----TSTSLVYINS 332
DB 304 VLDTTPDPPALDEVRKEMWPLVDCTGVTHGEQLT-----IHGKHESVFTSLWLCDDR 358
QY 333 ALRIKILCATVNVNINIDID-----KIYRTGIYHGEPLCNVNTQVRPCSNPR 382
DB 359 KFRVYK-----IGIDIPVLPRNTDLTVFEVANIQHGQVLCQRTSPKFTPEVL 408
QY 383 MNEWLNVDIYIPDLPRARLCLTICSVK---GRGKAKEHCPPLAMGNINLFDYDTLV- 437
DB 409 WNWMLERFQIKKIDPKGALNLQIYCGKAPALSKASAEPSSESCKGVRLLYVNNLLI 468
QY 438 -----SGKMLNLMPVPHGLEP--LINPIGVV--GSNPKE--TPCLELEFMDSSVYKF 486
DB 469 DHRFLLRGGEVYVLMHWQISGGEQDSFNADKLTSAITPDKENSMSISILDNVCHPIAL 528
QY 487 PDMSVTEHNAWVSREAGFSYSHAGLSNRLARQNEIARENKEDOLRAICTRDPSEITEQ 546
DB 529 PKHQPTPPEBGRV-----RAEMPRQQL-----KQLEAIITADPLNPLTAE 569
QY 547 EKDPLMSRHVYCVTLPEILPKLLSVKNSDEVAQWCL-----VKDMPRIKEQAMEL 601
DB 570 DEELMHRRYFSLKHPKAYPKLFSSVKKVGOEIVAKYQGLARREVMQSLADVLNQ 629
QY 602 LDCNTPDPMVGFAYRCLKLTLDKLSQYLIQIVQVLYKTYQYLDNLVLEFLKALYNQ 661
DB 630 LDCNNSDENAVAIAYQKES--LEDDDVHLYILQVQAKFPYHDSALARFLKGLKLNK 688
QY 662 RIGHFPPHMLKSEM-HNKTVSQRFGLLLESYRACAGMVLKH-LNRQVAMEKLIVLT-DI 718
DB 689 RIGHFLFLFRLREIAQSHYQORFAVILAEVLRGGTAMLDHFTQOVQVTEHQLQVTTDI 748
QY 719 --LKQEKDEIQKV--QKKFLVEQMRBPPDMALGCLFSPLNPAHQNLRLBECRIMSS 774

```

Db      749 KSLSAEYDVSSQVLSQKLEKLENSQLPES---FRVYDPELKGALAIKCKVMAS 805
QY      775 AKRPLMLNME--NPDISELLPONNE---IIFKNGDDLRODMELTIQIRIMENIMQNGE 829
Db      806 KKKPMLNLEPCAPPLALS-----NRTIGIIFKGGDLRODMILIQIRIMESWESESL 859
QY      830 DLMLPYGLSISDCVGLIVVNSHTIMQI--CKGGLKALQFNSHTLHOMLKDN-KG 887
Db      860 DLCLLYGCIISTDKIGMEIVDATTIAKIQOSTVANGTA--FKDEVLNHMLKEKSPTE 917
QY      888 EIDDAIMDLFTRSCAGCVATFLIGDRNNSNMVWDQQLPHIDGHLIDHKKKKFGY 947
Db      918 EKFQAAVERPVYSCAGCVATFVLGIGDRNDNMIMETETGNLPHIDGHLIGYKSFGLI 977
QY      948 KREERVFVLTDPLFIYVSKAOECTKREPERFOEMCYKAYLAIRQANLFIILFSMMLG 1007
Db      978 MKRERVFVLTPDLFLFWNGTSGKKTSP--HFQKQDIDCVKAYLALRHHTNLIILFSMMLM 1035
QY      1008 SGNPELQSFDDIAYIRKTLALDXTEDALRYFKOMNDAHGGMWTTGMWIFPTI 1062
Db      1036 TGMPLQTSKEDIYIRDALTVGKNEBDKXKYFLDQLEVCRCDKGMVQFVNFHLIV 1090

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RESULT 10
P11G_P1G STANDARD; PRT; 1102 AA.
AC 002697;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
D3 Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
D3 gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (Ptdins-
D3 3-kinase p110) (PI3K) (P120-PI3K).
GN PI3KCG.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Neutrophils;
RX MEDLINE=97248491; PubMed=9094719;
RA Stephens L.R., Egidio A., Erdjument-Bromage H., Lui M., Cooke F.,
RA Coadwell J.J., Strick A.S., Thelen M., Cadwallader K., Tempst P.,
RA Hawkins P.T.;
RT "The G beta gamma sensitivity of a PI3K is dependent upon a tightly
RT associated adaptor, p101."
RT Cell 89:105-114 (1997).
RL [2]
RP REVISIONS.
RA Stephens L.R.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-D-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidy1-D-myo-inositol 3,4,5-
CC triphosphate.
CC -!- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC PROTEINS.
CC -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL; Y10743; CAAT1731.1; -.
DR PDB; 1E7U; 01-DEC-00.
DR PDB; 1E8X; 01-OCT-02.
DR InterPro; IPR000403; PI3_P14_kinase.
DR InterPro; IPR002420; PI3K_C2.
DR InterPro; IPR000341; PI3K_res_bind.
DR InterPro; IPR001263; PI3K.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR Pfam; PF00792; PI3K_C2; 1.
DR Pfam; PF00794; PI3K_Ibnd; 1.
DR Pfam; PF00613; PI3K_A; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00144; PI3K_Ibnd; 1.
DR SMART; SM00145; PI3K_A; 1.
DR SMART; SM00146; PI3K_C1; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR TRANSFERASE; Kinase; Multigene family; 3D-structure.
FT DOMAIN 17 22 POLY-ARG.
FT DOMAIN 828 1073 PI3K/PI4K.
SQ SEQUENCE 1102 AA; 126657 MW; 9E7D4211FD626DFC CRC64;

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Query Match 25.7%; Score 1465.5; DB 1; Length 1102;
Best Local Similarity 33.5%; Pred. No. 3.7e-92;
Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

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QY 1 MPRPSSGGLWGIHLMPRIILVECLLPNGNIYT-----LBCLRATLITTYHLEFKEA 53
Db 23 MKRSTRAASLSSMELIP-----IEFVLPTQQRNKTPEATALHVAHGANEOMKAWQLRA 78
QY 54 RKXPL-----HOLDQESSYIFVSVQGEAREBFEPETRLDRLRQFP-----LKYI 102
Db 79 LRTSVADRYHRRGPHLILLYQKGGQWYIYDKYGVVQLDCLRYKWLHRSFGQIHV 138
QY 103 EPVGNNEEKI-INREIGFAGIPVCEFDVWKDPEVDFFRNILMVCKEAVDLADLSPHS 161
Db 139 QHRAPSEETLAPQRQNALIGVDVDSVNHDELEFTRRLVTPRMAVAGD----- 192
QY 162 RANVTYPPVNESPELPHKIIYNKLDKQIIVIIWIVTSFNNDKOKYTKINHDCVPEQVI 221
Db 193 PKLYAHHPWTSKP-LPEYLLKKTNNCVFIYI-----HRSITSGTIRVASDDTPTGL 245
QY 222 AEHLRK--KTRSMLLSSBDKLCVLEYGKYLKVGCGDEYFLKRPYQYKIRSCIML 279
Db 246 QSEFTYMARKKSLMDIPES-----QNERDPVLRVCGRDEYLVGETPIKRFQVWRQCLKN 299
QY 280 GRMPEMLL-----MAKESLYQLPM--DCEFTMPSYSRRISTATPYMNGE---TSTKSL 327
Db 300 GEIHLVLDTPDPALDEVRKEKEMPLVDCTGTGVTGHEQLT-----IHKDHESVPTVSL 354
QY 328 WINSALRIKILCATYVNVNIRIDID-----KIYVGTGYHGGELPLCDNVNTQRPV 377
Db 355 WCCDKRFKRVK-----INGIDIPVLPRTADLVFEVIANIYGOOVLQCRRTSPKPF 404
QY 378 CSNPRNENLNDIYIPDLPRAAKLCLST-C-----SVKRRKA-----KEBCHLAG 425
Db 405 TEEVLNFWLLEFSIKIDLPKQALLNLQYCGKAPRLSCKTSAEMSPESKKAQALLVY 464
QY 426 NINLPDYDTLVSGKALNLMPVPHGLSD--LLNPIGVYG--SNPNKE--TPCLELEFDWFS 481
Db 465 NLLILDRHLRHLNGEVLHLMQLSKGEGQSFNADKLTSTRNPDKENSMSISILLDNYC 524
QY 482 SVKRPDMSVIEEHNWVSYSREAGFSYSHAGLSNRLARDNELRENDKEQLAICTRDPIS 541
Db 525 HPIALPKRPTDPREGDRV-----BAEMNQRL-----KQLKALIIATDPPLN 565
QY 542 ELTDEKDLVHNRHNYCVIPIRLKLLSYKWSNRDVAQWYCL-----VWDMPRIKPE 596
Db 566 PLTAEDEKELLMFRRYBSLNDPRAVYPLPSVYWGQEEIYAKYQYLLAKREVDQSLADVG 625
QY 597 QAMELLDCNVPDPMVRGFAVRCLERYLTDDKLSQYLIQLVQYLKYEQYLDNLVRFLLKX 656

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Db 626 LTMQLDNCNSDENBVAIAVOKLES-LEDDVLAHYLLQLOVAVKFEYPHSAALARELLKR 684
Qy 657 ALTNOITIGHFFPHLSEM-HNKTVSORFGLLESYCRACGMVKKH-LNVOVAMEKLIN 714
Db 685 GLENKRIGHLFWPLSEIAOSRRHYOORFVILBAYRGCTAMHDFTOQVOVIDLQK 744
Qy 715 LT-DI--LKQEKDETOKV--OMKFVEQMRBDFMDALOGFLSPLNPAHQNLRLLEC 769
Db 745 VTIDISLSAEKDVSSQVLSQKQKLENQN--LNLPSFRVPYDGLKAGALVTEKC 801
Qy 770 RIMSASAPRLMLWE--NPIMSELLFQNN--IFKRNDDLRQMDLTQIIRIMNTW 824
Db 802 KVMASKKKPLMLEFKCADPTALS-----NETIGIIFKHGBDLPQMDLIIQIIRIMESIW 855
Qy 825 QNQGDLRLM.PYGLSTIGDCVGLIEVYRNSHTIMQI--QCKGSLKALQFNSHTLHQLKD 883
Db 856 ETESLDLCLPYGCISTGDKIGMTEIVKDATTAIKIOQSTVGTGA--FKDEVLSHMLKE 913
Qy 884 KMK-GEIYDAIDLFTRSCAGCVATFLLIGDRHNSINWKGDDGULFIHDFGHLDHKK 942
Db 914 KCPLEEFQAAVERFVUSCAGCVATFVLGIDHNNIMISEGNLPHIDFGHILGNVYK 973
Qy 943 KKEGYKEERYFVLTODFLIVISKGAOECTKREFPEROEKCYATYLAIRQHANLFINLP 1002
Db 974 SPGINKERVPFVLTPDFLFWMGTSKK--TSLHFQKQVQVAXYALRLHHTMLLITLF 1031
Qy 1003 SMMGSGMPELQSDDOIATIRKTLALDKTBOALEYFKXNDNAHGGWTKMDMIFHTI 1062
Db 1032 SMMIMTQMPOLTSKEDIEYRDALTALVGSEBDKAKFLDQLEVCGRDKMTVQFNMFLHVL 1091

RESULT 11
P3K1_DICD1 STANDARD; PRT; 1570 AA.
ID P3K1_DICD1 STANDARD; PRT; 1570 AA.
AC P54673;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Phosphatidylinositol 3-kinase 1 (EC 2.7.1.137) (PI3-kinase)
DE (Pcdins-3-kinase) (PI3K).
GN PI3A OR PIK1.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN NCBI_TaxID=44689;
RP SEQUENCE FROM N.A.
RX STRAIN=AX3;
RX MEDLINE=96009592; PubMed=7565716;
RA Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
RT discoideum: biological roles of putative mammalian p110 and yeast
RT vps34p PI 3-kinase homologs during growth and development.";
RL Mol. Cell. Biol. 15:5645-5656(1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy-1D-myo-inositol = ADP +
CC 1-phosphatidy-1D-myo-inositol 3-phosphate.
CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U23476; AAA85721.1; -
CC PIR, T18272; T18272.
CC DICTYDB; D001099; PI3A.
CC InterPro; IPR000403; PI3_P14_kinase.
CC InterPro; IPR002420; PI3K_C2.
CC InterPro; IPR000341; PI3K_ras_bind.
CC InterPro; IPR001263; PI3Ka.

```

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DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR Pfam; PF00792; PI3K_C2; 1.
DR Pfam; PF00794; PI3K_rbd; 1.
DR Pfam; PF00613; PI3Ka; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00144; PI3K_rbd; 1.
DR SMART; SM00145; PI3Ka; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
DR TRANSFERASE; Kinase; Multigene family.
KW TRANSFERASE; Kinase; Multigene family.
FT DOMAIN 41 48
FT DOMAIN 59 73
FT DOMAIN 161 168
FT DOMAIN 294 304
FT DOMAIN 308 324
FT DOMAIN 413 424
FT DOMAIN 503 510
FT DOMAIN 570 579
FT DOMAIN 821 828
FT DOMAIN 831 836
FT DOMAIN 1309 1570
SQ SEQUENCE 1570 AA; 178374 MW; 55B67B72B34D763 CRC64;

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Query Match 24.0%; Score 1370; DB 1; Length 1570;
Best Local Similarity 33.2%; Pred. No. 2e-85;
Matches 371; Conservative 199; Mismatches 363; Indels 184; Gaps 40;

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Qy 33 TLEGRATILITIKHELFKARKYPLHQLLQDSSYFVSTQV-AREEFPDETRLCD 91
Db 555 TIENTLKER---LSDYLFNNNSNNNNCKYAGDSYILLDPNDNPKMSLVKNSDYILD 611
Qy 92 LRL--FOPLKVIIEPVGNREKILNREIGPAIGMPVCF-----DWKDEPVQDFRR 141
Db 612 KRAOGLPKLVIE-----KSTILSDPSDELSPSEVEIIRKLI PGDTWRGEEVEYERR 666
Qy 142 NILNVCBAVDLRDLSNPHSRAMVYVPPNVESELEPKHYNKLDKQOIIIVIMVISP 201
Db 667 -----VTSRLRY-----EALP-----LIKSIQSTLVRISP- 693
Qy 202 NDKQYTLKINHDCVPEQVIAEAR-----KKTSMUL--SSEOL--KLCVLEY- 246
Db 694 -----LPIVGNKTLISFLDPIYVTKTLDELNETADQFTNRLFTNYS 739
Qy 247 -----QGYILNVCCEDEYFELEKYPDSQKYIRSCIMGRMNLMM--AKESLYSQ 297
Db 740 KHLRNVAHNLITLVGSSDPIHGHPIRTRESIRNHIQGTQPOLTIQRKPELDPOF 799
Qy 298 FMDCFMRS--YRRRISTATPVNAGETSTV-----SLWYINSLARKIKI 338
Db 800 FKPRDYPPELIIIDHS CNAINCNNNTNSNNNNINEDNDMDITHSIRIKKPRFKV 859
Qy 339 LCATYVNN-IRDD--KIYRTGIGHGEPLLCNVNTQRPV-----CSNPRAMEWL 387
Db 860 MGRTRIPISCKIDISSVIVISLVHGEICFSAFTQPIIPPPAPLAFLSLVDMCWL 919
Qy 368 NY-DIYIDLPPAARLCLICS-----VKGRKAKSEHCPPLANGINLFDYDTL 436
Db 920 VFTNIDYNSLVPDARLSISVSAWETVDVEIKNLDAATKKTFTIGINWITDFKYL 979
Qy 437 VSGKVALTWPYPHGLDPLNPIGTGNSP-NKETPCLELFDWSSVYKPPDMSVIEH 495
Db 980 RQGWELSLMP-----SDFSNPLDGYCSNPNPSGSGVGLTFEEFEEPLVLP- 1026
Qy 496 ANWVSREAGRSYSAGLSN--RLARDNELKENDKOLRAICTRPPLSEITOEKDFLMS 553
Db 1027 -----RKTKEFSTSVSVEQPTNINSNEMR--PEOITLAL--DPLSDLKQEKNOJMT 1076
Qy 554 HRHYCVTIPKILLSVKMSRDEVAQWYCLVQDWEPPIKPEQAMELLDCVYPPMVG 613

```

Db 1077 LRVHSLFPOVLPRLMLSVPTQATVADEALSLIDRPPKLPYSESLDLAKNANKVRE 1136
 QY 614 FAVRCLEKYLITDCLKSOYLQVLYVLYEYOYLDMLVLPFLKKAJNQRIGHPFHWLKS 673
 Db 1137 FAVTCLIED-LSEDELDLILQVLYVLYEYOYLDMLVLPFLKKAJNQRIGHPFHWLKS 1195
 QY 674 EMNKVYVSOFRGLLESYCRACGMYLGHNRQVAMKLNLDILKQER--KDETQVQ 731
 Db 1196 DLHDSNLSERFGLLESYLYACGHRLELKQ--MEVINNLTEVAKKIPKLQDHR-- 1250
 QY 732 MKFLVEQMRPRDFMDALQGFSLPNAHOLGNLRECRIMSSAKRPLMNWENPDLMSE 791
 Db 1251 -EFMIKFE---ESLFWKCRHLLTNPFBSNGLINKSKMDSKLPRLSFTNTDMAD 1306
 QY 792 LIFONNEIIFKNGDDLRQDMITLQIRIMENIWQOGLDRLMLPYGCLSIDCVGLEV 851
 Db 1307 PI----EVIFKAGBDDLQDMITLQIRIMENIWQOGLDRLMLPYGCLSIDCVGLEV 1362
 QY 852 RNSHTIMQIO-CGGLKGLALQFNSHTLHOMLKDNKKEI-YDAALDLPTRSCAGCYATF 909
 Db 1363 LNSEETAKLOKSSGCG--GAFRFQVSGPOLILOHNMKDMEOKAVDTFILLSCAGCVATY 1420
 QY 910 ILIGDRHNSINIVKODGOLPHIDFGHPLDKKKKFGYKERVVPLTODFLVYSKGAQ 969
 Db 1421 VLGIGDRHNDNLMTYKGRFLPHIDFGHPLGNYKKKFGYKERVVPLTODFLVYSKGAQ 1478
 QY 970 ECTKTEFERFEROECYKAYALAIROHANIPLNFSMMLSGMPELQSFDDIATIRKTLAD 1029
 Db 1479 ESFK---FSQFVNYCCGYNIVIRKNAKLPNMLFAMVSTGIPELQSMEDLNYLKESFIS 1535
 QY 1030 KTEQDALEYFMKONDAHGGMTTKDWTTHHTTKOHA 1066
 Db 1536 LSDAKAREKVALIHES-LATKTTQOLNPFPHL-AHA 1570

RESULT 12

P3K2_DICDI STANDARD; PRT; 1858 AA.

AC P54674;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Phosphatidylinositol 3-kinase 2 (EC 2.7.1.137) (PI3-kinase)
 DE (pdcins-3-kinase) (PI3K).
 GN PI3K OR PI3K.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN NCBI_TaxID=44689;
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RA MEDLINE=96009592; PubMed=7565716;
 RA Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
 RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
 RT discoideum: biological roles of putative mammalian p110 and yeast
 RT Vps34p PI 3-kinase homologs during growth and development.";
 RL Mol. Cell. Biol. 15:5645-5656 (1995).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP +
 CC 1-phosphatidyl-1D-myo-inositol 3-phosphate.
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: U23477; AAA55722.1;
 DR PIR: T18273; T18273.
 DR DictyDb: DD0100; PI3K.
 DR InterPro: IPR000403; PI3_P14_kinase.

DR InterPro: IPR002420; PI3K_C2.
 DR InterPro: IPR000341; PI3K_ras_bind.
 DR InterPro: IPR001263; PI3Ka.
 DR Pfam: PF00454; PI3_P14_kinase; 1.
 DR Pfam: PF00792; PI3K_C2; 1.
 DR Pfam: PF00794; PI3K_rbd; 1.
 DR Pfam: PF00613; PI3Ka; 1.
 DR SMART: SM00142; PI3K_C2; 1.
 DR SMART: SM00144; PI3K_rbd; 1.
 DR SMART: SM00145; PI3K; 1.
 DR SMART: SM00146; PI3K; 1.
 DR PROSITE: PS00915; PI3_4_KINASE_1; 1.
 DR PROSITE: PS00916; PI3_4_KINASE_2; 1.
 DR PROSITE: PS50290; PI3_4_KINASE_3; 1.
 DR Transferrase; Kinase; Multigene family.
 FT DOMAIN 34
 FT 166 172
 FT 185 226
 FT 227 235
 FT 246 253
 FT 259 268
 FT 294 303
 FT 361 364
 FT 369 384
 FT 425 429
 FT 439 444
 FT 445 454
 FT 562 570
 FT 715 727
 FT 982 990
 FT 1015 1049
 FT 1598 1858
 FT DOMAIN 1598 1858
 FT 1858 AA; 203945 MW; AEC033304CDDEA03 CRC64;
 SQ SEQUENCE

Query Match 22.1%; Score 1262.5; DB 1; Length 1858;
 Best Local Similarity 28.7%; Pred. No.5.6e-78;
 Matches 366; Conservative 197; Mismatches 317; Gaps 42;

QY 15 LMPRLIVECLPENGMI--VTLECRLEATLITIKHLFPEARVYR-LHQLODESSYTF- 70
 Db 657 LIBEYELKVLVSNSTISNETLP-LRRQTLM--OACNISRLFPKLHLIKSESTTILD 711
 QY 71 -SVTQEAEREERFEFDETRRLCDRL-----PQFLKVIPEVGN 107
 Db 712 GASTTTTTTTTTTTTANQSSNITTSNSLDTLNNSEIIVKGHIALEIFELIGT 771
 QY 108 REEKILNREIGAIGMPVCEFDWVQPEVQDFERN-----ILNVCKEAVDLRLNSPHSR 162
 Db 772 SPTRLVD-----QCEVVSFRDRPAQFLSNFTSTRNDL-----SQ 807
 QY 163 AMVYVPPNVSSPELKHLYNKLDKQOIIIVVIVVSPNNDKOKYTLKINHDCVPEOVLA 222
 Db 808 MIVV-----SSPLPLTTPNK-----ITIMVLL-PDQK-----IKRVDCPPSSVGC 849
 QY 223 EAIRKTRMLLSSEQLKLVLEYQCK--YLIKVCGEVEFL-----EKYP 266
 Db 850 DVYKELFKKPFAMIDR-----VHTQKRTQDDPVLKATGTGFRYILCIHELGNLTSGRPFIP 903
 QY 267 -LSQYKYSCTMLGMPNMLM----- 288
 Db 904 TSGGDFSLMDYDIYIQCVGKNQTVLSTNNLSILNVOSEKVSFIDKILETSDPDYD 963
 QY 289 -----AKSLYSQLPMDCFM----- 304
 Db 964 EDLDSINSNSFDLQKSIQOQOQOQOQIQTVINIKETKENKDSNKENKSSNNNNNNNN 1023
 QY 305 -----PSYRRISTATPYNNGETS-----TKSLMVI- 330
 Db 1024 NNN 1083
 QY 331 -----NSALRIKILCATY-VNV-NIRPID-----KIYVETGIY 361
 Db 1084 VQNFSLPNNSKLPINIVKRLFRVNIAGLRNLNPNNNEDARNFADKNNQPNVFWVAELTY 1143

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QY 362 HGCEPLCDVNTQVRPCSN-----PRNMENLVNDIYIPDLIPRAARCLSTICSVKGRK 413
DB 1144 YGEBELLTNPFTPLAQLASYGDSVEPPNMEKIAFTIPRIYLPBARASFTYVVTITSE 1203
QY 414 GAAEE-----HCPILANGINLPDYDTLVSGMALNLMFVHGLED--LNPIGVTGS 464
DB 1204 ALBSQMDVVSXSIPIQMSNCLMNHGMRMGFTAFRLM-----DDGRANPITGCVD 1257
QY 465 NPKKPEPCEL-EPDMFSSVVKFPDMGVIIEHAN--MSVREAGFSYSHAGLSNRLARDN 521
DB 1258 NQAAKQPIIILVEFESFIRPIVYDTLQSMNMNDSSISNNGVESISVSPSSAASSS 1317
QY 522 ELRE-----NDKEQIRAICTRDPISEITEQEKDFLMSHRHCVTIPELTPK 567
DB 1318 PLSSPLSPSPVGLKKLLDLBARRLKALMDSDPVLQVLSAEDKULVYGRHITKSKPKALAK 1377
QY 568 LILSVKXNSRDEVAQWCLYKDPPIRPEQAMELLDQNYDPWVRGFAVCLBKYLTDK 627
DB 1378 FLISVNMIDPDQVDAVRQMDMALIKPVQALBILDKKFDENHVRNPAIKINSF-SDAE 1436
QY 628 LSOYLQVNOVLKRYEQLDNLVFLFKKALTNO-RIGHPFPMHKESEMNKTVSQRFGL 686
DB 1437 FSDFLQTLQVLKKEPYHNSDLTHILQRLASNSRIGHPFPFLKSEMTPELEERYGL 1496
QY 687 LLESYCRACGMYLKHNRQVEAMEKLINTDLKQEKDETOXVQMKFLVEQMRPDPMD 746
DB 1497 LLBEGYLRSCGTHRQDLIKQNOVLKSLHTVANAQVKTGSSERK---KYLMEGLSKIRFPD 1553
QY 747 ALQGFSLPLPAHOLGMLRECEKINSASAKRPLMLNMENPDIMSELLFONNEIIFKNQDD 806
DB 1554 TFQ---PLDPBRWEAKGLIITDKCYMDSKCLPLWLVENEPHAKPL---TVLFKQGD 1606
QY 807 LRQOMLTLQIIRIMENIMONGLDLRLMRYGCLSIGCVGLIEVVRNSHTIMOJQCKGSL 866
DB 1607 LRQDITLQVLRKQDLKQKXNSGMDRLQPYKICATGDISGLLEVVLNANTIANINXQAG 1666
QY 867 KGALQFNSHTLQWLKQNKKEBI-YDAIDLFTRSCAGYCAVTFILGIDRHNSNIWVD 925
DB 1667 TGALEKTLVNLKQCNKTEAEYNKAVETFIISGAVVATVYMIGIDHSHNIMITK 1725
QY 926 DGQFLHIDFGHFLDKKKKFKGKRVFVLTOPLVVISGADQECTKREPERQEMCY 985
DB 1726 LGHFLHIDFGHFLNKKYKGFKRBAPFIPTPYMAV--GCKD---SENPKKFTVTTCC 1780
QY 986 KAYLAIQHANLFINLPSMILGSGMPELQSPDIAIYIKRTALDTEQDALEYMKQ--- 1042
DB 1781 SAYNILKKNLDFNLPLQMLSTGIPQLQVADIDLYLAKALPGLSDEAAEEFTKINISV 1840
QY 1043 -----MNDAAHGGW 1051
DB 1841 ALNTRKTVLNDIPH-GW 1856

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RT discoidium: biological roles of putative mammalian p110 and yeast
RT vps3p, p110-kinase homologs during growth and development.";
RT Mol. Cell. Biol. 15:5645-5656(1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP +
CC 1-phosphatidyl-1D-myo-inositol 3-phosphate.
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -----
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CC -----
DB EMBL; U23478; AA85723.1; -.
DB PIR; T18274; T18274.
DB DictyDb; DD01101; PI3K.
DB InterPro; IPR000403; PI3_P14_kinase.
DB InterPro; IPR002420; PI3K_C2.
DB InterPro; IPR000341; PI3K_cas_bind.
DB InterPro; IPR001263; PI3K.
DB Pfam; PF00454; PI3_P14_kinase; 1.
DB Pfam; PF00792; PI3K_C2; 1.
DB Pfam; PF00794; PI3K_Cbd; 1.
DB Pfam; PF00613; PI3K_A; 1.
DB SMART; SM00142; PI3K_C2; 1.
DB SMART; SM00144; PI3K_Cbd; 1.
DB SMART; SM00145; PI3K_A; 1.
DB SMART; SM00146; PI3K_C; 1.
DB PROSITE; PS00915; PI3_4_KINASE_1; 1.
DB PROSITE; PS00916; PI3_4_KINASE_2; 1.
DB PROSITE; PS02290; PI3_4_KINASE_3; 1.
DB KX Transferase; Kinase; Multigene Family; Repeat.
DB KW NON_TER 1
DB FT DOMAIN 58
DB FT DOMAIN 98
DB FT DOMAIN 110
DB FT DOMAIN 200
DB FT DOMAIN 235
DB FT DOMAIN 254
DB FT DOMAIN 345
DB FT DOMAIN 383
DB FT DOMAIN 390
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DB FT DOMAIN 488
DB FT DOMAIN 720
DB FT DOMAIN 737
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DB FT DOMAIN 1510
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DB FT REPEAT 1535
DB FT REPEAT 1539
DB FT REPEAT 1547
DB FT REPEAT 1560
DB SQ SEQUENCE 1585 AA; 180421 MW; 46898620D2484961 CRC64;

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Query Match 19.4%; Score 1109; DB 1; Length 1585;

Best local similarity 30.7%; Pred. No. 14e-67;

Matches 301; Conservative 189; Mismatches 374; Indels 118; Gaps 30;

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QY 146 VCKE-AVDLRDLSNPSHRAMVYVPPNVSSPELPKHLYNKLDKQIIVIVWVSP--NN 202
DB 562 LCKRLVLDLSLENNR-----PSIWK$-----HIDVLSFPRKRLRLMLAKPQSNV 610
QY 203 DKQRYTLKINHDCVPEQVY--AEAIRKRTS-----MLSSQQLKCVLEYG 248
DB 611 PAARLTYPPEPKTIPBEFVIRVHLFKQVTSRLRCANNHTAFSLMTTILSEKIKVTTPDPT 670
QY 249 KYILKVGCGCEYFLEKYPGLQYKIRSCJ-----MLGMPYLMIAKESLYSQLPMD 300
DB 671 QYRPLITGINQYVDNPVLLSVEYIVKIRKSGSIDLTWELLSGLIIQQOQQOQQOQQO 730
QY 301 CFTWPSYSRRISTAT-----PYMNGETSTKSLMVINSALRIKILCATY 343
DB 731 QQQQQQQQIENIDDENILKNNGLINVLKIEKPIREKQNCISLTVTEN--LQVRLHAHE 789

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QY 344 UNYN---IPDID---KIYVRGCIYHGEBPLCDNNTQVRPCSNPNWENLNDIYIPD 395
D 790 IFASKASEIIGTDSPIQIPIEAAYFGGELIATQSSKLVSFDYVYWNEMVINPLAVSN 849
QY 396 LPBAARLCISGVKGGKGAKEEHCPILAMGNINLFDITDPL-VSGKALNLMPPHLED 454
D 850 IPWGRKCLGL---NARYRGDIENIGWGRHFDGKILNFPAPSLIIMP-----G 898
QY 455 LINDPVGTSNPNKPTCLLEEDPWFSSVVKFPMSYIEEHANVSVRAGFSYSHAGLS 514
D 899 KINPIGICVNLSESKDAIIIAEFKDYV--PETHYEDDLIEJISKD----- 945
QY 515 NRIARDNEL---RENDXQLRAICTRDPYLSITEOEKDFLMSHRNYCVTIPILLPKLLS 571
D 946 ---ENGNELEPVVTMEEMDRVEQIILQDPLYSINKEEELLIMKSHYFCHTRQALSKLLQS 1002
QY 572 VKNNSREVAQMCVAVNDMPPIKEQAMELLDCYPRPM-VRGAVACLEKYLTDLDSQ 630
D 1003 VENTNRYQVGEARQQLKIMPTLSAVDALELDPEKFAQVCEIRETYVCLDQ-MSDYELI 1061
QY 631 YLQVLVLYEQLLDNLVRFLLKRALTN-ORIGHFEPHLLKEMNKTVSQRFGLLLE 689
D 1062 YLLQVLVAIGHDPHNSVLSFLIGRWQWQVULGHPFMHMRADIDNOYCEERFVLSS 1121
QY 690 SYCR-ACGMYLKHLNRQVAMEKILNLDLILKQEKDETQKVQMKFLVEQMRPDPMDAL 748
D 1122 GFLRYAPATQMESPKREITTLRIENLAKRKEVPEYKQVEMNLREBQSFE TEL--- 1178
QY 749 QGFLSPINAPHQGNLRECRIMSAAKRLMLNMBPDLMSILLFONNEIIFKNGDDL 808
D 1179 ---FVPEPDIRILINIPKCKSMDSAKVPMLVTFKNADEPAPPI---QMIATKGDDL 1231
QY 809 QDMULTQIITIMENINONOGDLRMLPYGCLSIGDCVGLLEVYNSHTIMQIOG-KGGK 867
D 1232 QDLITLQLLMLDMHMKSQDLDMHTTYRCIATGMGGLLEVYNSHTAARIQAGAGVS 1291
QY 868 GALQFNSHTLHOMLXDKNKSE-IYDAIDLFTSCAGYCATFLIGIDRHNSNIMVKD 926
D 1292 GA--FKQTPANMLKNNJOTENSQKAVSKFTLSAGYCATVYLGIDHNNINIMWDI 1349
QY 927 GQFLHIDFGHFLHKKKKFGYKREVPVLTODFLIYSKGADECTTREPERFOEMCYK 986
D 1350 GHLEFHDIFGHFNFKTFAGFOREKAPFLVLPDFVYI--GGK---SPNFAFEVDICK 1404
QY 987 AYLAIRQHANLFLNPEMLGSGMPEUQSPDIAYIKTLALDCTEOALEYFKKONDA 1046
D 1405 AFNIRSNNAHVFINMFEMLSTGIPERISNDIVYLRDKFRLDLDAASEYFKLIHES 1464
QY 1047 HHGQMTTKMDMIFPTIKQHALN 1068
D 1465 -IGTLTTTINFAIH-IMAHKN 1484

```

```

RT "A phosphatidylinositol-3-OH kinase family member regulating
RT longevity and diapause in Caenorhabditis elegans."
RT Nature 382:536-539(1996).
RN [2]
RN REVISIONS.
RA Morris J.Z., Tieszenbaum H.A., Ruvkun G.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Swinhorne J., Williams L.;
RU Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Durbin R.;
RU Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PHOSPHATIDYLIINOSITOL 3-KINASE HOMOLOG THAT REGULATES
CC LONGEVITY AND DIAPAUSE. COULD FUNCTION IN THE DEVELOPMENT OR
CC NEUROENDOCRINE SIGNALING OF THE DAUER PATHWAY.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-ID-myo-inositol = ADP +
CC 1-phosphatidy1-ID-myo-inositol 3-phosphate.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC -!- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U56101; AAC9459.1; ALT_INIT.
DR EMBL; Z66519; CA91377.2; JOINED.
DR EMBL; AL110499; CA91377.2; JOINED.
DR EMBL; AL110499; CAB57914.1; -.
DR EMBL; Z66519; CAB57914.1; JOINED.
DR PIR; S71792; S71792.
DR WormPep; B0334.8; CE23506.
DR GO; GO:0005942; C:1-phosphatidylinositol 3-kinase complex; NAS.
DR GO; GO:0007568; P:aging; IMP.
DR GO; GO:0040024; P:dauer larval development (sensu Nematoda); IMP.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000403; P13 P14_kinase.
DR InterPro; IPR002420; P13_C2.
DR InterPro; IPR003113; P13K_p85B.
DR InterPro; IPR003341; P13K_ras_bind.
DR InterPro; IPR001263; P13Ka.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00792; P13K_C2; 1.
DR Pfam; PF02192; P13K_p85B; 1.
DR Pfam; PF00794; P13K_Ibd; 1.
DR Pfam; PF00613; P13Ka; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; P13K_C2; 1.
DR SMART; SM00143; P13K_p85B; 1.
DR SMART; SM00144; P13K_Ibd; 1.
DR SMART; SM00145; P13Ka; 1.
DR SMART; SM00146; P13Ka; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
KW Transferase; kinase.
FT DOMAIN 851..1127 P13K/P14K.
FT VARIANT 826..826 S -> N (IN AGE1(MG109)).
FT CONFICT 1010..1010 F -> V (IN REF. 1).
SQ SEQUENCE 1146 AA; 132961 MW; 0D362E419407253A CRC64;

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QY Query Match 19.2%; Score 1096; DB 1; Length 1146;
Best Local Similarity 27.3%; Pred. No. 6,8e-67;
Matches 312; Conservative 219; Mismatches 430; Indels 182; Gaps 39;
39 EATLITIKIEFLK-DARKYPLHLQIDESSYFVSVTQEAEREERFDETRICDLRLFQ 96

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Db      | 70 EIKSDRKHQFELIAPKMGTSVXKPOD--YVFRQUNFGGEIIVIFNDQPLSKLEIHG 127
Qy      | 97 --PFLKXIEPVNGNEEKILNREIGFATGMPCVCEPDMVKDPVQFRRNIILNVCENADLR 154
Db      | 128 TFPWLFUYQDPGIRDKELMSDISHCLGYSLDKLEESLDEBELRQFASLWARTKTCULTR 187
Qy      | 155 DLNSPHBRAMVVPN--VESSPELPHKHYNKLKGOI-IYIWIWVSFNNDKOXYTLKI 211
Db      | 188 GL---EGTSIYAFEBEOYLVCGESCPKDLSEKVAKALISYGMF-----RKRAEI 235
Qy      | 212 NHDCVPROVIAEAIR---KKTSMILSS---EQLKLCYLEYQK---YILKVCCEBEYF 261
Db      | 236 NGVC--EKMKIQTIEFNPNETPKSLHFTLEVMKRLDYDITDDPADEWCFQLAGRTTEV 293
Qy      | 262 LE-KYPLSOXYIYNSCIMGRLMPLIMAK-----ESLYS-----QLPMDC 301
Db      | 294 TNPDKLTSYDGVSELESYRCPGFVVRQSLVKDYCRPKRLEPHYRAHERKLADV 353
Qy      | 302 FTM-----PSYSRIISTATPYMNGEISTK--SLWVINSALIKILCATYVWVNRID-- 352
Db      | 354 LSVSISTPKQSKSDMYMTDPRPTASLUQVSLMDLDANLMIR-----PVNISGEDFP 406
Qy      | 353 ---KIYRT--GIYHGEPLCDNVNTOFVPCSNBRMN--EWLNVDIYIPDEPRAARLCSI 406
Db      | 407 ADVDMYRIEFSVYVGTITLASK--STKVNQAFKMKEMWTFDLYKMDMPSA--VLSI 463
Qy      | 407 CSYGRKAKAEKCPLANGINLPDYDTLVSGKALNLV--PVPHGEDLIINPTGV--TGS 464
Db      | 464 RVLGKVLKSEEBEVEGVWVMSLTDMDRDELQGFPLHMAPEPTANRSIGENGARIGT 523
Qy      | 465 NPNKETPLLEFWMFSVVKFPDMS-----VIEHANNVSREAGFSYSHAGLSRLARD 520
Db      | 524 N-----AAVTIEISSYGRVMPGQYTYLVKRSTYET-----LNIKDD 566
Qy      | 521 NELRENDKEQURAICTRDPLSE-----ITEOKDFLMSHRHYCVTIPILP 566
Db      | 567 YE-----SCIRDPGRKKQMLVKMGHSGIVLEEDORHVMWMMRRY---IQKEP 612
Qy      | 567 KLL-----LSVKNMSRDEVAQMYCLVKDMPRIKEQAMELLIDCNPDMVGFVAVRCLEK 621
Db      | 613 DLLIVLSLAEVMTDRENFSELYVWLAEKMKPPSVAALTLTGKCTDVIKRFPAEKLNE 672
Qy      | 622 YLTDDKLSQVLIQVULKYEQYDNLVRLKALKALNORIGHFEFHLKSEMH----- 676
Db      | 673 QLSPTFHLPLPLIQAALKEPRASQEVGMILLTRALCDYRIGHFLWLAELIRLDC 732
Qy      | 677 --NKTVSQFGLLESYCRACGMVYKHLNROVEAMEKLINLIDIKOEKQD--ETQKV--Q 731
Db      | 733 DLKSEBYRISLLMAYLRGNEEHKITTROYDMDLSTRISTLYKGMKPVATMKLAD 792
Qy      | 732 MKFLVEQRRPDPMDALOGFLSPLNPAHQNLBLECRINSSAKRPLMLWENPDINSE 791
Db      | 793 LRSISHKEMND-----SPIDPVYKLGEMIDKAIIVGASARPLMLHKNNPKSD 843
Qy      | 792 LIPONNELIPKRGDLDRODMILTQIRIMENIMWQSGDLMLPRGCCSIDGCVLIVV 851
Db      | 844 LHLPCAMIFKRGDLDRODMILVQLVLEWMDNIMKANDICCLNPAVALPMEGMGIEV 903
Qy      | 852 RNSHTIWOICKGKIGAL--QFNSTLHOML-----KDKNKEI----- 889
Db      | 904 PNCKTIFETIQTGTMNTAVRSIDSPMKMIRKCGIIBDEKKKSKOSTKPIKIKDN 963
Qy      | 890 -----YDAIDLFTRSGAGYCVATFLLIGDRHNSNIMVKDQGLPHIDGHLDRKK 943
Db      | 964 TOAMKKYFESVDRFLYSCGVSVATYINGIKDRHSDNMLTDEGKYFHDGHLIGHGT 1023
Qy      | 944 KFGYKREVPVLTDDFLIVISKGOECKTREFRQEMCKATLARIQANLFINFS 1003
Db      | 1024 KLGIORDOPFLITLTHFTVIRSGSVGNSHLEOKFYLCEAVEVMMNNNDLVSLEF 1083
Qy      | 1004 MWLGSGBELQSFDDIAYIRKTLALD-KTEQALFYPMQNMDDAHGCGTTCMDVIFTI 1062

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Db      | 1084 LMDGMLPELSTRADLDHLKTLFCNGESKEARKFPAGIYEBAFNGSWSTKTNWLFHAV 1143
Qy      | 1063 KOH 1065
Db      | 1144 KHY 1146

RESULT 15
PK3B_HUMAN STANDARD; PRT; 1634 AA.
ID PK3B_HUMAN
AC 000750; O95666;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta
DE polypeptide (EC 2.7.1.154) (phosphoinositide 3-kinase-C2-beta)
DE (Ptdins-3-kinase C2 beta) (PI3K-C2beta) (C2-PI3K).
GN PI3KC2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Breast;
RC MEDLINE=97289668; Pubmed=9144573;
RA Brown R.A., Ho L.K.F., Weber-Hall S.J., Shipley J.M., Fry M.J.;
RT "Identification and cDNA cloning of a novel mammalian C2 domain-
RT containing phosphoinositide 3-kinase, Hsc2-PI3K."
RL Biochem. Biophys. Res. Commun. 233:537-544(1997).
RN [2]
RP SEQUENCE OF 26-1634 FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Monocytes;
RC MEDLINE=99047700; Pubmed=9830063;
RA Arcaeo A., Volinia S., Zvelebil M.J., Stein R., Waton S.J.,
RA Layton M.J., Gout I., Ahmedi K., Downward J., Waterfield J.D.;
RT "Human phosphoinositide 3-kinase C2beta, the role of calcium and the
RT C2 domain in enzyme activity."
RL J. Biol. Chem. 273:33082-33090(1998).
CC - FUNCTION: PHOSPHORYLATES PTDINS AND PTDINS4P WITH A PREFERENCE FOR
CC PTDINS. DOES NOT PHOSPHORYLATE PTDINS(4,5)P2.
CC - CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4-
CC phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4-bisphosphate.
CC - SUBCELLULAR LOCATION: FOUND MOSTLY IN THE MICROsome, BUT ALSO IN
CC THE PLASMA MEMBRANE AND CYTOSOL.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT LEVELS ARE HIGHEST IN
CC THYMUS AND PLACENTA AND LOWEST IN PERIPHERAL BLOOD, SKELETAL
CC MUSCLE AND KIDNEY.
CC - SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC - SIMILARITY: Contains 1 C2 domain.
CC - SIMILARITY: Contains 1 plox homology (PX) domain.
CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
CC
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CC
DR EMBL; Y11312; CAAT72168.1; -
DR EMBL; Y13892; CAAT74194.1; -
DR PIR; JC5500; JC5500.
DR HSSP; P21707; 1RSY.
DR Genew; HGNC:8972; PI3KC2B.
DR MIM; 602838; -
DR GO; GO:0005792; C:Microsome; NAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0016305; F:phosphatidylinositol 3-kinase, class II act. .; NAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000403; PI3_P14_kinase.
DR InterPro; IPR002420; PI3K_C2.

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DR InterPro: IPR000341: PI3K_ras_bind.
 DR InterPro: IPR001263: PI3Ka.
 DR InterPro: IPR01683: PX.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00454; P13_P14_kinase; 1.
 DR Pfam: PF00792; PI3K_C2; 1.
 DR Pfam: PF00794; PI3K_rbd; 1.
 DR Pfam: PF00613; PI3Ka; 1.
 DR Pfam: PF00787; PX; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00142; PI3K_C2; 1.
 DR SMART: SM00145; PI3Ka; 1.
 DR SMART: SM00146; PI3K; 1.
 DR SMART: SM00312; PX; 1.
 DR PROSITE: PS00499; C2 DOMAIN 1; FALSE_NEG.
 DR PROSITE: PS50004; C2 DOMAIN 2; 1.
 DR PROSITE: PS00915; P13_4_KINASE_1; 1.
 DR PROSITE: PS00916; P13_4_KINASE_2; 1.
 DR PROSITE: PS50290; P13_4_KINASE_3; 1.
 DR PROSITE: PS50195; PX; 1.
 DR Transferrase: Kinase; Multigene family.
 FT DOMAIN 1365 1481 PX
 FT DOMAIN 156 162 PRO-RICH.
 FT DOMAIN 169 174 PRO-RICH.
 FT DOMAIN 1079 1343 PI3K/PI4K.
 FT DOMAIN 1517 1608 C2 DOMAIN.
 FT CONFLICT 63 63 P -> S (IN REF. 2).
 FT CONFLICT 75 75 R -> W (IN REF. 2).
 FT CONFLICT 99 99 Q -> L (IN REF. 2).
 FT CONFLICT 246 246 V -> A (IN REF. 2).
 FT CONFLICT 278 278 K -> E (IN REF. 2).
 FT CONFLICT 567 567 P -> S (IN REF. 2).
 FT CONFLICT 664 665 DM -> BL (IN REF. 2).
 SQ SEQUENCE 1634 AA: 184856 MW: C0B5DF63C6688824 CRC64;

Query Match 18.6%; Score 1064.5; DB 1; Length 1634;
 Best Local Similarity 27.3%; Pred. No. 1,66-64;
 Matches 304; Conservative 181; Mismatches 392; Indels 237; Gaps 34;

QY 104 PVNGREKINIRELPAIGMVCDFMDKPEVDPPRNILNVCKEAVDLRLNSPSRA 163
 DB 311 PVGSRPHTVAN-----GHELFVSESEDEVAAF-CHMLDIRSGSDI0D---YFLT 358
 QY 164 MYVYPPVAVSESPDELPKHIVNKLKGQIIIVIVIVISNNNDQKXTLKLINHCVPEQYIAE 223
 DB 359 GYVMSATVPS---PEHLGEVNLKTVLC-----DLQNALITFTCC-----YFLT 397
 QY 224 AIRKKTSMILSSDQLKLVLEYO-----GKYLKVGCGDEYFLKRYPLSQYKIRSCI 277
 DB 398 ---SSTVDLIYO---TLCTHDDLRAVVDGDFVLKCGLEFLQNGHALGSHHEYIOYCR 451
 QY 278 MLGMPVLMMAKESLYSOL----- 297
 DB 452 KFDIDIRLOLMEQKVRSDIARIVNDOSPTLNVYLHQRPVKITISROALSILFDY 511
 QY 298 ---PMDCFM-----PSYSRRI-----STATPYNG----- 320
 DB 512 HNEVDALFLADGDFPLADRVQSVKALCNALAAVETPEITSALNQLPCPSRMQPKIOK 571
 QY 321 -----ETSTKSLWVINSAL--RIKLCAVYVNVNR----- 349
 DB 572 DPSVLAVRENRKVEALTAALDLVELYCNTE--NADPOTAVPGRKHDLVQEAHPARS 630
 QY 350 -----DIDKIYRTGIYHGGELCDNVNTQRYVFGSNPR-----WNEML 387
 DB 631 LAFTVYATRIPIIMATSYEDFYLSGLSHGKDMCSPLQTRRAHFSKYLFHLIYMDQOI 690
 QY 388 NYDIYIDLPRAARLCLGICSAV-----KGRKGAKEHCP--LAMGNINLFDYDTLVSG 439
 DB 691 CFPYQVNRRLRETYLLCAITVALPIPPGSSSEANKQRRVBPALGVTTPLPNERQVLTCG 750
 QY 440 KMALINMPVPHGLEDDLNLPIGVTSNPNKTP--CLELEPDMFSSVVKFPDMSVIEHA 496

DB 751 RKLGLMPATQE-----NP-SARWSADNFHQPPQSVIIQIDFPFGSAPDIKFTS-----PGCD 800
 QY 497 NMSVSRAGFSYSHAGLSNRLARNDELRENDKEOLRAICTRDPLSETTEDEKOFIWSHRH 556
 DB 801 KFSRPRYFEG-----SLEEDQKRLKQIMQKESLYWLTDDKRLMEKRY 844
 QY 557 YCVTIPEILPKLLSV--KMSRDEVAQWYCLVADMPKPEQAMELDCNTPDPMPWRG 613
 DB 845 YCHSEVSSLPVLVASASWEMACLPDI---YVLKQVTHNHQDALCLLHATFFDQEVRR 901
 QY 614 FAVRCLEKYLTDKLSQYLQIVQVLYKYEQYLDNLVRFLLKALINQRIQHFFFMHKS 673
 DB 902 MAVQWIGS--LSDAELIDYLPQVQALKECYLDSPVRFILKRAVSDRLRVTHYFFMLKD 960
 QY 674 EMNHKTVSOFGLLSEYCAAGCYVK--HINRQVAMEKILNLDILKQEKDETOYQOM 732
 DB 961 GLKDSQFSIRYQYLLALLCCCGKLEEFNRQC---WLVNALAKLAQOVRAPAPARQ 1016
 QY 733 KFLVEQMRPDMALQGFLS--PLNPAHQNLRLIECRINSSAKRPLMIMWENPDIMSE 791
 DB 1017 GILRTGLEEVKQFPALNGSRLPLSPSLVKGIVPRDCSFFNSAVPLKLSFQVNDPLGE 1076
 QY 792 LLEFONNEIIFKNGDDLEQDMLTQIIRIMENIWQNGLDLRLMPYGLSIGDCVGLIEV 851
 DB 1077 ---NIRVIFKCGDDLQDMLTQIMIRIMSKIWOQELDMRWVIFRCFSTGRGWTYEMI 1132
 QY 852 RNSFTIWQIQCKGKLGKALQFNSHTLQWLKDKXKGE--IYDAIDLFTRECAQCVATFI 910
 DB 1133 PNAETLKKIYVEHGVTS--FKORPLADWLQKNPGBDEYEKAVENFIYSACAGCCVATYV 1190
 QY 911 LGIGDRHNSNIMVWDGQLPHIDPGHFLDHRKKKFGYRREVPFVLTPQDFLIVISGAOE 970
 DB 1191 LGICDRHNDIMLKTGHMHIDGRRLGHAQMGNIKDRARFVFTISDAVYVINGDKP 1250
 QY 971 CTKTRFEERFQEMCYKAYLAIRQHANFLNLFMSMLQSGMPELOSFPDIAYIRKTLALDK 1030
 DB 1251 SSR---FHDVPLDCCQAYNLIIRKHTLFLNLGLMISCGIPELSDJEDLKYVDALRPD 1307
 QY 1031 TEOBALEYPMKQMDAHGCGTTKMDIIFTTIQ 1064
 DB 1308 TEAVATTYFTR--LIESLSIGVATKLNFEIHNLAQ 1340

Search completed: November 6, 2003, 14:43:14
 Job time : 23 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2003, 14:40:55 ; Search time 27 Seconds

(without alignments)
3807.567 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709

Sequence: 1 MPRPSSGELMGHLMPPRI.....GWTTKMDIETTKQHALNX 1069

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : PIR_76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	5708	100.0	1068	1 A43322	1-phosphatidylinos
2	5657	99.1	1068	1 T38110	1-phosphatidylinos
3	1966	34.4	1070	1 A54600	1-phosphatidylinos
4	1958	34.3	1043	2 T43502	1-phosphatidylinos
5	1677.5	29.4	1088	2 T13950	1-phosphatidylinos
6	1428	25.0	1050	1 A57134	1-phosphatidylinos
7	1370	24.0	1570	2 T18272	1-phosphatidylinos
8	1262.5	22.1	1570	2 T18273	1-phosphatidylinos
9	1109	19.4	1585	2 T18274	1-phosphatidylinos
10	1085	19.0	1164	2 S71792	1-phosphatidylinos
11	1064.5	18.6	1634	1 JCS500	phosphoinositide 3
12	1049.5	18.4	1658	2 T42642	phosphoinositide 3
13	919	16.1	1506	2 JCS985	phosphoinositide 3
14	859	15.0	1876	2 T13801	phosphoinositide 3
15	751	13.2	1607	2 T21982	hypothetical prote
16	684	12.0	801	1 T52538	1-phosphatidylinos
17	684	12.0	887	1 S57219	1-phosphatidylinos
18	677.5	11.9	664	2 PC4002	phosphatidylinosit
19	661.5	11.6	816	1 A59003	phosphatidylinosit
20	648.5	11.4	875	1 A36369	1-phosphatidylinos
21	645	11.3	814	2 T07761	phosphatidylinosit
22	635	11.1	814	2 B96630	phosphatidylinosit
23	633.5	11.1	873	2 T25442	hypothetical prote
24	629	11.0	812	2 T07745	phosphatidylinosit
25	625.5	11.0	897	2 T43628	phosphatidylinosit
26	602	10.5	1020	2 T18260	1-phosphatidylinos
27	491.5	8.6	732	2 T08420	1-phosphatidylinos
28	474	8.3	2051	2 F96529	probable Phosphat
29	473	8.3	2028	2 T52022	1-phosphatidylinos

30	442	7.7	854	2 A55404	1-phosphatidylinos
31	442	7.7	1466	2 S65741	1-phosphatidylinos
32	442	7.7	1900	2 S45530	probable 1-phosphat
33	434.5	7.6	133	2 PC4348	phosphoinositide 3
34	423	7.4	1877	2 T40550	probable phosphatid
35	411.5	7.2	2121	2 T27406	hypothetical prote
36	392.5	6.9	525	2 F96547	probable phosphat
37	362.5	6.3	131	2 PC4346	phosphoinositide 3
38	343.5	6.0	131	2 PC4345	phosphoinositide 3
39	331.5	5.8	131	2 PC4347	phosphoinositide 3
40	310	5.4	379	2 T07607	probable 1-phosphat
41	303	5.3	828	2 JCS706	1-phosphatidylinos
42	297	5.2	1066	2 A49335	1-phosphatidylinos
43	291.5	5.1	1121	2 T52631	1-phosphatidylinos
44	268.5	4.7	1093	2 T18275	1-phosphatidylinos
45	265	4.6	604	2 F89453	protein F35H2.4 (

ALIGNMENTS

RESULT 1

A43322 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - bovine

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QY 421 PLAMGNINLFYDITDLTVSGMALNLPVPHGLEDLNPIGVTSNPKETPCLEBDFW 480
DB 421 PLAMGNINLFYDITDLTVSGMALNLPVPHGLEDLNPIGVTSNPKETPCLEBDFW 480
QY 481 SSVKKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
DB 481 SSVKKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
QY 541 SEITEQKDLMSHRHYCVTIPETLPKLLSVKMSNDEVAQWCLVKDMPPIKPEQAME 600
DB 541 SEITEQKDLMSHRHYCVTIPETLPKLLSVKMSNDEVAQWCLVKDMPPIKPEQAME 600
QY 601 LLDONYPDPWGRGAVNCEKYLITDDKLSOYLIOLVOLKYEOLDLNVLVFLKKAALTN 660
DB 601 LLDONYPDPWGRGAVNCEKYLITDDKLSOYLIOLVOLKYEOLDLNVLVFLKKAALTN 660
QY 661 QRIGHFFFMHLKSEMHKKTYSQRFGLLESYCRACGMVYKHLNRQVAMEKLIINTDILK 720
DB 661 QRIGHFFFMHLKSEMHKKTYSQRFGLLESYCRACGMVYKHLNRQVAMEKLIINTDILK 720
QY 721 QEKKDETQYQMKFLVEQMRPDMALQGFSLPLNPAHQGNRLBECRIMSSAKRPLW 780
DB 721 QEKKDETQYQMKFLVEQMRPDMALQGFSLPLNPAHQGNRLBECRIMSSAKRPLW 780
QY 781 LMNENPIMSELLFONNEIIFKNGDDLRODMLTQIIRIMENIMONQGLDRLMYPGCLS 840
DB 781 LMNENPIMSELLFONNEIIFKNGDDLRODMLTQIIRIMENIMONQGLDRLMYPGCLS 840
QY 841 IGDGVGLIEVVRNSHTIMQIOCKGKLGALQFNSHTLHQLKDNKKEIYDAIDLFTRS 900
DB 841 IGDGVGLIEVVRNSHTIMQIOCKGKLGALQFNSHTLHQLKDNKKEIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNIMVXDQGLPHIDGHLIDHKKKKFGYKREVPVLTQDF 960
DB 901 CAGYCVATFIIGIDRHSNIMVXDQGLPHIDGHLIDHKKKKFGYKREVPVLTQDF 960
QY 961 LIVISKAGQECTKREPERFQEMCKAYLAIRQHANLFINLSMMLSGMBELQSFDDIA 1020
DB 961 LIVISKAGQECTKREPERFQEMCKAYLAIRQHANLFINLSMMLSGMBELQSFDDIA 1020
QY 1021 YIRKTALDKTEQALLEYFMKQNDAAHGGWTTKMDWIFHTIKQHALN 1068
DB 1021 YIRKTALDKTEQALLEYFMKQNDAAHGGWTTKMDWIFHTIKQHALN 1068

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RESULT 2

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138110
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) alpha isoform - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I38110; S44127
C:Accession: S.; Hiles, I.; Ormondroyd, E.; Nizetic, D.; Antonacci, R.; Rocchi, M.; Waterf
Genomics 24, 472-477, 1994
A:Title: Molecular cloning, cDNA sequence, and chromosomal localization of the human pho
A:Reference number: A55636; MUID:95229146; PMID:7713498
A:Accession: I38110
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1068 <RES>
A:Cross-references: EMBL:Z29090; NID:g472990; PIDN:CAA8233.1; PID:g472991
C:Genetic8:
A:Gene: GDB:PIK3CA
A:Cross-references: GDB:370915; OMTW:171834
A:Map position: 3q26.3-3q26.3
C:Superfamily: phosphatidylinositol 3-kinase
C:Keywords: phosphotransferase

```

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Query Match 99.1%; Score 5657; DB 1; Length 1068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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```

QY 1 MPPRSSGELMGILHMPRIILVECLLPNGMITVLECLRAATVITIKHELFEKARKYPLHQ 60
DB 1 MPPRSSGELMGILHMPRIILVECLLPNGMITVLECLRAATVITIKHELFEKARKYPLHQ 60

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DB 1 MPPRSSGELMGILHMPRIILVECLLPNGMITVLECLRAATVITIKHELFEKARKYPLHQ 60
QY 61 LLDDESSYIFVSTQAEAREEFDETRRLCDLRLFQPLKVLIEPVGNREKILNREIGFA 120
DB 61 LLDDESSYIFVSTQAEAREEFDETRRLCDLRLFQPLKVLIEPVGNREKILNREIGFA 120
QY 121 IGMVCEFDWVXDPEVQDFPRNILLNVCKEAVDRLDINS PHSRAMYVY PPNVSS PELPKH 180
DB 121 IGMVCEFDWVXDPEVQDFPRNILLNVCKEAVDRLDINS PHSRAMYVY PPNVSS PELPKH 180
QY 181 IYKLDKQCIIVYIWIYVSNNDKQKTYLKLINHDQVPEQVIAAIRKTRSMLSSEQLK 240
DB 181 IYKLDKQCIIVYIWIYVSNNDKQKTYLKLINHDQVPEQVIAAIRKTRSMLSSEQLK 240
QY 241 LCVLLEYQKYLILVYCGDEYFLEKYPISQYKIRSCIMLGPMNLMMAKESLYSOLPMD 300
DB 241 LCVLLEYQKYLILVYCGDEYFLEKYPISQYKIRSCIMLGPMNLMMAKESLYSOLPMD 300
QY 301 CFMPYSRRIISTATPYMNGESTKSLWVINSALRIKILCATYVNVNIRIDIKIYVRTGI 360
DB 301 CFMPYSRRIISTATPYMNGESTKSLWVINSALRIKILCATYVNVNIRIDIKIYVRTGI 360
QY 361 YHGGEPICDQVNTQRYPCSNPRNEMLVNDIYIPDLPRARLCLSTCSVKGKGAKEHC 420
DB 361 YHGGEPICDQVNTQRYPCSNPRNEMLVNDIYIPDLPRARLCLSTCSVKGKGAKEHC 420
QY 421 PLAMGNINLFYDITDLTVSGMALNLPVPHGLEDLNPIGVTSNPKETPCLEBDFW 480
DB 421 PLAMGNINLFYDITDLTVSGMALNLPVPHGLEDLNPIGVTSNPKETPCLEBDFW 480
QY 481 SSVKKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
DB 481 SSVKKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
QY 541 SEITEQKDLMSHRHYCVTIPETLPKLLSVKMSNDEVAQWCLVKDMPPIKPEQAME 600
DB 541 SEITEQKDLMSHRHYCVTIPETLPKLLSVKMSNDEVAQWCLVKDMPPIKPEQAME 600
QY 601 LLDONYPDPWGRGAVNCEKYLITDDKLSOYLIOLVOLKYEOLDLNVLVFLKKAALTN 660
DB 601 LLDONYPDPWGRGAVNCEKYLITDDKLSOYLIOLVOLKYEOLDLNVLVFLKKAALTN 660
QY 661 QRIGHFFFMHLKSEMHKKTYSQRFGLLESYCRACGMVYKHLNRQVAMEKLIINTDILK 720
DB 661 QRIGHFFFMHLKSEMHKKTYSQRFGLLESYCRACGMVYKHLNRQVAMEKLIINTDILK 720
QY 721 QEKKDETQYQMKFLVEQMRPDMALQGFSLPLNPAHQGNRLBECRIMSSAKRPLW 780
DB 721 QEKKDETQYQMKFLVEQMRPDMALQGFSLPLNPAHQGNRLBECRIMSSAKRPLW 780
QY 781 LMNENPIMSELLFONNEIIFKNGDDLRODMLTQIIRIMENIMONQGLDRLMYPGCLS 840
DB 781 LMNENPIMSELLFONNEIIFKNGDDLRODMLTQIIRIMENIMONQGLDRLMYPGCLS 840
QY 841 IGDGVGLIEVVRNSHTIMQIOCKGKLGALQFNSHTLHQLKDNKKEIYDAIDLFTRS 900
DB 841 IGDGVGLIEVVRNSHTIMQIOCKGKLGALQFNSHTLHQLKDNKKEIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNIMVXDQGLPHIDGHLIDHKKKKFGYKREVPVLTQDF 960
DB 901 CAGYCVATFIIGIDRHSNIMVXDQGLPHIDGHLIDHKKKKFGYKREVPVLTQDF 960
QY 961 LIVISKAGQECTKREPERFQEMCKAYLAIRQHANLFINLSMMLSGMBELQSFDDIA 1020
DB 961 LIVISKAGQECTKREPERFQEMCKAYLAIRQHANLFINLSMMLSGMBELQSFDDIA 1020
QY 1021 YIRKTALDKTEQALLEYFMKQNDAAHGGWTTKMDWIFHTIKQHALN 1068
DB 1021 YIRKTALDKTEQALLEYFMKQNDAAHGGWTTKMDWIFHTIKQHALN 1068

```

RESULT 3

```

AS4600

```

1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110k chain beta isoform - human
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: A54600
 R/Hu, P./ Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
 Mol. Cell. Biol. 13, 7677-7688, 1993
 A>Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase
 A/Reference number: A54600; MUID:94067128; PMID:8246984
 A/Accession: A54600
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1070 <Hu>
 A/Cross-references: GB:567334; NID:g455759; PIDN:AA829081.1; PID:g455760
 A/Note: Sequence extracted from NCBI backbone (NCBIN:140879, NCBIPI:140880)
 C/Genetics:
 A/Gene: GDB:PIK3CB; PIK3C1
 A/Cross-references: GDB:136233
 C/Superfamily: phosphatidylinositol 3-kinase
 C/Keywords: phosphotransferase

Query Match 34.4%; Score 1966; DB 1; Length 1070;
 Best Local Similarity 40.1%; Pred. No. 3e-126;
 Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;

Qy 1 MPPRPS-GEIKGTH--LMPPRIYECCLIPNGMIVTLBCLREAYLTITIKHELFKEARKY 56
 Db 7 MPPAMADIDIMWAVDSQIASDGSIPVDPLPTGTIYQLVPRREXTISYIKQIMLKKQVHNY 66
 Qy 57 PLHQQLDDESSYIFVSTQAEERBEFFDETRRLCDLRFQPLKYTEIPVGNREKILNRE 116
 Db 67 PMNNLMIDISYFACNOQAVVEELEDETRRLCDVAFPLVKLIVRSCDPEEK-LDSK 125
 Qy 117 IGFALMPVCEPDMVQDEVDFFRNILNCKEAV-DLRDLPNSPESRAMYVVPVNESSP 175
 Db 126 IGVLIQKGFHEPFLMDPEVNEFRMRKRKSEKILSLVGL-SMDMLKQTIYP--EHEP 182
 Qy 176 ELRKAHLYNKDKQOIIIVIVIVISPNNDKQYTLKINHCVQVIAEAIIRKTRSMWLS 235
 Db 183 SIPEINDELKLYGSKLIVAVHVF--ENCQVFSFQVSPNNMFIKVNELAIQKR----- 231
 Qy 236 SEQLKLCVLEVOGK-----YILKVCQGDVEYFLEKYRPSQYKTRSCIMLGMPYML 287
 Db 232 -----LTIHKEDEVSPPYDVVLOVSGVEVEFGDHPIQOYLRNCCVNNRALLPFI 283
 Qy 288 MAKESLYSOLPMDCFMPSYRSRISTATPYMNGETSTK--SLWVINSALRIKILCATYV 344
 Db 284 VECCKIKKRYVEQGMIAEAINNSNMLRPLRPKTRITISHWENNPPQIVLVGN-- 341
 Qy 345 NNINRIDIKIYVVTGYHGGEPFLCDVNTQRPVCSNPR-WNEMVINYDIYIPDLPRARLC 403
 Db 342 KINTEBTVKVVHVRAGLFHGTETLCTIVSEVSGKNDHINPELFDINICDLPRMARLC 401
 Qy 404 LSTCS-----VKGRKGAK-----EEHCPLANGNINLFDYDTTLVSGKRALNL 445
 Db 402 FAYVAALDKVKYKKSRTKTNPSKYQTIIRKAGKHYVAVWNTVDFPKGOLRTGDIILHS 461
 Qy 446 W-FVPHGLEDLNPICVGTGSPNPKETPCLELEFDWSSVYKFEPM-----SYVE 493
 Db 462 MSSFPBELBMLNPMGTVOINPTTENAT-----ALHVKPEPKKOPRYVPPFKILIE 513
 Qy 494 EHAMSVSREAGSYSHAGLSNRLARDNLENDKQLRAICTRDPDLSITEOEKFLMS 553
 Db 514 KAAEIASDSANVS-SRGG-----KKFLPVILKEILDRDPLSLQCEHEMLMIYT 560
 Qy 554 HHNYCYTT-PEILPKLLSYKNSRDEVAQMYCLVQDWPPIKPEQAMELLDCNPPMVR 612
 Db 561 LKQDCSEIFPQSIPKLLSIKMKKEDVQQLQILQIWPGLPPREALLELDFHYPPQYVA 620
 Qy 613 GRAVRCLEKYLFDKLSOYLIOQVOYLKKEQOYLDNLVLPFLKKAALTNRIGHFFMHLK 672
 Db 621 EYAVGCL-RQMSDEEISQILQIVQVQLKEPFLDCLSRFLERALGNRRITIGGLFWHLR 679
 Qy 673 SEMANKTVSQRFGLLESYCRACGMYLKLINRQVEAMEKXILNLTILKQEKKEDETOKVOM 732

Db 680 SEVHIPIAVSVQFGVITIEAYCRGSGVGMKVLISKQVEALNKLKLTNSLTKLNAVKLNRKAKG 739
 Qy 733 KFLVEQRRPDPMDALQGFLSPINPAHQGNLLEBECRIMSASRPLMLWMPDINSSEL 792
 Db 740 EAMHTCLQSAVREBALSDLOSIPCVITSELVEKCKYKDSKKPLMYLVNN-KVFG- 797
 Qy 793 LPONNELLFNGKGDRLKQDMLTLQIIRIMENIWONOGDMLMLPYGCLSIDCVGLLEVR 852
 Db 798 -DSVGVIYFNGSGDLDQMDMLTLQMLMLDLWKKEAGIDLFMLYGGCLATDRBGLIEVS 855
 Qy 853 NSHTIWOIQ-C-KGGLKCALQFNSHTLHOWLKDKNKEIYDAIDLFTRSCAGYCVATEIL 911
 Db 856 TSETIADIQLNSGNVAAAFAFNKDALMLWKEVNSGDDLDRAIEEFTLSGAGYCVASYVL 915
 Qy 912 GIDDRHNSNIMVDDQDLPHIDRGFLDHDKKKKFGYKREVPVVLQDFLIVISKAQEC 971
 Db 916 GIDDRHSDNIMVKKTQLPHIDGHILGNFKSKFGIKREKRPVPLITLYDFHVIQCG--KT 973
 Qy 972 TKTRFEERFOEMCYKAVLAIRQHANLFINLFSMWLGSQMPQLQSPDDIAYIRKTLALDKT 1031
 Db 974 GMEKRGRRPQCCEDAYLIRKGNLFTITFALMLTAGLPBELTSVADIOYLKDSIALGKS 1033
 Qy 1032 EOEALYIFMKQNDAAHNGGWTTKMDWIFPTIKQ 1064
 Db 1034 EEBALKQFKQFDEALRESWTTKVMWMAHTVRK 1066

RESULT 4

T43502
 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110k chain - mouse
 N/Alternate names: p110delta protein
 C/Species: Mus musculus (house mouse)
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C/Accession: T43502
 R/Chanrky, D.; Vojtek, A.; Kaeshian, A.; Holtzman, D.A.; Wood, C.; Gray, P.W.; Cooper, J. Biol. Chem. 272, 19236-19241, 1997
 A>Title: p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit that associates with p85 and p50
 A/Reference number: Z22519; MUID:97382246; PMID:9235516
 A/Accession: T43502
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1043 <Cha>
 A/Cross-references: EMBL:U86587; NID:g2331237; PID:g2331238; PIDN:AA05676.1
 A/Experimental source: spleen
 A/Note: highly expressed in lymphocytes and lymphoid tissues
 C/Superfamily: phosphatidylinositol 3-kinase
 C/Keywords: phosphotransferase

Query Match 34.3%; Score 1958; DB 2; Length 1043;
 Best Local Similarity 39.7%; Pred. No. 1e-125;
 Matches 429; Conservative 187; Mismatches 391; Indels 74; Gaps 19;

Qy 16 MPP-----RILVECLIPNGMIVTLBCLREAYLTITIKHELFKEARKYPLHQ 60
 Db 1 MPPGVCMEHFWTKESQSVVVDLPLPTGVYINLFPISRNALSTIKOVLMHRAQYPLH 60
 Qy 61 LQDESSYIFVSTQAEERBEFFDETRRLCDLRLFPPLKVIIEPVGNREKILNREIGA 120
 Db 61 MLDPEAVYFTCVNQAEQOELEDEQRRLCDIOPFLVRLVARBEDRVKKLINSQISLL 120
 Qy 121 IGMVCEPDMVQDEVDFFRNILNANCKEAVDLRLDINSHNSAMYYIPVNVSSPELPR- 179
 Db 121 IAKGLHEPDSLNDPEVNDRTKROFCERAAHRLQGLGVNEMLOYSFPLQELSPARGWA 180
 Qy 180 ---HIYNKLDKQOIIIVIVIVISPNNDKQYTLKINHCVQVIAEAIIRKTRSMWLS 236
 Db 181 GLLRVSNR-----ALLVWVKFEGSSSEFTFQYSTKMPALAMACHARKK-----A 225
 Qy 237 EOLKLCVLEVOGKYLKVCQDEYFLEKYRPSQYKTRSCIMLGMPYMLMAKSLYSQ 296
 Db 226 TVRQPLVQEPREVALQVGRHEVLYGNVPLCHFOYICSLHSGLSPHLTVHSSILAM 285


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QY 297 LEMDCFTMPSYSRRISTATPYMNGETSTKSLMVINSALRIKILICATYVNVNTRDIDKIYV 356
DB 286 RDEQSNPAQOVQPRAKPPPIPAKKSSSVSLMLEQPSIELIEGRKXVADER--MKLVY 343
QY 357 RRGTYNGSGPLCDNVQTV--PCSNPRNMENLVYIDLPAAALCLSTIGV----- 409
DB 344 QAGLFNGNMLCTCTTSSSEVNVCSSEPMWQORLEFDISVCDLPMAALCFALYAVVERKAK 403
QY 410 --KGRGAKEEHCPGLMGNINLPDYDTLVSGKALNLP--VEHGLEDLNP1GVTGSPN 466
DB 404 AASTKKSKKACDPIANALMLFDYDOLKTGERCLYMPSVDEKGEILNPAGTVGRNP 463
QY 467 NNETPCLLEDFMSSVVKFPMDSVIEEHANMSVSRBAGFSYSHAGISNRLANDNELREN 526
DB 464 NRESAA-----ALVILYLP---VAHPVPPALKEILIEGRHGGRHIT--EEEL--- 508
QY 527 DKEQLAICTRDPLSEITEOKDFLMSHRHYCT--IPELIPKLLSVKMSRBEVQWMC 585
DB 509 ---QLREIILERRSGELYEHEKDLVWKMREHVEQEHPEALARLLLVTKMKHEDVAKMLY 565
QY 586 LVKDWPRIPKEQAMELLDCNYPDPMYRGFAVRCLEKYLTDKLSQYLQILQVLYKYEQYL 645
DB 566 LKCSMBELPVLSTLELDSSFPDCCYGSFAIKSLRK--LTDELFOYLQILQVLYKYESYL 624
QY 646 DNLLVFLKKAALTNRIGHFFFWHLKSEMNKNTVSQRFGLLESTYGRACGYLKEHLNRQ 705
DB 625 DCLTLFPLGRALANRKIGHFLFWHLHSEMHVPSVALRFGILMEAYCRSGSTHMKVLMKQ 684
QY 706 VEMAEKILINTDLKQEKDETOQVOMKFLVEO--MRPRDMDLQSLPLSNPAHQGNL 764
DB 685 GEALSKIKALNDPVKYSQ--KITKPKQTKEMWMCMEQETMEALSHLQSLPDSSTLBEV 743
QY 765 RLBCRIMSASAKPPLTMNMENPDIEMSELFPONNEIIFKNGDDLQMDLTIQIRIMENI 824
DB 744 CVECTTMDSKMPLTMSYSEBAGSA---GNVGIIIFKNGDDLQMDLTIQMDQVLM 800
QY 825 QNQGDLRLM.PYGLSTIGDCVGLIEVVNRNSHTTMOIC--KGLKCALQFNSHTLHQMLD 883
DB 801 KQSLDLRMTPYGCLPTPGDRTGLIEVLHSDTIANIOLKSNMATAAFNNDALNMLKS 860
QY 884 KKKGEIYDAIDLFTSCAGCYCATFTLIGIDRHNSINIMKDDGOLPHIDGFLDKKK 943
DB 861 KNPBEALDRAIEEFTLSCAGCYCATYVLGIDRHSDIMIMRESGOLPHIDGFLDKPKT 920
QY 944 KFGGRERVPFVLQDFFLIVISKGAOECTKREPERFOEMCYKAYLAIRHANLFINLFS 1003
DB 921 KFGINRRVFFILYDFVHVIQOG--KTNNSEKFERPRGVCERAVTILRRGGLFLHFA 978
QY 1004 MMLSGMPELQSFDDIAYIRKTLALDKTEQALEYFMKQMDAHNGGTTVMNIFHTIK 1063
DB 979 LMRAGAPBELSCSDIOYLKDSLALGKTEBALKHFRVFNBEALRESWTKVNNLHVNS 1038
QY 1064 Q 1064
DB 1039 K 1039

RESULT 5
T13950
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13950
R:Leevers, S.U.; Weinkove, D.; MacDougall, L.K.; Hafen, E.; Waterfield, M.D.
EMBO J. 15, 6584-6594, 1996
A:Title: The Drosophila phosphoinositide 3-kinase Dp110 promotes cell growth.
A:Reference number: 217828; PMID:97133288; PMID:8978685
A:Accession: T13950
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1088 <LBB>
A:Cross-references: EMBL.Y09070; NID:g1707447; PIDN:CAA70291.1; PID:g1707448
C:Genetics:

```

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A:Cross-references: FlyBase:FBgn0015279
A:Map position: 3
C:Superfamily: phosphatidylinositol 3-kinase
C:Keywords: phosphotransferase

Query Match          29.4%; Score 1677.5; DB 2; Length 1088;
Best Local Similarity 35.1%; Pred. No. 1.7e-106;
Matches 364; Conservative 217; Mismatches 385; Indels 107; Gaps 28;

QY 24 CLIPNGMTVTELEBEATLITTKHELFEAKRYPLHQLIDSSSYIFPSVTOEAREBEFF 83
DB 49 CLIPNGFLELEAVNPANTIQIVIKEMVNOAKQMPGVYKEACEQVYGIS--TFNIBPT 107
QY 84 DETRLCDLRLOPLFKVIEPVGNREE-----KILREIGFALGMVCEFDYK 132
DB 108 DETRLSEV---QPPGILS--LGERDVTSSSDYELTMVNGMGIG-----TTFDHR 156
QY 133 ---DPEVQDFRRNINLVCKEAVDLRLDLSPHSRAMVYVPNVSESELEPKIYNKLDKQ 189
DB 157 THGSEPIDDFRLYMTQCNILERSAYWQORLLEHFLRLANGSTKPELIRERHPT 216
QY 190 IIVVIVIVISPNNDKQYTLKINHDCVPEQVIAEAIKRTSRMLSSBOLKLCVLEYQK 249
DB 217 FLIV---VKNEHQSTFLISVNEODTPPSLTSTLOKXNRSGOMKXNR-----TSD 264
QY 250 YILKVCCEBEYLEKYPLOYKYIRSCIMLGMPNIMLAKSILYSQLEPMDCFMPSYSR 309
DB 265 YILKVSGRDEYLLGDPLLOFLYIQMLSDSAVPNVL--QSVR--LESTINHNHQ 318
QY 310 RISTATPYMNGET----STKSLMVINSALRIKILICATYVNVNTRDIDKIYRTGIYHG 364
DB 319 AMYTKRPLRKRIYVHLHKISLSIMDMGNFQLTLSISVNFQTRALKGVAVCLYHGD 378
QY 365 EPLCDNVNTQRYPCSPRNEMW-----NYDIYEDLPAAALCLSTIGV---KGRG 414
DB 379 KKLCAQSTD---SPGNEDTFLENDLVMPFDIQMNLPRMTLCVIEEVTMKSSKXS 435
QY 415 AKSEHC-----PLMGNINLPDYDTLVSGKALNLPVPHGLE--DLLNPIGV 462
DB 436 SNKIDIALKDPVKNPDLAVNNTTIDDKDLRTGHTLTYYADDIGVEVPHLGTI 485
QY 463 GSNPKETPCLLEDFMSS---VVKFPMDSVIEEHANMSVSRBAGFSYSHAGISNRLAR 519
DB 496 EPRPRKE--ECALVDLTLFSSGCTGTVAPSEEVLYQA--ADREQ-----VNRQR 542
QY 520 DNELRENDKQDLAICTR---DPLSEITEQEKDFLMSHRHYCT--IPELIPKLLSVK 574
DB 543 QLAGPEKRIKELKELMANYGLDKIYEMVQDNRNAIWERNDTILRELPELSLILHCVW 602
QY 575 NSRDEVAQWCLVKDWPIRPEQAMELLDCNYPDPMYRGFAVRCLEKYLTDKLSQYLQ 634
DB 603 KERDDVADMWYLLKQWPLISERSLELDYAPDPVARRRAICLH--FLDDEDLILYLLQ 661
QY 635 LVQVLYKYEQYLIDNLVFLKKAALTNRIGHFFFWHLKSEMNKNTVSQRFGLLESTYGR 694
DB 662 LVQAIKHESTLBSLVFLFLRALRNQRIGHYFFWHLRSMQTPSMQTRFGLLEVLK 721
QY 722 CKHHVAPLRQQLHVLKQKSLAKKSKKEXKVTMLQDFLRQDRNSAVF---QNTQNP 777
DB 755 LNPAAHQGNLRLECRIMSSAKPPLTMNMENPDIEMSELFPONNEIIFKNGDDLQMDL 814
QY 815 QIRIMENIMONQGLDRLM.PYGLSTIGDCVGLIEVVNRNSHTTMOICQGLKCALQ--FN 873
DB 834 QMLRVMDLKRQDGMDRAMINYNISMSKSGIMLEVVNRHMETIANIKKKGMSFATSPFK 893
QY 874 SHTLHQLDKDKK--GEIYDAIDLFTSCAGCYCATFTLIGIDRHNSINIMKDDGOLPHI 932
DB 894 KGSLSMLKHNKRNADKLKAIINFTLSAGYCATYVLGIDRHSDINIMKNGOLFHI 953

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Db 694 -----LPIVGNKILISIFLPITQVTKLTLELEMTADQFNRLFTKQYS 739
Qy 247 -----OGKILKVCGEDEFLEKYPISQYKIRSCIMLGRMPLMLM-AKESLYQL 297
Db 740 KHLNPNVSNHPLIKVGGSDFIHGPHDIRTEPSIRNHIIQGTQPLTIQSPKPELDOP 799
Qy 298 PMDCFTMPS---YSRRISTATPYNGESTK-----SLAWINSALRIKI 338
Db 800 FKRPEDIPPELLIDHSCSNALINCNNNTNNTNNINPNDMQDITHISIREIKKPRKXV 859
Qy 339 LCATYVWVN-IRDI-D-KIYVRTGIYHGEPICDNVNTQRPV-----CSNPRNEML 387
Db 860 MGSIRIPLSCIKIDISSSVIVISILYHGIECFSKAFQPIIPPPAPLAETLSVWCBL 919
Qy 388 NY-DIYIPDLPRARLCISCS-----VKRKAKEHCPLAGNINLPDYDTTL 436
Db 920 VFTNIDVSNLPVDALISIVYSANETVDVEIKNLDATKRLPIGINWITDFKYL 979
Qy 437 VSGKALNLMVPPHGLDLPNPIGVTSNP-NKETPCLEFPDMFSSVYKFPDMVIEBH 495
Db 980 RQGVNELSLMP-----SPFSNPLGCSNPPSSQSGVLTLEFEENLVLFP----- 1026
Qy 496 ANMSVSRAGPSYSHAGLSN--RLARDNLEBNDKEQLRAICTRDPLSEITEQKDFLWS 553
Db 1027 -----RKTKFTSVSVEIQEPPTNINSNEMRE-FEQITLAL---DPLDLKQEKYNOQMT 1076
Qy 554 HRHVCVTIPEILPKLLSVKNSRDEVAQMYCLVQWDPPIKPEQAMELLDCYPPMWRG 613
Db 1077 LRHYSILPPOVLPRLMLSVPTQATVADVAISLDRMPKRLKYSELELLDKHAKRKRE 1136
Qy 614 FAVCLEKYLTDKQYLQIOLVOYLKYEOYLDNLVFLKKAALTNORIGHFFMHLKS 673
Db 1137 FAVTCLDQ-LSEDELLDILQVLQVLYKTEPRHDSKLSFLKAKALLNNIGHSPWYLS 1195
Qy 674 EMHNKVSQREGLLESYCRACMYLKHINROVEAMEKLIINTDLKQEK--XDETQXQV 731
Db 1196 DLHNSNLBERGILLLESYLVACGARIETLQ---MEVINNLTEVAKKIKPLKQDDR-- 1250
Qy 732 MKFLVEQRRPDMALQGPLSPNPAHOLGNLREBCRIMSSAKRPLMLKENDIMSE 791
Db 1251 -EFMIKER---ESLEWPKRPHLTLPNRPESNGLIINKSKYMSKPLRLSTNTNDMMAD 1306
Qy 792 LTFQNNETIPKNGDRLQDMLTIOIRIMENIMQOGDLRLPYGCLSIGDVCGLIEV 851
Db 1307 PI---EYIFKAGDRLQDMLTIOIRIMENIMQOGDLRLPYGCLSIGDVCGLIEV 1362
Qy 852 RNSHTIMOIO-CKGKALQAFNSHTLQWMLKDKKKEI-YDAALDELFTSCAGYCVATF 909
Db 1363 LNSHTAKIOKSEGG--GAFPRQVGSFGQLILQHNKSDMEYQKAVDTFILSCAGYCVATY 1420
Qy 910 ILGIDRHSNINMYKDDQQLPHIDGHLIDHKKKKFYKREVPVLYQDPLIYISKAGQ 969
Db 1421 VLIGIDRHSNINMYKGGFLPHIDGHLIDGHLGNYKKKFGFRERAPVPVFPDFCYVN--GQK 1478
Qy 970 ECTKREERFEREMCYKAYLAIROHANLFINFNMWLSGMPLESPFDIAIRITLAD 1029
Db 1479 ESFK---ISQFVNYCTGGINIVKNAKLPNNLPAMNVTGIELOSMEELNYLKESFSE 1535
Qy 1030 KTEQEALEYFMKONDAHHGGWTTKMDWIFHTIKOHA 1066
Db 1536 LSDAKAREKVALIHES-LATKITQLNNPFHHL-AHA 1570

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RESULT 8

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T18273
1-phosphatidylinositol 3-kinase (BC 2.7.1.137) 2 - blime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18273
Rizhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A:Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bid

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A:Reference number: 206411
A:Accession: T18273
A:Status: Preliminary; translated from GS/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1858 <ZHO>
A:Cross-references: EMBL:U23477; NID:9733521; P1D:9733522; P1DN:AAA65722.1
C:Genetics:
A:Gene: PIK2
C:Keywords: phosphotransferase

Query Match      22.1%; Score 1262.5; DB 2; Length 1858;
Best Local Similarity 28.7%; Pred. No. 1e-77; Indels 317; Gaps 42;
Matches 366; Conservative 197; Mismatches 397;

15 LMPRIIVECLPNGMI--VTECLREATLITIGHLEFKARKYP-LHOLQDESSYIF- 70
Db 657 LIPHEYLKUSVNSTISNETLP-LRQOTLM---QACNISRLLPKHLILKSSSTIILD 711
Qy 71 -----VSVOAEREEREPDETRLCDRL-----FOPLKYIEPVGN 107
Db 712 GASTTTTTTTTTTTTANQSNITTKNSSIDLTINNSNEIIDVKCHIQALELIEFELIGT 771
Qy 108 REEKILNREIGFALGMVCEFDWKDPEYODFRN-----ILNCKEAVDLRLDLSHSR 162
Db 772 SFTRVLD-----QGEVVSFRDFAQFRLSNFTSTRNDL-----SQ 807
Qy 163 AMYVYPNVSSEPELPKHIVNKLDKGQIIVIVIVASPPNDKQKYTLKINHDCVPEQVIA 222
Db 808 MIVY-----SSEPLPLTPRK-----ITIMWL- PGDGK-----IKKRVDCPPNSVG 849
Qy 223 EAIRKTRSMILSSEQLKCYLEYQK-----YILKVCGEDEYF-----EKYP 266
Db 850 DVKKEIFKPMIDR-----VHQGKTODPVLKVGFRYLICHELGNLTSRQFYF 903
Qy 267 -----LSQKIRSCIMLGRMPLMLM----- 288
Db 904 TSGGDESLMDYDIKQCVGKQVLELSTNNSILSLNQSEKVSFIKILLETSDPDYD 963
Qy 289 -----AKESLYQLPMDCFPM----- 304
Db 964 EDLSINSNSFDLKQSIQOQOQOQOQIOTVINIKRTNKENKDNKENKDNSSNNNNNNNN 1023
Qy 305 -----PSYSRRISTATPYNGETS-----TKSLWYI- 330
Db 1024 NNNNNNNNNNNNNNNNNNNNNNNNNNSNSISGSLDEGSGSGSGSEQPTLIG 1083
Qy 331 -----NSALRIKILCATY-VNV-NIRPD-----KIYVRGIY 361
Db 1084 VQNFSLPNNSKLPINIVGRLEFRVNIAGRLNFPNNEDARKKADGKNQGNVAVMAELY 1143
Qy 362 HGEPLCDNVNTQRPVCSN-----PRNEMINVDIYIPDLPRARLCISGVGRK 413
Db 1144 YGSELINPVETTPPIAQLASVDSGSEVPENWEKGLAFTIPRIYLPRARASTVVTITSE 1203
Qy 414 GAKEE-----HCPLAGNINLPDYDTTLVSGKALNLMVPHGLD--LNPIGVTS 464
Db 1204 ALBSQMEVVSCKSLPIGNSNCLMNHKMLMGTAFLRW-----DGRBRANDIGTCVD 1257
Qy 465 NPKNETPCLEL-EFDWBSVYKFPDMSVIEBHAN--MSVSEAGPSYSHAGLSNRLARON 521
Db 1258 NOAKOPITLLVBESEFIRPIVYVDTALQSMKVVNDSSISSNGVESPEIVSFSSAASS 1317
Qy 522 ELRE-----NDKEQLRAICTRDPRLSEITFOEQDFLMSHRHYCVTIPILPK 567
Db 1318 PLPSSEPLSPVGLKLLDDEARRRLKALMDSPLVOLSLMEDKVLVYGRHLYKSPKALAK 1377
Qy 568 LLLSVKNSRDEVAQMYCLVQWDPPIKPEQAMELLDCYPPMWRGFAVRCLKXYLTDK 627
Db 1378 FLTSLNWDIPQVNDAYAQMDMALKRYQALDELIDAFABEHVNRFAIKIINSP-SDAE 1436
Qy 628 LSOYLIQVLYKYEOYLDNLVFLKKAALTNQ-RICHFFPHLKSMEHNKTYSORGL 686
Db 1437 FSDFLQTLQVLYKTEPEYNSDLTILIORALNSRSRIGHFFFWFLKSEMHPTIEIBRYGL 1496

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QY 687 LLESYRACAGMYLKHNRQVEAMEKLIINTDILKQEKDETOXYQMKFLVEQNRPDMD 746
DB 1497 LLEGYRSCGCTHRODILIKONQVLSKSLHTVAMAVQCTGSSERK---KYLEGSLKIKFPD 1553
QY 747 ALGGLSPSPARQGLSLREBGRIMSSACRPMLTMENPDIMSHLLFQNNELIFKRGDD 806
DB 1554 TFO---LPLDPRWEAKGLIIDCKRYMDSKPLMLVLENVEPHAKFP---TYIFKGGD 1606
QY 807 LRQDMTLQIIRIMENIMQNGDLRLMLPYGCLSIGCVGLIEVYRSHTIMQIOCKGL 866
DB 1607 LRQDILITQYLRIMDRKWKSGMDRLQPYKCIATGSGIGMLEVYLNANITANINKAGG 1666
QY 867 KGLAQNSHTLHOMLKDKNKEI-YDAIDLFRSCAGCVATFIIQIGRHSNINWGD 925
DB 1667 TGLAL-LEEKTLVWMLKECNKTEAEYNKAVETFILSCAGVATYVMGIDGRHSNIMITK 1725
QY 926 DQGLFHIDEGFIDHKKKKRGYKREYFVLTDPLIVISKGAQECTKTEFERFQEMCY 985
DB 1726 LGHLFHDHFGHFGNKKKYGFRERAPFTFPQYMAIV--GGKD---SENFRFVYTTCC 1780
QY 986 KAVLAIRQHANLFINFSMMLSGMPLOSPDDIAYIRKTLALDKTEQALVEYFMKO--- 1042
DB 1781 SAVNIIRKNTDLFINFQMLSTGIPBELQVABEDIDYRKALAGLSDEBAAEFTKNTSV 1840
QY 1043 -----NNDAAHGGW 1051
DB 1841 ALNTKTVLNDIFH-GW 1856

RESULT 9
T18274
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18274
R:Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A:Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bic
A:Reference number: 206411
A:Accession: T18274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1585 <ZHO>
A:Cross-references: EMBL:U23478; NID:G733523; PID:G733524; PIDN:AAA85723.1
C:Genetics:
A:Gene: PIK3
C:Keywords: phosphotransferase

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Query Match 19.4%; Score 1109; DB 2; Length 1585;
Best Local Similarity 30.7%; Pred. No. 2.6e-67;
Matches 301; Conservative 189; Mismatches 374; Indels 118; Gaps 30;

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QY 146 VCKE-AVDLRDLNPSHRAMVYPPNVSSPELPKHINYKLDKGQIIVITWIVSP--NN 202
DB 562 LCKERLVLDQSLRINNGR-----PSIMWS-----HIDVLSFRKLRRLAMLAKQSNV 610
QY 203 DKQKYLTKINHDCVPEQVI--AAAIKRTS-----MLSSBGLKCVLEYGQ 248
DB 611 PAARLTPYPPKTIPEFVIRVHLFFNQKTSLRCAANNHTAFSLMTILSEKTKKTPDPPT 670
QY 249 KYILKVGCGDEYLEKPYLSQYKYIRSCI-----MLGRPMNLMLMAKESLYSGLPMD 300
DB 671 QYRFLITGNOYVDPVPLSVYIYVKIRKGEIDLTVWELSLSTGLIIQQQQQQQQQQQ 730
QY 301 CFTMSYSRRISTAT-----PYNNGETSTKSLWINSALRIKILICATY 343
DB 731 OQQQQQQQIENIDENILKINGLINVLSKIEKPIREKDNCSISLVTYEN-LQVRLHAHE 789
QY 344 VVNN-----LRDID---KIYVRGIYHGEPLCDNNVTQRPVCSNRRMWEMLVYDIID 395
DB 790 IFASKASIIITGDSPTQILTEAIVAFYGGELATQSSKLVSFQDTYVMWENWVPLAVSN 849

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QY 396 LPRARICLSICSVKRGKAKEEHCPLAWGNINLFYTDTL-VSGKMLNMLWVPHGLE 454
DB 850 IPRGARMCGL-----NARYGDI-FNIGWYGRHLFDSKGLINTFAPSLILWF-----G 898
QY 455 LNPICVTSNPKKETPCLELEFDMSSVYKFPDMVIEEHAWVSREGFSYHAGLS 514
DB 899 KINPIGCVNLSKQALIIAFEFQDYV--EKTIHYEDDLIELISKD----- 945
QY 515 NRLARNEI---RENKEQLRAICTRDPISLEIENQEDFLMSRHVCVTIPEILPKLLS 571
DB 946 ---ENGNEPLPVYTMEDMRVEQIILDDPLYSLKKEBRLIWSKRYCHTQFQLSKLLQS 1002
QY 572 VKNSRDEVAQMYCLVYKDPPIKPEQAMBLDNCYPPM-VRFPAVCKEKLVTDDGLSQ 630
DB 1003 VEWNTYKQVGEARQQLKIWPTTLSAVDALLEDLPKPDCAVEIRRYTKCLDQ-MSDYELI 1061
QY 631 YILQVQVLKYEGYLDNLVRLFKKALTN-QRIIGFFPHHLKSEMNKNTVSGRFGILL 689
DB 1062 YILQVQALKHDFNHSVLSLFLIGRWOMQVGLGHFFWHLRADIDNOECERFVTLSS 1121
QY 690 SYCR-ACGMVLYKHNRQVEAMEKLIINTDILKQEKDETOXYQMKFLVEQMRRPDMDAL 748
DB 1122 GFLRYAPQUMESFKSEITTLRIENLAKRVKVEPYEKQYVENNIREOSFPTBL--- 1178
QY 749 QGFLSPNPAHQGLNLREBGRIMSSAKRPLMLWENPDIMSELFPQNNELIFKRGDDL 808
DB 1179 ---FVPFDSIRIRLNTIIPKCKMSDAKVPWLTFFKNADFAFPL-----QMIKTGDDL 1231
QY 809 QDMLTQIIRIMENIMQNGDLRLMLPYGCLSIGCVGLIEVYRSHTIMQIOCK-KGGLK 867
DB 1232 QDITLQQLRLMDHMKWKSODLDLHMTIYRCIATGMSGTGLEEVVNSETAARIOAGAGVS 1291
QY 868 GAGQNSHTLHOMLKDKNKEI-YDAIDLFRSCAGCVATFIIQIGRHSNINWGD 926
DB 1292 GA-FQOTPIANMLKHNQNTENSQKAVSKFTLSGCVATYVLIIGRHSNINWIDH 1349
QY 927 GQLEFHIDEGFIDHKKKKRGYKREYFVLTDPLIVISKGAQECTKTEFERFQEMCY 986
DB 1350 GHLFHDHFGHFGNFTFPAFGQEKAPFVLTTPFVVI--GGKD---SPRFAPVYDICK 1404
QY 987 AVLAIRQHANLFINFSMMLSGMPLOSPDDIAYIRKTLALDKTEQALVEYFMKMDA 1046
DB 1405 AFNIIRSNHAFVETNMFELMLSTGIPRLRENDIVYRDKRFLDLDAAESYFKLIIHES 1464
QY 1047 HHGQWTKNDMIFHTIKOHALN 1068
DB 1465 -IGTLTTTINFAIH-IMAHKN 1484

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RESULT 10
S71792
1-phosphatidylinositol-3-OH kinase AGE-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 01-Dec-2000
C:Accession: S71792; T31476; T18707
R:Morris, J.Z.; Tissenbaum, H.A.; Ruvkun, G.
Nature 382, 536-539, 1996
A:Title: A phosphatidylinositol-3-OH kinase family member regulating longevity and diapau
A:Reference number: S71792; NCID:96320556; PMID:8700226
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1164 <MOR>
A:Cross-references: EMBL:U56101
R:Williams, L.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21038
A:Accession: T31476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-263, 'YEMK', 270-285, 'L', 'Q', 289-307, 324-328, 'LESY', 332-1164 <WIL>
A:Cross-references: EMBL:AL110499; PIDN:CA857914.1; CESP:B0334.8
A:Experimental source: clone Y62PSA

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Submitted to the EMBL Data Library, October 1995

A:Reference number: Z19009

A:Accession: T18707

A:Status: preliminary; translated from GS/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1089-1164 <M12>

A:Cross-references: EMBL:Z66519; NID:G1044812; PIDN:CAA91377.1; GSPDB:GN00020; CESP:B0334

A:Experimental source: clone B0334

C:Gene: CESP:B0334.8

C:Genetic: B

A:Map position: 2

A:Insertion: 22/2; 117/3; 307/3; 748/2; 835/2; 960/2; 1077/2; 1121/3

C:Superfamily: phosphatidylinositol 3-kinase

Query Match 19.0%; Score 1085; DB 2; Length 1164;
Best Local Similarity 26.6%; Fred. No. 7.1e-66;
Matches 310; Conservative 221; Mismatches 424; Indels 212; Gaps 37;

39 EATITITIGHELPK--EARKYPLHLOLODESSYIFVSVQBAEREFEFDETRLDLRLFQ 96
70 EIKLSDFHQLFELIAFMKWTYSVKPD--YVFQQLNPFELIVIFNDDQPLSLTEHG 127
97 --PELVIEPVGNREKILNREIGPAIGMPVCEFDMPKDEPVODERRNILLVCCAEADLR 154
128 TFFMLFLYQPDGINDDKELMSDISHCLGYSIDKLDESLDEELRQFRAISLMARTKTCULTR 187
155 DINS-----PGRAMV---YPPNVSSPELPKAITN---KLDGQI-----IVVIWV 196
188 GLEGTSHYAFPEEOYLVCGESCPKDESVKXAKLSYGMFMKRRKRAELINGVCEKMKLQI 247
197 IVSPNDNQ-----KYTLKINHDCVPEOVIAEAIIRKTR-----SMILSSEQ 238
248 EFNPNETPKSLIHLTSLRINAIKLDVYDTDDADBGKPSSELAGTTFTYTNDDVGLTSYD 307
239 LKL-----CVLEYGQKYLKVCQDEFELEKY-----PLSQYKYS----- 275
308 VRLQGNIFVQLKLTQGVASERLRCPGVVARQSLVLKDCRPKPLVEPHYRAHERKL 367
276 -----CIMLRMPNIMLMAKESLYSQLPMDCTMBSYSRRISTATIPYMGESTSISWVI 330
366 ALDVLSVSDSTP-----KQSKNSDMVMTDRPTASLKHQV-----SLMDL 407
331 NSALRKIKLCATYANNINDDIP-----KIYART--GIYHGBPLCDNVATQPCSPNRP 383
408 DNLMIR-----PNISGFDFPADVDVMIYERFSVYGTLLTMSK--STKYVNAOFKYN 459
384 N--EWLNYYDIYDPLPRAARLCISICVSKRKQKKECHCLAWGNINLPDYDTLVSGXA 442
460 NKEMYTFDLKMDMPSA--VLSIRVLGKVKLKSEEPVGWNNMSLTIMRBLRQGGQL 517
443 LNLN--EVPHGLBDLLNPIGV--TGSNPNKETPTCLELEFDMFSSVYKPPDMS---VIEEIA 496
518 PHMAPEPTANRSGRIGENGARIGTN-----AAVTIISYSGGRVMPGQYTVLVKRS 572
497 NMSVSREAGSYSHAGISNRLANDELRENDKQLAICTRDPLSE----- 542
573 TWTEET-----LNTMGDDYE-----SCRDRGYKLOMLYKKESSGIV 609
543 ITTQGEQDFLMSHRHYCVTIPETLPKL-----LSVKNSRDEVAQWYCLVKDMPKIPKQ 597
610 LEEDEQGHVMMWRRY---IQQEPDLLIYSELAPWTDRENSSELYMLEKKKPPSVAA 666
667 ALLDLGKRCLDRIYRKFAVEKLNBOQLSPVFHFLIPRLIQLATKYERPAQGEVGMMLITBA 726
658 LTNORIGHFFFWHLKSEMH-----NKTYSQRPGLLSEYCAQGYLKLHARQVEAME 710
727 LCDYRIGHRLFMLIRAIARLDCDLKSEEFYRRISLIMEAYVLGNNEEHIKIITROYDMVD 786
711 KLINLTDLKQEKD--ETQKY--QMKRLVQMRPPDMALQGLSLPNRHOGLGNIRLE 767

[illegible]

```

QY 298 --PMDCTM-----PSYSRR1-----STARPYNG-----320
Db 512 HNEVDALFLDGDPLADRVOSVKAICNALAAVEPILTSALNQLPPCSRMQPKIQK 571
QY 321 -----ESTKSLWYNSAL--RIKILCATYNNVIR-----349
Db 572 DPSVLAVRENRKVEALTAIDLVELYCNTF--NADQTAVPGRKHDLVQEACHARS 630
QY 350 -----DIDKIYRTGIYHGEPICDNVNTQVPCSNP-----WNEML 387
Db 631 LAFTVATHRIPITWATSYEDFYLSCLSHOGKMCSPLOTRRALFISKYLFHLIWMQOI 690
QY 388 NYDIYIPDLPPARLCLSTICSV-----KGRKAKEHCPC--IAMGINLPDYDTLVSG 439
Db 691 CFPQVVRRLPRETLICATYVALPIPPGSSSEANKQKRVPEALGMVTPPLNFQVLTG 750
QY 440 KMALNIMPVHGLEDLNPIGVTGNSNPKETP---CLELFPDMSVYKPPDMSVIEHA 496
Db 751 RKLGLMPATQOE-----NP--SARWASAPNFQPSVILQIDPFTSAFDIKETS---PPGD 800
QY 497 NMSVSRAGESSYHAGLSNRLARDNELRENDKEQLRAICTRDPLSEITBOEKDFLMSHRH 556
Db 801 KFBPRVYFG-----SLREEDQKTKOIMOKESLYWLTDDKRLMEKRY 844
QY 557 YCATIPEILPKLLSV---KMSRDEVAQWYCVKQWPIKPEQAMELDCNYPDPWVRG 613
Db 845 YCHSEVSSLPLVLASASPMEMACLPDI---YVLLKQTHNHQDALCLLHATFPDQVVR 901
QY 614 FAVRCLEKYLTDKLSQYLQVQVULKYBOYLDNLVRFLLKALTNQRIIGHFFHMLKS 673
Db 902 MAQWQIGS--LSDDELLADYLPOLVQALKYBCYLDSPVLRFLKRAVSPLRVTHYFFMLKD 960
QY 674 EMNKTYVSQFGLLBSYCRACGMYLK--HNRQVEAMEKLINLTDIKOKKDETQVQVM 732
Db 961 GLKDSQESIRYOYLALALCCCGKGLREBFNRQC---WLVNALAKLAQOVRKAPASARQ 1016
QY 733 KFLVEQRRPDMALOGFLS--PLNPAHQGNLRLBECRIMSSAKRPLMWNENPDIMS 791
Db 1017 GIARTGLEEVKQFFALNGSCLRLPLSPBLVKGIVPRCSYFNSNAVPLKLSPOVPLGE 1076
QY 792 LLFQNNELIFKNGDDLRODMTLTQIRIMENIMONQGLDRLMPLPYGLSIGDCVGLIEV 851
Db 1077 ---NIRVIFPKCDDLRQDMTLQIRIMSKIRWOBELDMRWIVIFRCFSGRGRGWEMV 1132
QY 852 RNSHTIMOIOCKGGLKALQFNSHTLHOMLKDKNKG--IYDAALDLFTRSCAGCYATFI 910
Db 1133 PNAETLRKIOVEHGVTS--FKDRPLADWLOKINPGDEYEKAVENFIYSCAGCCVATYV 1190
QY 911 LGIGDRHNSNINWVDGQLPHIDFGHLDHKKKFGYKREVRPFVLTDPLIVISKGAQ 970
Db 1191 LGICDRHNDIMLKTGHMFHIDFGHFLGHQMGFNIRKDRAPFVLTSDMAVYINGDKP 1250
QY 971 CTTTRFEPFQEMCYAYLAIROHANLFINLFSMMLGSGNPELOSFDIAVIRKTLALDK 1030
Db 1251 SSR---FHDPEVDLCCQAYNLIRKHTHFLNLILMLSCGIPELSELEDLKYVDALRPQD 1307
QY 1031 TEOEALYFMKQMDAHGGMWTKMDIFHTIKQ 1064
Db 1308 TEANATTYFTR--LISSSLGSVATKLNPFHTINLAQ 1340

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RESULT 12

T42642
 phosphotransferase (EC 2.7.1.-) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_rev: 11-Jan-2000 #text_change 11-May-2000
 C:Accession: T42642
 R:Motif: L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
 J. Biol. Chem. 271, 13892-13899, 1996
 A:Title: Cpk is a novel class of Drosophila ptdline 3-kinase containing a C2 domain.
 A:Reference number: Z17659; M01D:96278830; PMID:8662856
 A:Accession: T42642

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1658 <MOL>
 A:Cross-references: EMBL:US2193; MID:g1272421; PID:g1272422; PIDN:AAC52604.1
 A:Experimental source: strain balb c
 C:Genetic:
 A:Gene: cpk
 C:Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
 C:Keywords: phosphotransferase

Query Match 18.4%; Score 1049.5; DB 2; Length 1658;
 Best Local Similarity 33.1%; Pred. No. 3,2e-63;
 Matches 270; Conservative 141; Mismatches 297; Indels 107; Gaps 24;

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QY 296 QLPMDCTMSY-----SRISTATPRMNETSKSLWYNSALRIKILCATYNNV 347
Db 614 QVSMIDLTLTAIYOLLRLHANSRSCSTGCP--RSSRNKEMATTEOQFTVAAHGSSN 671
QY 348 -IRIDIKIYRTGIYHGEPICDNVNTQVPCSNP-----RNMENLYDIYIPDLPPAR 401
Db 672 WSNYKRYVILCSLSHNGDLFPKIQSKVGYTKNFFYLLKMBELIFPIQISQPLESV 731
QY 402 LCLSTICSV-----KGRKAKEHCPLAMGNIN--LPDYDTLVSGQVALNLP 447
Db 732 LHLTLFGVLNQSSGSSPDSNKKQKQ-----PALGKVSILTFDFPKRFLTGKTLVLT 785
QY 448 VPHGLEDLNPIVGTGNSNPK---ETPCLLEFPDMSVYKPPDMSVIEHANMSVRE 503
Db 786 SSH-----TNSIPALPKKSYMERIVLYQVNF-----PSPAPDII-----820
QY 504 AGFSYHAGLSNRLADNEHR--END--KEQLRAICTRDPLSEITBOEKDFLMSHRHCVT 560
Db 821 ---YTSPOIDRNIIOODKLETLESQIKGLDIIHRDSSFGSKEDKVPLEMRKYCLK 876
QY 561 IPEILPKLLSV---KMSRDEVAQWYCVKQWPIKPEQAMELDCNYPDPWVRGAVR 617
Db 877 HPCLEPKILASAPNWKAN---LAKTYSLLHQWPPCLPLAELBLAKAFDQGVRSIAGS 933
QY 618 CLEKYLTDKLSQYLQVQVULKYBOYLDNLVRFLLKALTNQRIIGHFFHMLKSEMN 677
Db 934 WMEA--LSDDELLADYLPOLVQALKYELIYNSLVRFLPSALGNIQIASHLYMLLKALHD 992
QY 678 KTVSQRFGLLBSYCRACGMYLK--HNRQVEAMEKLINLTDIKOKKDETQVQKFLV 736
Db 993 THGSGRYEHLVGLALISVGKGLREBELSKQKLVQGLGVAEKVKQASGSTRQVYLOK---1049
QY 737 EQRRPDMALOGFL-----SPLNPAHQGNLRLBECRIMSSAKRPLMWNENPDIMS 790
Db 1050 -----SMERVOQFPLRKRCRLPLKPSLVAKEINIKSCSPSSNAMPKVTVMNADPLG 1102
QY 791 ELLFQNNELIFKNGDDLRODMTLTQIRIMENIMONQGLDRLMPLPYGLSIGDCVGLIEV 850
Db 1103 EEL---NMFVKVGBDLRQDMTLQIMIKIMDIKIMLEGBDLRNVIFRCISTGSDRGWVEL 1158
QY 851 VRNSHTIMOIOCKGGLKALQFNSHTLHOMLKDKNG--EYDAALDLFTRSCAGCYATFI 909
Db 1159 VPASDTLRKIOVEHGVTS--FKDKPLAEMLKRNPDSEBEYEGASNFYSCAGCCVATY 1216
QY 910 IIGIGDRHNSNINWVDGQLPHIDFGHLDHKKKFGYKREVRPFVLTDPLIVISKGAQ 969
Db 1217 VLGI CDRHNDIMLKTGHMFHIDFGKFLGHQMGFSFRDRAFPVLTSDMAVYINGGSK 1276
QY 970 ECTTRFEPFQEMCYAYLAIROHANLFINLFSMMLGSGNPELOSFDIAVIRKTLALD 1029
Db 1277 ---FTIRFQLFVLDLCCQAYNLIRKQTNLFINLILMLISGPELSTIDKLKYVDALQPO 1333
QY 1030 KTEOALYFMKQMDAHGGMWTKMDIFHTIKQ 1064
Db 1334 TIDAETITFTR--LISSSLGIATKFNPFHTINLAQ 1367

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RESULT 13

JCS985

phosphoinositide 3-kinase C2gamma - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-May-1998 #sequence_rev100 29-May-1998 #text_change 30-Apr-1999
 C/Accession: J05985
 R:Hitawa, H.; Ohnubo, M.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Yoshimura, A.
 Biochem. Biophys. Res. Commun. 244, 531-539, 1998
 A>Title: Cloning and characterization of a novel class II phosphoinositide 3-kinase cont
 A:Reference number: J05985; MUID:98189216; PMID:9514948
 A:Accession: J05985
 A:Molecule type: mRNA
 A:Residues: 11506 <MNA>
 A:Cross-references: DDBJ:AB008791
 A:Experimental source: liver
 C:Comment: This protein exclusively expressed in the liver, and a N-terminal truncated fo
 C:Genetics:
 A:Map position: 6
 C/Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
 F:978-1239/Domain: catalytic #status predicted <CAT>

Query Match 16.1%; Score 919; DB 2; Length 1506;
 Best Local Similarity 24.7%; Pred. No. 2,4e-54;
 Matches 308; Conservative 204; Mismatches 414; Indels 322; Gaps 44;

QY 4 PSSGSELWGHLPRLVLECLPFGMIVTLECLREKATLITIKELTKKARKYPLHQ--L 61
 DB 127 RNPSSGKHGIEY--PRF--DALPPSSGQGECPPOSGGKHNHYCGE-----HEGNL 175
 QY 62 LQDESSYIPVSVQOAREEFEDTRRLCDRLFPQPLKV-----IEP 104
 DB 176 PHHSSYSIDISIPNR-----EKRSQDNVLEPSEKDFLRTSNVSESTER 227
 QY 105 VGNNEEKILNREIGFALGMPVCEPDVYKDPEDVDFRNILNVCEAVDLR-----DLS 158
 DB 228 IG-----CPRIEVEVP--QCSNKLAFCKVKKIKRESYHASDINS 266
 QY 159 PHSAMTV--YPPNVSSPELPKHIVYKDKGQIIVIVIVPBNNDKQYTKLKHND 215
 DB 267 NSGKIMATTVAIPGRILFADTKFR-----XKISTENSAQILLMPHANY 309
 QY 216 VPBOVIAEAIKKRSMILSSEOLKLCVLEYQKYLKVCSCDEFEYLPESQYKYL-- 273
 DB 310 LVKDLIAEIL--LICANEPLS-----PKETLVSCSEBELQMDHLSGKIKFOX 357
 QY 274 -RSCIMLRMPLMLMAKESLYSQ-----LPMDCFT--MPSYSRI 311
 DB 358 NKSVIQLQKQNRDPKGLSRKSEDDHSPHNLQLEFTHIWKIKRQCLSTWKKYNLAH 417
 QY 312 S-----TATYV----- 318
 DB 418 EHLTKPQKMEKXLSMWSGNQHTSOPHNVNLEEVNICSVLGCIETKOVSDAVKELN 477
 QY 319 -----NGRTSTK-----SLWVINSALRIKIKCATYVNVNINDIKI 354
 DB 478 LILQPSQNFQNSSTSKKGLTERVATLSRSIYOL-----IDVYCSSECT--DPQPV 528
 QY 355 YVRGTGIYH-----GGEPLCDNVNTORV 376
 DB 529 HTPGGSVHYNAGLOSLSTVCSLINVPEITMAHYKAFSCWLTGYAAGKLCQVASCPL 588
 QY 377 PCSNP-----RWNEMLNIDYIPDLPRARLCLSTCSYKRGAKAEHRCPLAWGINFLD 431
 DB 589 PVTGKFSLLVNNNEIINFLPIKSLPREBMLVIKLF--GIDSAGHSTNLMLMTCLPLRP 645
 QY 432 YVDTLVSGM-ALNLMPPVPHGLDILNPIGVGNSNPKETPCLELFPWFSSVVKFPDMS 490
 DB 646 ROESVLGSLFSTVLTQSEPP--IEMTAPVWDGSOQSP--LTLQID-----PPD-- 690
 QY 491 VIEBHAMNSVREAGFSYSGAGLSNLRARDNELRENDKEQLRAICTRD--PLSE----- 542
 DB 691 -----AGREY-----LKPSEENRTRDHEPRREGCKIKHIAKSQKSPIL 729
 QY 543 ITEOEKDFLMSHRHCVTIPILLPKLL-LSVKNSSDEVAQMYCLVXKMPPIKPEQAMLL 601

DB 730 LSEKRRYLMFYRLVCNNENSSLPVLGASPGMD--EEVSEMAHAILLRMTFSHPWEALGL 788
 QY 602 LDCNVDPVWRGPARCLETLYLTDKLSOYLQLOVQVLEQYLDNLVRFILKKTATNQ 661
 DB 789 LRSRFPDQDIREVAVOQLDILLTDE-LDCLPQLOVAQFENLSEPLVLELPRRLQSI 847
 QY 662 RIGHFFFMHLK--SEMNKTVSOPRFGILLSEYCRACGYLKLHNLQVAMEKILNLTDI 718
 DB 848 RVNHCILYMLRDAQSAYKSMYQELALAQ-FCAG-----EALNELSKEQVLVLGD 901
 QY 719 LKQEKDETQVQWKFVQW--RRDPMDALQGLSPINPAHQSLRLBECRIMSASAR 777
 DB 902 IGEKVSASDPPQKDKVLKKEIGSELPFDIKCHPLPAPALCTIKGIDBACSYFNAS 961
 QY 778 PLTMENENDPMSLELPPONNEIFKXGDDLRQDMLTQIIRIMENIQWQGLDRLMPYG 837
 DB 962 PLKITPIMNPMW-----KIVSVIFKAGDDLRQMLAQIIVQNDNMLQEGLDMMQITYG 1017
 QY 838 CLSITGCVGLIEVVRNSHTIMQIOCKGLKALQFNSHTLHQLKDKNK-GEIYDAIDL 896
 DB 1018 CLSTGRAGQFIEMVPAVTLAKIHLISGLIPKEN--TIKKVFSQNHLEKEDYKALRN 1075
 QY 897 FTRSCAGYVATPILIGIGHNSINIVKDDQLPHIDFGHPLDKKKKGYKREVPVL 956
 DB 1076 FVYSCAGWCVVTILGVCDRHNDNIMLTSGHMFHIDFGKFLGHAQTFGGIKDRAPFIF 1135
 QY 957 TQDFLVISGAGDECTKREFEFQEMCYKAYLAIRHANLFINLPSMMLSGMPLOSF 1016
 DB 1136 TSEMEVFITEGK--NIQHFQDFVELCCRAVIVRGHGLIISLEMLHAQLPELRGI 1192
 QY 1017 DDIAVIRKTLALDKTEQDALEYFMKQNDNAHSGWTTKMDMIFHTIKQ 1064
 DB 1193 EDLKYVNNLRPODTLEATSHFTKKIKESLE-CFVKLANLJHTLAQ 1239

RESULT 14
 T13801
 phosphoinositide 3-kinase (EC 2.7.-.-) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 13-Aug-1999 #sequence_rev100 13-Aug-1999 #text_change 17-Nov-2000
 C/Accession: T13801; T13351
 R:MacDougall, L.K.; Domini, J.; Waterfield, M.D.
 Curr. Biol. 5, 1404-1415, 1995
 A>Title: A family of phosphoinositide 3-kinases in Drosophila identifies a new mediator
 A:Reference number: Z17764; MUID:96362138; PMID:8749393
 A:Accession: T13801
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1876 <MAC>
 A:Cross-references: EMBL:X97892; NID:92113837; PIDN:CAA63485.1; PID:92113838
 R:Moiz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
 J. Biol. Chem. 271, 13892-13899, 1996
 A>Title: Cpk is a novel class of Drosophila ptdins 3-kinase containing a C2 domain.
 A:Reference number: Z17659; MUID:96278830; PMID:862856
 A:Accession: T13351
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-295; 'P', 297-331, 'R', 333-576, 'T', 578-641, 'S', 643-1876 <MOU>
 A:Cross-references: EMBL:U52192; NID:91272419; PID:91272420; PIDN:AAC47117.1
 A:Genetics: P13K 68D; cpk
 A:Cross-references: FlyBase:FBgn0015278
 A:Map position: 3L
 C:Keywords: phosphotransferase

Query Match 15.0%; Score 859; DB 2; Length 1876;
 Best Local Similarity 31.2%; Pred. No. 4.3e-50;
 Matches 230; Conservative 129; Mismatches 281; Indels 98; Gaps 27;

QY 378 CSN-----PRWN--EWLNIDYI-IDLPRAARLCLSTCSYKRGAKAEH----- 419
 DB 893 CSNDTSGGLPRLNFSAMLTEDQHPICITLPRARLTFLV--YGQAASEGPNDQNGE 949

Qy 420 -----CPLANGNTLFPYDTDTLVSGKALMLMPVPHGLEDLINFGVTGSPNPKK-TPCL 473
 Db 950 RROVTELTGMCSTQLPDKFRWMLGCPYLLSLMPM--TDKMLGPAPARGCHPDPFCVLL 1007
 Qy 474 ELEDFWSSVYKPFDMVIEBHAMWSREAGFSYSHAGLSNRLARONELREN--DKEQL 531
 Db 1008 SIEVPPYGGRIEPEHOBVPPAP-----HYDFASL-----DANLOEBELDTAEL 1052
 Qy 532 RAICTRDPLEITEOEKDFLMSHRHYCVTIPETLPKLLSV-KMNSRDEVQMYCLVKDW 590
 Db 1053 -----GYGATERREVEF-MEKRLVYQSYFNALPKYLAHNSWDYAN-LIDHALLHSHW 1103
 Qy 591 PPIKPEOAMELDCNYDDPMYRGAVRCLEKYLTDKLSQYLQYLVQVLYKYBOYLNDMLV 650
 Db 1104 APISPLCSTLELPPRYPDAKREKAVEMISK-MENDQLVDFLPQLVOSLKHDTEGSAWA 1162
 Qy 651 RPLIKKALTNORIGHFFW-----HLKSEMHX-----TVSQRFG-----LLL 688
 Db 1163 RPLSKCLSEPRFHHMYLLVHSLPDDPHNSIGAAVNDQYDSQVTVRYRANKMML 1222
 Qy 689 ESYCRAG-MYKHLNBOVEAMEKLINLTDILKOEKDETQKVQMKFLVEQMRAPDPMDA 747
 Db 1223 RALMALCGEKMLQRFMYQHNMCKLTTIAESVKAESMKRSLAAGMDV--HODLLE- 1279
 Qy 748 LQGLSLPNAHQULNLEBCRIMSSAKRPLMLNMPDIMSLELFPONNEIFKNGDDL 807
 Db 1280 -OPTCLPGLBELEVTVGVSVNCSYFNSNTLPLKINFPQDA-----ESLPAIFKCGDL 1332
 Qy 808 ROMLTLQIIRIMENIWNONGLDRLMPLYGCLSLGDCVGLIEVYRNSHTIOLQCKGKLG 867
 Db 1333 QOQOOLITQILIRINKMLARLDLKVTFNCVPTGYKSGMELVSEKETAARKIQVEGGLT 1392
 Qy 868 GALQFNSTHLOWLKDKNKEBI-YDAIDLFSTRSACGYATFLIGIDRHSNIMVKDD 926
 Db 1393 GS--FKORPAEWMGKNPSELYQSAVRNFTLSACGYATVYLGICDRNDNIMKTS 1450
 Qy 927 GOLPHIDGPHLDHKKKKFGYKREVRPVLTDQLIYISKAQECTYTREREPOEMCYK 986
 Db 1451 GHLPIDGFKFLGDAQFNGFNRDRTFVLTSDMAVYINGDKPST--DEHYVVDLCR 1507
 Qy 987 AYLAIRPHALFNLFSMMLGSGMPELQSPDIAVITKTLALDTEDEALEYFPKQNMDA 1046
 Db 1508 AFNIVRNADLLHTLHAMTACMGVNS-NAVQYVRALLPSQSNDEAATFAKMIQSS 1566
 Qy 1047 HHGWTKMDMIFHTIKQ 1064
 Db 1567 LK-SMFTQFNPPLHMLAQ 1583

RESULT 15

T21982

hypothetical protein F39B1.1 - *Caenorhabditis elegans*

C/Dates: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C/Accession: T21982; T22312

R:Lightning, J.

- submitted to the EMBL Data Library, February 1996

A:Reference number: Z19497

A:Accession: T21982

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Cross-references: EMBL:Z69660; PTDN:CAA93489.1; GSPDB:GN00028; CESP:F39B1.1

A:Experimental source: clone F39B1

R:Thomas, K.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19545

A:Accession: T22312

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1607 <M12>

A:Cross-references: EMBL:Z69903; PTDN:CAA93776.1; GSPDB:GN00028; CESP:F39B1.1

A:Experimental source: clone F46F2

C:Genetics:
 A:Gene: CESP:F39B1.1
 A:Map position: X
 A:Introns: 15/2; 65/2; 134/1; 190/1; 261/3; 298/1; 374/2; 417/3; 472/2; 512/1; 661/3; 71
 C:Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology

Query Match 13.24; Score 751; DB 2; Length 1607;
 Best Local Similarity 22.8%; Pred. No. 8.5e-43;
 Matches 261; Conservative 213; Mismatches 429; Indels 240; Gaps 39;

Qy 35 ECLREATLITIKHELFREAKYRPLHOLQDESSYTFVSTQEARERFETRALCLRL 94
 Db 300 ECVGAKLI-----QENIEFP-----SSFCILDCPNGLIE-----EQVKLCRNL 340
 Qy 95 FQ-----PLKATIEPVGNREEKIL-----NREIGALGPVCEFDVVKDPEV 136
 Db 341 IRKDMTDFFLAPVDVMTTASTAVKVVYKDSMKANKSKNGAM--ICAIID-----EK 392
 Qy 137 QDFERNILNVCKEAVDLRDLNPSHR--AMVYVPPN--VSSPELPKHIVN----- 183
 Db 393 MDI-----ITQALSLFDESELPDKEYGLKIGLNGFLSSDSLGSNLVTHGCLNGDD 446
 Qy 184 -KLDKQIIVIVIVYSPNN-----DKQYTLKINHDCVPEOV--IAAIR 226
 Db 447 VKLDLG-----VFAPNSRIYEQTLESNMLKKSQVKYSTVVDKEDVENTLGHLAGEMS 498
 Qy 227 K-----KTRSMLSSEQLKLVLEYGKYLKVGCC-----DEYF--LEKYPISQY 270
 Db 499 QYELAFNDGSTLKLSSSQKVK-----QVINLCKCHGIVPEKLYVEMQKYLAST 550
 Qy 271 K-----YIRSCIMLGRMPLMLMAKESYSQLPMDCTFMSYRR 310
 Db 551 EDQLVHNRNDFLREHISFLCYRCCTSRVNIPLQITIPKVEVLSKMPFQI----- 604
 Qy 311 ISTATPMMNGETSKSLVINSALRIKILCATYVNNIRIDIKIYATGTGIYHGGEPLCDN 370
 Db 605 -----MLNSVHSIPEHMQ-----SQYSEFYMSLDYHGTQVLDGF 639
 Qy 371 VNTQGVCSNPRNMENLVNIY-----IPDLPRARLCLSTC-SYKGRKAKEECP- 421
 Db 640 SNKYVPKTIKNDHFFPRPLDLVAKFKRLNLCQYPRETRIVASISGTVNSAQANENPDP 699
 Qy 422 ---LAMGNINLPDYDTLVSGKALMLMPVPHGLEDLINFGVTGSPNPKETPCLELEFD 478
 Db 700 IWLGLYCSVPLDENLPMRGSRPLPLTLTKK--QPLKRFPGYPRYIKDARDPLIMSF 757
 Qy 479 WFSVVKFP---DMGYI-BEHANWSVREAGFSYSHAGLSNRLARDNELRENDKEQLRA 533
 Db 758 IMDTETIYFPNVVIMQCIPODFATLDIETQ-----EYLL 792
 Qy 534 ICTRDPLEITEOEKDFLMSHRHYCVTIPETLPKLLSVKMSRDEVQMYCLVKMPPI 593
 Db 793 LIENQDTSTLETDDQDLIMQKRLHLTNQPALPLVSLSDWSFGFPMRYQLIEEVAFL 852
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QY 942 KKKFGYKREVRPFVLJODFLIVISKGAOECTKREPERFOEMCYKAYIAIROHANLFTNL 1001
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Search completed: November 6, 2003, 14:44:52
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:42:46 ; Search time 35 Seconds

(without alignments)
5245.714 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1978.5	34.7	1044	12	US-10-337-192-2 Sequence 2, Appl1
3	1978.5	34.7	1044	12	US-10-027-591-2 Sequence 2, Appl1
4	1976.5	34.6	1044	15	US-10-162-160-1 Sequence 4, Appl1
5	1467	25.7	1110	12	US-10-101-235A-4 Sequence 1, Appl1
6	1465.5	25.7	1102	11	US-09-974-573-1 Sequence 1, Appl1
7	1322	23.2	1076	12	US-10-101-235A-6 Sequence 48, Appl1
8	1089	19.1	1167	9	US-09-205-658-48 Sequence 48, Appl1
9	1089	19.1	1167	9	US-09-844-353A-48 Sequence 48, Appl1
10	1089	19.1	1167	12	US-09-963-693-48 Sequence 2, Appl1
11	1014.5	17.8	1686	10	US-10-092-219-2 Sequence 2, Appl1
12	685	12.0	887	10	US-09-771-161A-192 Sequence 192, App
13	685	12.0	887	10	US-09-771-161A-193 Sequence 193, App
14	675.5	11.8	803	10	US-09-921-232-2 Sequence 2, Appl1
15	675.5	11.8	803	10	US-09-921-330-2 Sequence 2, Appl1

16	675.5	11.8	803	10	US-09-921-329-2	Sequence 2, Appl1
17	545.5	9.6	756	10	US-09-771-161A-101	Sequence 101, App
18	442	7.7	1900	10	US-09-801-368-390	Sequence 390, App
19	357	6.3	195	12	US-10-101-235A-9	Sequence 9, Appl1
20	357	6.3	204	9	US-10-101-235A-2	Sequence 2, Appl1
21	341.5	6.0	150	9	US-09-205-658-17	Sequence 17, Appl1
22	341.5	6.0	150	9	US-09-844-353A-17	Sequence 17, Appl1
23	341.5	6.0	150	12	US-09-963-693-17	Sequence 17, Appl1
24	314.5	5.5	508	10	US-09-771-161A-102	Sequence 102, App
25	304	5.3	816	12	US-10-205-219-3	Sequence 3, Appl1
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27	283.5	5.0	817	12	US-10-342-276-28	Sequence 28, Appl1
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33	261.5	4.6	119	10	US-09-765-298A-14	Sequence 14, Appl1
34	202.5	3.5	2654	15	US-10-227-610-2	Sequence 2, Appl1
35	199.5	3.5	1140	11	US-09-950-634-4	Sequence 4, Appl1
36	196.5	3.4	2549	11	US-09-950-634-3	Sequence 3, Appl1
37	188.5	3.3	1710	12	US-10-032-585-7238	Sequence 7238, Ap
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39	180.5	3.2	4128	9	US-10-205-194-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1
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; Sequence 8, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Satyamangla V.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OR INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRS
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-235A-8

Query Match 99.1%; Score 5657; DB 12; Length 1068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
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DB 301 CFPMPSYSRISATAPYNGESTSKSLMWINSAIRIKILCATYVNVNIRIDIKIYRTGI 360
QY 361 YHGEPLCDVNTQVPCSNPRNMWLNVDIYIPDLPPAARLCISGVKRRKAKKEHC 420
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DB 361 YHGEPLCDVNTQVPCSNPRNMWLNVDIYIPDLPPAARLCISGVKRRKAKKEHC 420
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DB 421 PLAMGNINLPYDTTIVSGKALMLMPVPHGLBLLNPIGVTSNPKETPCLELEDFME 480
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PRIORITY APPLICATION NUMBER: 60/238,057
PRIORITY FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1044
TYPE: PRT
ORGANISM: Human p10delta protein
US-10-337-192-2

Query Match      34.7%  Score 1978.5; DB 12; Length 1044;
Best Local Similarity 39.9%; Pred. No. 1,3e-170;
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

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QY 233 LLSSEQKLCVLEYGKTYILKVCCEDEYFLEKYPLSOYKATRSCTMLGRMPLMLAKES 292
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QY 353 KIYRTGTYHGEPLCDVNTQVPCSNPRNMWLNVDIYIPDLPPAARLCISGV-- 409
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DB 340 KLVVQAGLFHENEMLCITVSSSEVSCEPVAKORLEFDINICLPPMARICFPLVAVIE 399
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RESULT 2
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Sequence 2, Application US/10337192
Publication No. US20030195211A1
GENERAL INFORMATION:
APPLICANT: SADBHU, Chanchal et al.
TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
FILE REFERENCE: 27866/39033
CURRENT APPLICATION NUMBER: US/10/337,192
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: 60/199,655
PRIOR FILING DATE: 2000-04-25

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DB	910	IDFGHFLNGFKTKFPIINRVRVFLITYPFVHIQOG--KTNNSEKFEFRPGICEAAVITL	967
QY	992	ROHANLFINLPSMVLGSGMPELQSFDDIAYIRKTLALDKTEQALAEYPMQMNDAHHGW	1051
DB	968	RRHGGLFLHLFALMAAGPELSCSKDIQYLMKSLALGTTEBALKHFRVKNENALRESM	1022
QY	1052	TTKMDMIFHTIKQ 1064	
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; Publication No. US20020161014A1			
; GENERAL INFORMATION:			
; APPLICANT: SADHU, Chanchal et al.			
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA			
; FILE REFERENCE: 27866/36170C			
; CURRENT APPLICATION NUMBER: US/10/027,591			
; CURRENT FILING DATE: 2001-10-19			
; PRIOR APPLICATION NUMBER: 09/841,341			
; PRIOR FILING DATE: 2001-04-24			
; PRIOR APPLICATION NUMBER: 60/199,655			
; PRIOR FILING DATE: 2000-04-25			
; PRIOR APPLICATION NUMBER: 60/238,057			
; PRIOR FILING DATE: 2000-10-25			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: PatentIn version 3.0.			
; SEQ ID NO 2			
; LENGTH: 1044			
; TYPE: PRT			
; ORGANISM: Human p110delta protein			
US-10-027-591-2			
Query Match 34.7%; Score 1978.5; DB 14; Length 1044;			
Best Local Similarity 39.9%; Pred. No. 1,3e-170;			
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;			
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QY	293	LVSQLEPMDCTFWPSYSRRISTATPYMNGESTSKSLMVINSALRIKILCATYVNVNIRID 352	
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QY	353	KIYVATGIYHGGEPLCDNVNTRQV--GSPRANEMLVNDIYIPDLPPARILCLSLCSY-- 409	
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Db 460 RSNPPTDSAAALLICLP---EVAHPVYVYPALEKLE-----L 494
QY 518 ARDN-----LRENDKQLRAICTRDPLESETTEOEKPLMSHRHYCVT-IPEILPKLLLSYK 573
Db 435 GRHSCVAVTEEBEQULREIELEBRSSGELYEHKQLVWKLHVEVENEPEALRALRLLYTK 554
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Db 555 WNKHEDVAQMYLCSWPDELPLYLSALBELLDSPDCGVGFAIKSLRK-LTDELFOYLT 613
QY 634 QLVQVLXEQYLDNLVPLFKKALTNRIGHFFFWHLKSEHAKTVSORFELLLESYCR 693
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QY 694 ACGWLLKRLNQNQVBEAMEKLINLTDLKQEKDETOXVMKFLVBO-MRPDMDALQGLF 752
Db 674 GSTHHMKVLMKQGBALSKLALNDVKLSSQ-KTKPKPTKELIMHCKMOEAYLEALSHIQ 732
QY 753 SPLNPAHOLGNRLREECRIMSSAKRPLMLNENPDIMSELFPONNEIIFKONGDDLRQDML 812
Db 723 SPLDPSTILAEVCYQCTFPMDGSKMKPLWIMWSNBAGSG---GSIGIILFKONGDDLQDML 789
QY 813 TLOITRIMENIWONOGDLRLMLPYCCLSIGDCVGLIYVVRNSHTTMOIQ-KGLKALQ 871
Db 790 TLOMTQMDVYLMKQGBDLRMTPYCGLPTGRTGLIEVLRSDTIANIQLNKSNNAAATPA 849
QY 872 FNSHTLHQMLDKKNKGETYDAIDFTPSGAGYCATFLLIGIGDRHNSINIMKDDGOLF 931
Db 860 FKXDALNLMLSKQKPEALDRALIEFTLSCAGYCATVYVLGIDHNSINIMKRESGOLF 909
QY 932 IDFGHFLDHKKKKKFEQYKERYPVFVLTODFLIVISKAQOECTKTRFEFERFOEMCYAYLAI 991
Db 910 IDFGHFLGNFKTRKGINERVPFLITYPVHVIQGG-KTNSEKFEERFRCGCEAYTL 967
QY 992 ROHANLFINLFSMMLGSMPELOSFDDIAYIRKTLALDKTQOALEYFMKQNDAAHGGW 105
Db 968 RRGHGLFHLPALNRAAGLPELTSCKDIOYLDKSLALGKTEEBALKHFRVXFNALRESM 102
QY 1052 TTKXDMWIFHTIKQ 1064
Db 1028 KTKVWMLAHNVSK 1040

RESULT 4
US-10-162-160-1
; Sequence 1, Application US/10162160
; Publication No. US20030093627A1
; GENERAL INFORMATION:
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. US20030093627A1el Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-160-1

```

Query Match 34.6%; Score 1976.5; DB 15; Length 1044;
 Best Local Similarity 39.9%; Pred. No. 2e-170;
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

16 MPP-----RIVECLPNGMIVTLECEATLITIKHELEFKAERYPLHQ 60
 1 MPPGVDCRMEFWTEKBNQSVVDFLLPRGYLNPVSRNNALSTIKOLMHRBAQYELPH 60
 61 LLODESSYIVSVYQBAEREEFFDETRLCDLRLFOPLKIEFVGNREKILNREIGFA 120
 61 MLSPEAVYFTICINQTAEOQLEDEORRLCDVQPLPLRLVAREGDRVKILINSQISLL 120
 121 IGMVCFDMDKDEYODFRNINLVCKEAVDLDLNSPHSRAMVYVPPNVESPE---- 176
 121 IKGKIHFEFDSLCDPEVDFRAKMOCFEAAARQOULGWEMLQYSPFLQLEPSAQWGP 180
 177 ----LPHNIVKLDKGQIIVIVIVIVSPNNOKYTKLKNDCVPEQVIAIRKTRSM 232
 181 GTLRPNR-----ALVNVKREGSESEFTPOVSTKQVPLAMACALRRK----- 224
 223 LLSSEQLKLCVLEYQKYLKVCDCDEYFLEKYPLOSQYKTRSCIMLGRMPLIMAKES 292
 225 ---ATVRQPLVEQPEDYTLQVNGRHEYLGSYPLQFOYICSLHSGILPHTLVHSSS 281
 293 LYSOLPMDCTMPSYSRISTATPYMNGESTKSLMIVNSALRIKILCATYVNNINRID 352
 282 ILAMRDEOSNPAPOVOKERAKPPPIPAKPSVSLMSLEQFRLELQGSKYVNDER--M 339
 353 KIYVRTGIYHGGEPICDNVNTQVRP--GSPRNEMVANDIYIPDLFRAARCLGISCV-- 409
 340 KLVOAGLFGHNMELCKTSSSESVSCSEPVKQPLEDINICULPRARLCLFALYANIE 399
 410 -----KGRKAKEHCPLAMGNINLPDYDTLVSGKALNMP--VPHGLDLNPIGVT 462
 400 KAKKARSTKSKKADCPILAMNMLFDYKQDKTGERCLVMPVPDEKGLMLPTGTV 459
 463 GSNPKETP-----CLELFPDFSSVYKPPDMSVTEENANMSVSEAGFVSHAGLSRL 517
 460 RSNPTDGAALLCLP---EVAHPVYVYPALEKLE-----L 494
 518 ARDNE---LRNDKQRLAICTRDPLSEITEQKDFLMSHRHYCVT--IPEILPKLLSVK 573
 495 GRHSCVATHEEOQLREILERSGSGELYEHKQLWKLNHEVQHPREALARLLVTK 554
 554 WNSRDEVAQMYCLVXDMPPRIKEQOMELIDCNYPRMVRGFAVRCLKEYITDDKLSQYLI 633
 555 WNKEDVAVQMYLILCSWPELPLVLSALBELDFSPDCHVGSFAIKSLRK--LTDELDFQYLL 613
 634 QLVQVLKTEQYLDNLVRLPKKALTNRIGHFFPMHLKSEMHKNTVSGRFGILLSEYCR 693
 614 QLVQVLKTESYLDCELTFELDRALANRKIGHFLMHRSEMHVSVSVALRFGILLEAYCR 673
 694 ACGWTLKLNROVAMEKLINLTDLIKQKDEQKQVQMKFLVEQ--MRPRDMDALQGL 752
 674 GRTHMKVLMKQGBALSKULANDVYKLSQ--KTEPKQTKELMLCMRGEALVLELSHQ 732
 753 SPLNFAHQGLNLRLEECRIMSASAKPLMLMNPIMSELLFONNEIIFKNGDDLRQDM 812
 733 SPLDSTLLAEVCVOCSTFMDSKMKPLWIMYSNEBAGS---GSVGIIFKNGDDLRQDM 789
 813 TLQITRIMENIWNQGLDKMLPYGCLSIGDCVGLIEVVRNHTTMOJOC--KGGLKGLAQ 871
 790 TLQITQIMQVLMKQGBELDLRMTPYGCLPYGDRGTGLEVLRSDTIANIOLKNSMAATAA 849
 872 FNSHTLHQLKDKNGEYIDALIDLFTBSGAGCVATFLIGIDRNSNINVMYDQGLPH 931
 850 FKDALNMLKSKNPEALDRAIEFTLSGAGCAVATVVGIGDRSDIMIMRESQULPH 909
 932 IDFGHFLDKKKKFGYKREVRVFLTQDPLIVISKAQOCTKREFERPQEMCYKAYAI 991
 910 IDFGHFLGPKTKFGINREVRVPIILYDVVHVIQOQ--KTNNSEKERRFRGCEAYTIL 967
 992 ROHANLFINLFSNMLSGMPELOSFDIAYIRKTLALDXTQEALEYFPKQKNDANHGGM 1051

DB 968 RRRGLFLFLFALMRAAGLPELSCSKDIQYLKDSIALGKTEBEALGHFRVXFNEALRESW 1027
 QY 1052 TTKMDWIFHTIKQ 1064
 DB 1028 KTKVNMILAHNVSK 1040

RESULT 5
 US-10-101-235A-4
 ; Sequence 4, Application US/10101235A
 ; Publication No. US20030182669A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rockman, Howard A.
 ; APPLICANT: Naga Praasad, Sathyanangla V.
 ; APPLICANT: Laporte, Stephanie A.
 ; APPLICANT: Barak, Larry S.
 ; APPLICANT: Caron, Marc G.
 ; TITLE OF INVENTION: Phosphonositide 3-kinase mediated inhibition of GPCRs
 ; FILE REFERENCE: 033072-064
 ; CURRENT APPLICATION NUMBER: US/10/101,235A
 ; CURRENT FILING DATE: 2002-03-19
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1110
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-101-235A-4

Query Match 25.7%; Score 1467; DB 12; Length 1110;
 Best Local Similarity 35.3%; Pred. No. 5.7e-124;
 Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;

QY 107 NREKILNREIGFAIGMPCFEDVVKDEYODFRNINLVCKEAVDLDLNSPHSRAMVY 166
 143 SEESQAFORCLTALIGYDVTVDSNVHDELEFTRGLVTPRMAEVARSD-----PKLYA 196
 167 YRPVSESPLEPKIIVKLDKGQIIVIVIVIVSPNNOKYTKLKNDCVPEQVIAIR 226
 197 MHPVWTKP--LPEYLMKRIANNCFIYI-----HRSSTQILVSPDPTGALQSF 249
 227 K--KTRSMILSSQQLKLCVLEYQKYLKVCDCDEYFLEKYPLOSQYKTRSCIMLGRMPL 284
 250 KMAKKKSLMDIPES-----QSEDDFVLVRGREGYLVGEPIKNPQVRRCLKNGEIH 303
 285 LML-----MAKESLYQLEP--DCFTMPSYSRIISTATPYMNGE---ISTKSLWVINS 332
 304 VVLDTPPDPAUDEVRKEEMEPVLDCTGVTGYHBOLT-----IHGKHESVFTSLMDCDR 358
 333 ALRKILCATYVNNINRID-----KIYVRTGIYHGGEPICDNVNTQVRPSCNPR 382
 359 KFRYK-----IRGIDIPVLPNTDLTVFVEANIOHQOVLQCORRTSPKFTPEVL 408
 383 WNEIMVNDIYIPDLFRAARCLGISCVK---GRKGAKEHCPLAMGNINLPDYDTLV- 437
 409 WNWLEFETIKDLPKGMLNLQIYCGKAPALSKASAESSSSKGVRLLYVNLILI 468
 438 -----SGKALNIMVPVPHLED--LNPPIGVT--GSPNKE--TPCELELEDWSSVYKF 486
 469 DHRFLREGYVLLHMWQISGKGEQGSFNAOKLTSATNPDKENMSISILLDNCHPILAL 528
 487 PDMSVTEBHAWSVSREAGFSYHAGLSNRLARONELRENNKEQRLAICTRDPLSEITEQ 546
 529 PHSQPTPPEBGRV-----RAMPNQLR-----KQLEALITADPLPLTA 569
 547 EKDFLMSHRHYCVTIPILPKLLSVKNSSRDEVAQMYCL-----VKDMPPIKEQAMEL 601
 570 DKEILMHRFYESLKHPRKAYPKLFSSVVKMGQOEIYAKTQOLLARREVMQSLDVGELTQ 629
 602 LDCNVPDPMVRGFAVRCLKEYITDDKLSQYLIQLVQVLKTEQYLDNLVRLPKKALTNO 661
 630 LDCNFSDENVRALAVQKLES--LEDDDVHLVYLLQVAVKFEFYHDSALARFLKRLGRLNK 688

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Qy 662 RIGHFFFWHLKSEM-HNKTIVSQRFGLELLESYCRACGWYKJ-LNROYAMEKLIINTL-DI 718
Db 689 RIGHFFFWHLKSEM-HNKTIVSQRFGLELLESYCRACGWYKJ-LNROYAMEKLIINTL-DI 748
Qy 719 --LKQEKKDETOKV--QMKFLVEQMRPDPMDALOGFLSPNPAHQUNLRECRIVSS 774
Db 749 KSLSAEKYDVSSQVYSOLKXLENIJONSQLES---FRVPYDGLKAGALAEKCKWAS 805
Qy 775 AKRPLMNMW--NDIMSELIFONNE--IFKNGDDLRQDMLTLOIRIMENIMONGL 829
Db 806 KKRPLMEFKADPTALS-----NETIGILFKHGDDLRQDMLTLOIRIMENIMONGL 859
Qy 830 DLRLMPLGCLSGIDGCVGLIEVYRNSHTIMQI-QCKGKLKALQFNSHTLHQMLEDKN-KG 887
Db 860 DLGLPLPGCISTGDKIGMIEIVKDATIATKIQOSTVGTGA--FKDEVLMNMKEKSPTE 917
Qy 888 EYDAIDLTFRSCAGYCVATFIIIGIDRNSNIMVKGDLQFLHIDGHFLDHKKKFGY 947
Db 918 EKFOAAVERFYSCAGYCVATFVLIGIDRNDNIMITETGNLPHIDGHILGNYSFJGI 977
Qy 948 KREVRPVLTPDPLIVISKAQECTRREPERQEMCYKAYLATROHANLFINLPSMWLG 1007
Db 978 NKERVPLVLPDPLFVMTGSKKTSR--HFQKPDICVKAYLATRSHHTNLILFSPMLM 1035
Qy 1008 SGMELQSPDIAIYIRKTLADKTEOBALYEFMKQMDAHNGWTTKMDWIFHTI 1062
Db 1036 TGMPLQSLKEDIEYIRDALTYGKNEBDAKKYFLDQIEVCRDKGWTQVQPNWFLHLV 1090

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RESULT 6

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US-09-974-573-1
; Sequence 1, Application US/09974573
; Publication No. US20030022344A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Roger
; APPLICANT: Ried, Christian
; APPLICANT: Walker, Edward H
; APPLICANT: Stephens, Len
; TITLE OF INVENTION: PHOSPHOINOSITIDE 3-KINASES
; FILE REFERENCE: ONYX1048-US
; CURRENT APPLICATION NUMBER: US/09/974,573
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/242,801
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 1102
; TYPE: PRT
; ORGANISM: Porcine P13K
US-09-974-573-1

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Query Match 25.7%; Score 1465.5; DB 11; Length 1102;
Best Local Similarity 33.5%; Pred. No. 7.7e-14;
Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

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Qy 1 MPPRSSGELMGHTLMPRIIVECLPNGMIVT-----DECLEATLITIKHLEKREA 53
Db 23 MKRPSTASLSSMELIP---IEFVLPTSQRTKTPETALHLVAGHGNVEQMKQAQWLRA 78
Qy 54 RKYDL-----HOLLQDESSYIFVSVTOEAREEFDETRELCDLRFOPF-----LKVI 102
Db 79 LENSVSADYFHRRLQDHFLLLYQKKGQWELDYKQVYVOTIDCLRKYKVLHRSQGHV 138
Qy 103 EPVGNREKTI-LNKEIGFALGMPVCEFDWYKDEPVQDFRNILNVCKEAVDLRLNSPHS 161
Db 139 QRHAPSEETLAFQQLNALIGYDVTVSNVHDELEFRRLRLVPRMAEVAAGR-----192
Qy 162 RAMVVPNNVSSPELKRHIYKNDKQOIVIVIVIVISPNNDKKTGLKINHDCVPEQVI 221
Db 193 PKLYAMHPWTSKP-LREYLLKKTNNCVFIVT-----HSTTSQTIKVSADDTPTGTL 245

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Qy 222 AEAIRK--KTRSMLLSEQULCVLEYQGRYILKVCQCDVEFLEKPLSQYKIRSCIML 279
Db 246 QSFPTKXAKKSLMDIES-----QNERDFVLKVCQDEYLVGETFLKPNQWROGLCKN 299
Qy 280 GRMPLML-----MAESLYSQLPN--DCFTMPSYRRJSTATPYMNGE---TSTKSL 327
Db 300 GEBIHLVLDTPPPALDEVRKEEWPVLDCTGVGYHEQLT-----IHKDHESVFVSTL 354
Qy 328 WVINSLRKILCTAYNNVNRID-----KIVYTGTYHGGEPICDNNVTRVP 377
Db 355 WDCDKRFRK-----TRGIDIPVLPRTADLVFVENAIQYGOQVLQORTSRKPF 404
Qy 378 CSNPRNEMLYNDIYIPDLPRAPALCLSI--C-----SVYKRGK-----KEBCKPLAWG 425
Db 405 TEVLANVWVLEFSIKIDLPKGLNLNQIYQKAPALSGTSAEMSPESGKXQQLLYV 464
Qy 426 NINLFYDTPLVSGKALNMPVPHGED--LNPICVT--GSNPNK--TCLLEFWMFS 481
Db 465 NLILIDHRLRGEYVLAHWOLSGKGDGSPFADKLTSAIYNDKENSMSISILLNYC 524
Qy 482 SVYKFPMSYIEBHANSVSRAGFSYSHAGLSRLARDNBLRENDKEQJRAICTRPLS 541
Db 525 HPIALPKHRTPTDEGDRV-----RAEMPOLR---KOLEAIIATDPLN 565
Qy 542 EITEOKDFLMSHRHYCVTTPILLPKLLSVKNNSDEVAQMYCL-----VKDMPPIKPE 596
Db 566 PLTAEDEKELMHFRYBSLXDPKAVPKLFSSVKKQGGITVAKTQYLLAKREWDQSDALVG 625
Qy 597 QAMELDCNYPDMWNRGFAVRCLEKYLTDKLSQYLIQIVQVLYKYOYLDNLVRLFKK 656
Db 626 LTMQLDNCFSDENVRAIAVQKLES--LEDDVLYHYLIQIVQAVFEPYHSALARFLKR 684
Qy 657 ALTMORIGHFFFWHLKSEM-HNKTIVSQRFGLELLESYCRACGWYKJ-LNROYAMEKLIINTL-DI 714
Db 685 GLRKRIQHLFLFELRSELAQSRHYQRFVILEAYRGGCTAMLHDTQOVQYIDMLQK 744
Qy 715 LT-DI--LKQEKKDETOKV--QMKFLVEQMRPDPMDALOGFLSPNPAHQUNLRECRIVSS 774
Db 745 VTIDIKSLSAEKYDVSSQVYSOLKXLENIJONSQLES---FRVPYDGLKAGALAEKCKWAS 805
Qy 770 RINSSAKRPLMNMW--NDIMSELIFONNE--IFKNGDDLRQDMLTLOIRIMENIMONGL 829
Db 802 KVMASKKKPLMEFKADPTALS-----NETIGILFKHGDDLRQDMLTLOIRIMENIMONGL 855
Qy 825 QNGCLDRLMPLGCLSGIDGCVGLIEVYRNSHTIMQI-QCKGKLKALQFNSHTLHQMLEDKN-KG 887
Db 856 ETSLELDCLPFGCISTGDKIGMIEIVKDATIATKIQOSTVGTGA--FKDEVLMNMKEKSPTE 917
Qy 884 KNK-GEIYDAIDLTFRSCAGYCVATFIIIGIDRNSNIMVKGDLQFLHIDGHFLDHKKKFGY 947
Db 914 KCPLEBKFOAAVERFYSCAGYCVATFVLIGIDRNDNIMITETGNLPHIDGHILGNYSFJGI 977
Qy 943 KRGYKREVRPVLTPDPLIVISKAQECTRREPERQEMCYKAYLATROHANLFINLPSMWLG 1007
Db 974 SFLGINERVPVLPDPLFVMTGSKK--TSLHFGQFQOVQVAYLATRSHHTNLILFSPMLM 1031
Qy 1003 SGMELQSPDIAIYIRKTLADKTEOBALYEFMKQMDAHNGWTTKMDWIFHTI 1062
Db 1032 SMMLMTGMPLQSLKEDIEYIRDALTYGKNEBDAKKYFLDQIEVCRDKGWTQVQPNWFLHLV 1091

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RESULT 7

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US-10-101-235A-6
; Sequence 6, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangia V.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Barak, Liaty S.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Phosphoinositide 3-kinase mediated inhibition of GPCRs
; FILE REFERENCE: 033072-064

```


CURRENT APPLICATION NUMBER: US/10/101,235A
 CURRENT FILING DATE: 2002-03-19
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 1076
 TYPE: PR1
 ORGANISM: Homo sapiens
 US-101-235A-6

Query Match 23.2%; Score 1322; DB 12; Length 1076;
 Best Local Similarity 33.4%; Pred. No. 8,7e-11;
 Matches 339; Conservative 175; Mismatches 340; Indels 162; Gaps 35;

107 NREKILNREIGFALGMPVCEFDWKDEYODFRNINLVCKEAVDLPDLSPHRAMV 166
 143 SEESQAFQRLTALGYDVTDSNHDELEFTRGALPRMAEASD-----PKLYA 196
 167 YPPNVSSPELPKHLYNKLDKQQLIVVWVSPNNQKQYTLKINHCVPEOVAEAI 226
 197 MHPWTSKP-LPEYLMKKIANNCIFIV-----HRTSQTIKVSPTDGTGALIQSFT 249
 227 K-KTRSWLSSBQIKLCVLEYQKYLKVCQDEYFLKYPPLSOYKTRSCIMLGMPN 284
 250 KMAKKKSLMDIPES-----QSEDFVLKVCGRDEYLVGETPIKQFQWRHCLKKEEIH 303
 285 LML-----MAKESYSLPM--DCFTMPSYRRISTATPMNGE-----TSTSLMVINS 332
 304 VLLOTPPALDEKVEKEMPLVDCTGYTGHEQLT-----IHGDHESVFTVSLMDCR 358
 333 ALRKILCATVYVNNIRID-----KIYVTGIYHGGEPLCDNVNTQVPCSNR 382
 359 KFRVX-----IRGIDIPVLRPNNDLVYFVNAVNOHQGVLCQGRTPKPTTEVL 408
 383 WNEWNIYIPDLPRARLCLSTICSVK---GRKAKEEHCPLAMGNINLFDTDTLV- 437
 409 WNVWLEFRIKIDLPKALNLQIYCGKAPALSSKASSESSKGVRLIYYVNLILI 468
 438 -----SGKALNIMPRPHGED--LNPICVT--GSMNKE--TGCLELEFDMFSVVKF 486
 469 DHRFLRGEYVLMHMOISGKEGDSFNADKLTISATPNKENSISILDNVCHPAL 528
 487 PDMSTIEEAMSVSREAGFSYSHAGLSNRLARDLEBNDEQRAICTRDPSEITEO 546
 529 PKHOPTPEBGDRV-----RAEMPQAR-----KQLEAIANDPLNPLAE 569
 547 EKDFLMSHRHYCVTTPILLPKLLSVKNSRDEVAQMYCL-----VKDMPRIKEQAMEL 601
 570 DKELIMHFRYESLKHPRKAYPRLFFSSVKGQOEIVAKTYQLARREVMOQALDVLTMQL 629
 602 LDCNVPDMVWGFANRCLEKYITDDKSOYLILQVQVLYKBOYLDNLLVRLFKKALTNQ 661
 630 LDCNVSDBNVAIAVOKLES--LEDDVLAHYLLQVQVAKFEFYHDSALARFLKGLKLNK 688
 662 RIGFFPMLKSEM-HNKTVSQRFGLLESYCRACAGMLKH-LNRQVAMEKLINLT-DI 718
 689 RIGHFLFPLSLSEIAQSHYQRFVILAEYIRGGTAMLDHFOQOVVIENTLOKVTLDI 748
 719 --LKOEKDETOKV--QMKFLVEQMRDPMDALOGPLSPNLPAHOLANLREECRISS 774
 749 KSLSEKVDVSSQVLSQKLENLQNSQLPES--FVVPYDGLKAGALAIEKCKVVAS 805
 775 AKRPLMLWE--NPRINSELLFQNN-----IFKNGDDLRQDMLTQIIRIMENIQNGL 829
 806 KKKPLMLFKCADPALS-----NETGILIFKHDDLRQDMLTQIIRIMESIWETSL 859
 830 DLRLMPLVCLSGDCVGLIEVVRNSHTIMQI-QCKGKLGALQFNSHTLHQLKXN-KG 887
 860 DLCLLPYCISITGDKIGMIEIVKATIAKTQOSTVNGTGA--FDEVLANHMLKSKSTE 917
 888 EYDAIDLPTKSCAGYCVATPILIGIRHNSNIMVKDGOGLFHLDFHLDHKKKKFGY 947
 918 EKFGAAVERFYVSCAGYCVATFVLGIGD----- 945

QY 948 KRERVPVLNODFLIVISKAQECTKTRFEFEQEMCYKAYLAIROHAN-LFINLFSMML 1006
 DB 946 ---RVFFVLTPDLFLVWGTSGKTSR--HFQKQDLCVAKAYLALRHHTNLLIILFESMML 1000
 QY 1007 GSGMPELQSFDDIAVIRKTLALDKTEQEALEYFMKONDAHHGGWTKMDIPIHTI 1062
 DB 1001 MTGMQQLTSKEDIIEYIRDALTGVGKNBEDAKKYPDQLEVCGRDKGWTQFVWFLHLV 1056

RESULT 8
 US-09-205-658-48
 Sequence 48, Application US/09205658
 Patent No. US20010029617A1
 GENERAL INFORMATION:
 APPLICANT: Ruvkun, Gary
 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
 TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 FILE REFERENCE: 00786/351004
 CURRENT APPLICATION NUMBER: US/09/205,658
 CURRENT FILING DATE: 1998-12-03
 EARLIER APPLICATION NUMBER: 08/857,076
 EARLIER FILING DATE: 1997-05-15
 EARLIER APPLICATION NUMBER: 08/888,534
 EARLIER FILING DATE: 1997-07-07
 EARLIER APPLICATION NUMBER: US98/10080
 EARLIER FILING DATE: 1998-05-15
 NUMBER OF SEQ ID NOS: 328
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 48
 LENGTH: 1167
 TYPE: PR1
 ORGANISM: Caenorhabditis elegans
 US-09-205-658-48

Query Match 19.1%; Score 1089; DB 9; Length 1167;
 Best Local Similarity 27.2%; Pred. No. 1,7e-89;
 Matches 311; Conservative 219; Mismatches 411; Indels 182; Gaps 39;

QY 39 EATLITTKHLEFK--EARKYPLHOLLDESSYIFVSTQEAEREFEFDETRRLCDLRLFO 96
 DB 91 EIKLSDFKHQJLFELIAMKGTYSVKPD--YVFRQLNNGEIEVINDDQPLSKLELHG 148
 QY 97 --PPLKVIPEVNGNEEKLINREIGFALGMPVCEFDWKDEYODFRNINLVCKEAVDLR 154
 DB 149 TFWLFTYQPDGINRDKELMSDISHCIGYSLDKLEESLDELRQFRASLWARTKTLTR 208
 QY 155 DLNSPHSRAMVYVPPN--VESSPELPKHLYNKLDKQOI-IVVWVSPNNQKQYTLKI 211
 DB 209 GL--EGTSHAFAFEEGYLQVGSCEPKDLESKYVAALSYQMFV-----RKRAEI 256
 QY 212 NHDVPEOVAEAIK--KTRSWLSS--EQLKLCVLEYQK--YILKVCQCEYF 261
 DB 257 NGVC--EKMKIQIEFNPNEPSPKSLHTFLYEMKLDVYDTDDPADEGWFQLAGRTTFV 314
 QY 262 LE-KYPLSOYKTRSCIMLGMPMLMAX-----ESLVS-----QLPMDC 301
 DB 315 TNPVKLITSDGVSELESYRCPGFVVRROSLVLKDYCRPKLYEPHYRAHEKKLADV 374
 QY 302 FTM-----PSYSRRISTATPMNGESTK--SLWVINSALRIKILCATVYVNNIRID- 352
 DB 375 LSVSISDTPKQSKSDMWMDDFRTAALQKSLMDLDANLIR-----PVNISGFDFP 427
 QY 353 ---KIYVFT--GIYHGGEPLCDNVNTQVPCSNRAN--EWLNDIYIPDLPRARLCLSI 406
 DB 428 ADVDMYVRIEFSYVGLTILASK--STTKVNAQFAMKMKEMVTFEDLVNKKDMPPSA--VLASI 484
 QY 407 CSVGRGAKAEHEHFLAMGNINLFDTYDTLVSGMALNLW--PVPHGLEDLNPICGV-TGS 464
 DB 485 RVLGKVKYKLSSEBEVEGVNNSLTDMRDELROGQFLHLWABETANRSRIGENGARIGT 544
 QY 465 NPNKETPCLLELDFMFSVVFPMDS-----VIEEAMSVSREAGFSYSHAGLSNRLARD 520

```
Db 545 N-----AAVTIEISSYGRVRMPGQGYTYLVKHSRTWTET-----LINIGDD 587
Qy 521 NELRENDKEQLRAICTRDLSE-----ITOEKDFLMSHRHYCVTIPILP 566
Db 588 YE-----SCRIDPGYKLOMLVKKHESGIVLEBEDQRVMMWRRY---IOQEP 633
Qy 567 KLL-----LSVKNSRDEVAQMYCLVQWDPRIKPEQAMELLDCNYPDPWVRGFAVCLER 621
Db 634 DLLIVSELAFVWTDRENSELYWMEKKRPSVAALTLGKRCCTDRVIRKFAVEKLN 693
Qy 622 YLTDDKLSOYLLOLVOLKYEOYLDNLVFLKKAITNORIGHFFFWHLKSEMH----- 676
Db 694 QLSPVTFHFLPLIOALKYEPRAQSEVGMMLTRALCDYRIGHFLWMLRAETARLDC 753
Qy 677 --NKTVSORFGLLESYCRACGMYLKHLNROVEAMEKLINLTDILKOEKD-ETQVY--Q 731
Db 754 DLKSEBYRISLMEAYLRGNBEHIKITROVDVDELTRISTLVKGMPPDVATMKLRDE 813
Qy 732 MKELVEQMRPDPMDALQGLSPLNPAHOLGNLREBCRIMSSAKRPLMNMENPDIMSE 791
Db 814 LRSISHKEMND-----SPLDPVYKLGEMIDKAIVLGSAKRRPLMLHMKNKPKSD 864
Qy 792 LIFONNEIIFKNGDDLRODMTLTQIIRIMENIMONOGDLRLMLPYGCLSIGDCVGLIEVY 851
Db 865 LHLPCAMIFKNGDDLRODMTLVQVLEVMONIKWKAANIDCLNPAVAVLPMGEMIGLIEVY 924
Qy 852 RNSHTIMOJCKGGLKGLAL--QFNSHTLHOWL-----KDKNKGEI----- 889
Db 925 PNCKTIFELIOVGTFPMNTAVRSIDPSFMNWKIRKOCGIEDEKKSKSDSTKNPIEKKIDN 984
Qy 890 -----YDAIDLFTSCAGYCVATFIIGIDRHSNSINWKGDCQLFHDIFGHFLDHKKK 943
Db 985 TQMKKYFESVDLFVSCVSVATYIMGIXDRHSDMLMTEDQKYNHIDFGHILHGKGT 1044
Qy 944 KEGYKEERVPVLTQDFLIYSKGAOECYTRFEPEQEMCYAYLAFIRHANLFINLFS 1003
Db 1045 KGIQDRDOPFIITEHMTVIRSGKSYDGNSELQKFKTLCEAYEWMNNRDLFVSLFT 1104
Qy 1004 MMUGSMPELOSDDLAIRKTLALD-KTQEALVFMKQMDAHNGWTTKDMIFHTI 1062
Db 1105 LMLGMLPELSTAKDDLHKLTLFCNGESKEERKFPAGIYEBAFNGSWSTKTNWLFHAV 1164
Qy 1063 KOH 1065
Db 1165 KHY 1167

RESULT 9
US-09-844-353A-48
; Sequence 48, Application US/09844353A
; Patent No. US20020037585A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Kouitarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tisbendaum, Heidi
; APPLICANT: Morris, Jason
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005
; CURRENT APPLICATION NUMBER: US/09/844,353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857,076
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
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; ORGANISM: Caenorhabditis elegans
US-09-844-353A-48

Query Match 19.1%; Score 1089; DB 9; Length 1167;
Best Local Similarity 27.2%; Pred. No. 1.7e-89;
Matches 311; Conservative 219; Mismatches 431; Indels 182; Gaps 39;

Qy 39 EATLITIKHELFK--EARKYPLHOLLDESSYIFVSVTQAEERBEFDETRRICKDLFLQ 96
Db 91 EILSLDFKHLFELIAPMKRGYTSVKPD--YFROLANGGELEVLFPNDQPSLBLEHG 148
Qy 97 -PFLKIEBPVNGREKILNREIGFALGMPVCEFDWYKDEVDQFRNINLVCKEAYDLR 154
Db 149 TFPMLFLYCPDGINRDKELMSDISHGLGYSLDKLESIDELRQFRASLWARTKTCULTR 208
Qy 155 DLMSHRSRMYVVPN--VSSPELPRHLYNKLDKQOI-IVVIVWIVSPNNDKOKYTLKI 211
Db 209 GL--EGTSHYAPPEBOYLCVGESCPDLESKYAAKLSYQWFW-----RKRAEI 256
Qy 212 NHDCEPOVIAEAIR--KKTREMLSS--EOLKUCVLEYGOK--YLYKCGCEYF 261
Db 257 NGVC--EKMKKIOLENNPNETPKSLHTFLYENRKLVDYDTPDPADEGMFLDLAGRTTFV 314
Qy 262 LE-KYPLSOYKYIYRSCIMLGRMPLIMAK-----ESTYS-----OLPMDC 301
Db 315 TNDPVKLTSDYGRSELESYRCGPFVVRQSLVKDYCRKPLREPHYVAHERKLALDV 374
Qy 302 FTM-----PSYRRITATPYNNGESTK--SLWVINSALRIKILCATVYNNVIRID-- 352
Db 375 LSVSISDTPKQSKSDMWMTDFRPTASLKVSSIMDDANIMIR-----PVNISGDFP 427
Qy 353 ---KIYVR--GIYHGGEPLCDVNTQVPCSPRRN--EULANDIYIPDLRAARCLST 406
Db 428 ADVDMTVRIEFSYVGTLLTASK-STTKVNAQPAKKNKEVYTDLYMKDMPSA--VLST 484
Qy 407 CSYKGRGKAKEHCPLAMGNINLFDYTDLVSGKALNLM--PVPHGLELDNIPGV-TGS 484
Db 485 RVLVGVKLSKEFEFGWVNMSTLDRDELROQQLFHLMAPEPTANRSRISGNARIGT 544
Qy 465 NPKKTEPCLLEFEDMSSVYKPPDMG---VIEEHANMSVSRAGFSYSHAGLSNRLARD 520
Db 545 N-----AAVTIEISSYGRVRMPGQGYTYLVKHSRTWTET-----LINIGDD 587
Qy 521 NELRENDKEQLRAICTRDLSE-----ITOEKDFLMSHRHYCVTIPILP 566
Db 588 YE-----SCRIDPGYKLOMLVKKHESGIVLEBEDQRVMMWRRY---IOQEP 633
Qy 567 KLL-----LSVKNSRDEVAQMYCLVQWDPRIKPEQAMELLDCNYPDPWVRGFAVCLER 621
Db 634 DLLIVSELAFVWTDRENSELYWMEKKRPSVAALTLGKRCCTDRVIRKFAVEKLN 693
Qy 622 YLTDDKLSOYLLOLVOLKYEOYLDNLVFLKKAITNORIGHFFFWHLKSEMH----- 676
Db 694 QLSPVTFHFLPLIOALKYEPRAQSEVGMMLTRALCDYRIGHFLWMLRAETARLDC 753
Qy 677 --NKTVSORFGLLESYCRACGMYLKHLNROVEAMEKLINLTDILKOEKD-ETQVY--Q 731
Db 754 DLKSEBYRISLMEAYLRGNBEHIKITROVDVDELTRISTLVKGMPPDVATMKLRDE 813
Qy 732 MKELVEQMRPDPMDALQGLSPLNPAHOLGNLREBCRIMSSAKRPLMNMENPDIMSE 791
Db 814 LRSISHKEMND-----SPLDPVYKLGEMIDKAIVLGSAKRRPLMLHMKNKPKSD 864
Qy 792 LIFONNEIIFKNGDDLRODMTLTQIIRIMENIMONOGDLRLMLPYGCLSIGDCVGLIEVY 851
Db 865 LHLPCAMIFKNGDDLRODMTLVQVLEVMONIKWKAANIDCLNPAVAVLPMGEMIGLIEVY 924
Qy 852 RNSHTIMOJCKGGLKGLAL--QFNSHTLHOWL-----KDKNKGEI----- 889
Db 925 PNCKTIFELIOVGTFPMNTAVRSIDPSFMNWKIRKOCGIEDEKKSKSDSTKNPIEKKIDN 984
Qy 890 -----YDAIDLFTSCAGYCVATFIIGIDRHSNSINWKGDCQLFHDIFGHFLDHKKK 943
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Db      985  TOAMKKYFESSVDRLVSCVGSVATYIMGIKDRHSDNMLTENGKYYHIDFGHILGHGKT 1044
Qy      944  KFGYKERVFPVLTQDPLIYISKGAOECTKTRREFEFOEMCYAYLAIRHANLFINLFS 1003
Db      1045  KLGIGDRQPFILTEHMTYIRSGKSVDSGSHLOQFKTLCEAYEVMNNRDLFVSLFT 1104
Qy      1004  MMLGSGMPELQSPDDIAYIRKTLALD-KTBOALEYFMKOMNDAAHGGATTKADYFHTI 1062
Db      1105  LMLGMELPELSTKADLHLKTLFCNGESKEARKFAGIYEBAFNGSWSTKTMWLFHAV 1164
Qy      1063  KQH 1065
Db      1165  KHY 1167

RESULT 10
US-09-963-693-48
/ Sequence 48, Application US/09963693
/ Publication No. US20030181364A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruvkun, Gary
/ APPLICANT: Osg, Scott
/ TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
/ TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
/ FILE REFERENCE: 00786/351004
/ CURRENT APPLICATION NUMBER: US/09/963,693
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US/09/205,658
/ PRIOR FILING DATE: 1998-12-03
/ PRIOR APPLICATION NUMBER: 08/857,076
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: 08/888,534
/ PRIOR FILING DATE: 1997-07-07
/ PRIOR APPLICATION NUMBER: US98/10080
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 328
/ SOFTWARE: FastSeq for windows Version 4.0
/ SEQ ID NO 48
/ LENGTH: 1167
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-09-963-693-48

Query Match      19.1%; Score 1089; Db 12; Length 1167;
Best Local Similarity 27.2%; Pred. No. 1.7e-89;
Matches 311; Conservative 219; Mismatches 431; Indels 182; Gaps 39;

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Db      428  ADVDMVRIEFSVYVYGTLLTASK-STTKVNAQFAKMKEMYTFDLYMKDMPSA--VLSI 484
Qy      407  CSVKRKAKKEHCPPLAMGNILFPYDTLVSGXNALM-LPVPGLJEDLNPIGY-TGS 464
Db      485  RVLGVKVLKSEEFEGVWVMSLTDMRDELROQQLFPHLMABEPANRRIENGARIGT 544
Qy      465  NPKETPCLELEFDMSSVAKFPDMS---VIEBANMSVSSEAGFSYHAGLSNRLAD 520
Db      545  N-----AAVTIELSSVGRVMPSSOQGYTVLVKHSWTJET-----LNIWGD 587
Qy      521  NELRENDKEQLRAICTRDLSE-----ITOEKDFLMSHRRYCVTIPILP 566
Db      588  YE-----SCIRDPGYKQLQMLVKHSGIYLEDDEORHVMWRRY--IQOBP 633
Qy      567  KLI-----LSVKNSRDEYAOYCLVKNMPPIKEBQAMELLDCCNYPDPWGFVAVCLEK 621
Db      634  DLIIVISELAFWTTDENFSELVYMLEKKPSSVAAALTLTGKCTDRIVIRKFAVAKLME 693
Qy      622  YLTDDLSOYLIOYOVULVYEQYLDNLVRFLLKALTQRIQGFPEFHLKSEMH----- 676
Db      694  QLSPVTFHLFILPLIQALKEPRAOSEVGMILTRALCDYRIGHRLFVILRAIARLRC 753
Qy      677  --NKTVSOREGLLBSYCAQGYTLKHLNROYEAMEKLINLDILKQEKD-BTOYV--Q 731
Db      754  DLKSEEVRIISLMEAYLRGNEHIXITROVDMVDELTRISTLVKGMPPDVATMKLRDE 813
Qy      732  MKFLVEOMRPPDMDALOGPLSPNPAHQGNLRLEECIMSSAKRPLVMNMPIMSE 791
Db      814  IRLISHMENMD-----SPLDVYKLGEMITOKAIVLGSAKRPLMLMKKPKPSD 864
Qy      792  LLFQNNELIFKNGDDLRQDMLTQIRIMENIMONOGLDLRMLPYCLSIGDCVGLIEV 851
Db      925  PNCKTIFELVQGVNMTAVRSIDSPMNKIRKQCGIEDEKKSKXDSTKNLEKKIDN 984
Qy      890  -----YDAAILDLFTRSCAGYVATPFLIGDRHNSIMWKDGOPLHIDFGHLDHKK 943
Db      985  TOAMKKYFESSVDRLVSCVGSVATYIMGIKDRHSDNMLTENGKYYHIDFGHILGHGKT 1044
Qy      944  KFGYKERVFPVLTQDPLIYISKGAOECTKTRREFEFOEMCYAYLAIRHANLFINLFS 1003
Db      1045  KLGIGDRQPFILTEHMTYIRSGKSVDSGSHLOQFKTLCEAYEVMNNRDLFVSLFT 1104
Qy      1004  MMLGSGMPELQSPDDIAYIRKTLALD-KTBOALEYFMKOMNDAAHGGATTKADYFHTI 1062
Db      1105  LMLGMELPELSTKADLHLKTLFCNGESKEARKFAGIYEBAFNGSWSTKTMWLFHAV 1164
Qy      1063  KQH 1065
Db      1165  KHY 1167

RESULT 11
US-10-092-219-2
/ Sequence 2, Application US/10092219
/ Publication No. US20020115114A1
/ GENERAL INFORMATION:
/ APPLICANT: Domin, Jan
/ TITLE OF INVENTION: No. US20020115114A1el Lipid Kinase
/ FILE REFERENCE: 1064HG/50947
/ CURRENT APPLICATION NUMBER: US/10/092,219
/ CURRENT FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: PCT/GB98/00244
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: 09/355,160
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 9701652.1
/ PRIOR FILING DATE: 1997-01-28
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 1686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-2

Query Match      17.8%; Score 1014.5; DB 14; Length 1686;
Best Local Similarity 32.5%; Pred. No. 1.8e-82;
Matches 263; Conservative 131; Mismatches 293; Indels 123; Gaps 23;

QY 298 PMDCPTMPSYRSRISTATPYMNGSTSKSLMVNSALRIKILCTYNNV-IRIDIKIV 356
DB 666 PMDC-----AQSSEYKEMWTTTEQOFTIFAHAGISSWWSYEVKYYL 709
QY 357 RTGIYHGEBELCDNVNTQVPCSNP-----RWNEMLNVDIYIPDLPRARLCSISGV-- 409
DB 710 IGLSHNGKDLFPKIQKQVGYNNFPYLLKMDLIIFFQISDLPRESVLHLTLPILN 769
QY 410 -----KGRKAKEHCPLAMGNIN--LEDYDTLVSGKVALNLPVPHGLEDLN 457
DB 770 QSSGSSPDSNKKRG-----PEALGVSLPLCDFRFRFLCGTYLALYMTSSH----- 816
QY 458 PIVTGSNPKKP-----CLELEF--DMSSVVKFP--DMSVIEEAMNSVSREAG 505
DB 817 -----TMSVPGVTVKGYMERIYLVDPSPAPFDIITTTQVDRSIIQOH----- 862
QY 506 FSYSHAGLSNRLARDNELREND--KEQDRAICTRDPLEISETEOEKDFLMSRHVCVTIPEI 564
DB 863 -----NLETLENDIKGKLDLILHKDSSIGLSKEDKAFIMKRYICFKHPNC 908
QY 565 LPLKLLSV--KNSRDEVAQMTCLVKNPPIKPEQAMELLDCNYPDPWVRGFAVRCLK 621
DB 909 LPLILASAPMKWGN--LAKTYSILHQPALYPLALBELDLSKFADQEVRSILAVTIEA 965
QY 622 YLDDLSQVLIQLVQVLYKEQYLDNLVRFLLKALTNRIGHFFPMHLKSEHAKTVS 661
DB 966 -ISDDELTDLDPVQALKYEIYNSLVQFLSRALGNIOIAMLWMLKDLHDVQFS 1024
QY 682 QREGLLESYCRACGMYLKHLNROVEAMEKILNLTDLKOEKDETQKQVMEKFLVEQMR 741
DB 1025 TRYENHVGALLSVGG--KRLREBELKQTLVOLLGVAEKVAKOAGSARQVVLQNSMER 1081
QY 742 PDFMDALQGFLS-----PLNPAHQLGNLLEECRIMSSAKRPLNWMENPDINSELFPQ 795
DB 1082 -----VQSFQKXKCRPLKPLKSLVAKELNISKCSFFSSNAVPLKVTMVADPLGEEL-- 1133
QY 796 NNEIIRKNGDULRQDMTLTQIRIMENINQGLDMLPYGCLSIGDCVGLIEVVRNSH 855
DB 1134 --NVMKRVGEDELQDMIALQMIKIMKIMLKEGLDLMVIFKCLSTGRDRGMVELVPSD 1191
QY 856 TIMQIOCKGGLKCALQFNSHTLHQLKDKXKG--EYDAALIDLFTRSAGVCVATPILIG 914
DB 1192 TLRKIVGVGVTS--FKDKPELAEMLRKINPSEETEKASENTIYSCAGCCVATYVIGIC 1249
QY 915 DRHNSINMVDQQLPHIDFGHFLDHKKKFGYKREKRVFVLTODELIVISKAQECTKT 974
DB 1250 DRHNDINIMRSTGMFHIDRGKFLGAQMGSKFRBRAPVLTSDMAVYVNGEKK--PT 1306
QY 975 REPERQEMCYKVALIRQHANLFINPSMGLSGMPELOSPPDLAIYRKTALDKTEQE 1034
DB 1307 IRQQLTVDLCCQAYNLIIRKQTNLFMLLSIMIPSGBELTSLDKVVRDALQPTTDAE 1366
QY 1035 ALEYFMKONMDAHGGMTTKMDWIFPTIKQ 1064
DB 1367 ATIFFTR-LIESSLSIATKFNFIHNLQ 1395

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; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-192

Query Match      12.0%; Score 685; DB 10; Length 887;
Best Local Similarity 23.4%; Pred. No. 6.8e-53;
Matches 203; Conservative 158; Mismatches 312; Indels 194; Gaps 23;

QY 354 IYVRTGIYHGEBELCDNVNTQVPCSNP--RWNEMLNVDIYIPDLPRARLCSISGVKGR 412
DB 57 LYVTCQVFAEGKPSALPVRTSYKAFSTRMWNEMLKLPVXPDLPRNAQVALTIMVYGP 116
QY 413 KGAKESHCPLAMGNINLPDITLVSGKVALNLP--VPHGLEDLNPIGVTSNPKKETP 471
DB 117 GKA-----VPVGGTVVLFPGYKMSRQGMHDLKWPVVEADGSPPTVPGRTSTLSBDQM 172
QY 472 CL-----ELEDFSSVVKFPDMSVIEEAMNSVSREAGFSY----- 508
DB 173 SRLAKTLKARQGMKQVMDLRLT--FRELEWINE-----SVKSSNFMILMGFRVCYKCD 227
QY 509 -----SHAGLSNRL--ARDNELR 524
DB 228 DKEXGIVYEEKODESSPILTSFELVKVDPDQMSLENLVESKHNLPRLSRGSPSDHLK 287
QY 525 --ENDKEQLRAICTRDPLEISETEOEKDFLMSRHVCVTIPELLPKLLSVKNMSRBEVAQ 582
DB 288 PVPSPDQKNIIVSYPPSKPPTYEEDLVWEFRYYLTNODKATKTLISVTIMLPQAKQ 347
QY 583 MYCLVNDWPPPIKPEQAMELLDCNYPDPWVRGFAVRCLKELYLTDBKLSQVLIQLVQVLYKE 642
DB 348 ALALLKKNMPDVEDSELISHTYTPYKRVAVARL--ROADDEDLMLTSLQVQALKYE 406
QY 643 QY----- 644
DB 407 NFDIDKNGLEPTKDSQSSVSGNVSNGINSAEIDSSQIITSPLEVSPPASKTKEVP 466
QY 645 ----LDNLVRFLLKALTNRIGHFFPMHLKSEHAKTVSQRFGLLSYCRACGMYLK 700
DB 467 DGENILQDQDCLFLISASKNSTLANLYWVYVECDQDQOQDPKTHEYTLNVMRRFSQ 526
QY 701 HL--NRQYEAM-----EKLINLTDLKOEKDETQK--VQMKFLVEQMRBDEM 745
DB 527 ALLKGRKSVRWKSLAQAOTFVDRVLHMKAVQGRKKKNKNEQLQLLGDNENQANIS 586
QY 746 DALQGLPLNPAHQLGNLLEECRIMSSAKRPLNWMENPDINSELFPONNE-----II 800
DB 587 D-VELIPLPLEPVQKIRGIIPEFATLFSKALMP-----ADLPFKTEBGKGVPI 634
QY 801 FRNGDULRQDMTLTQIRIMENINQGLDMLPYGCLSIGDCVGLIEVVRNSHTIMOJ 860
DB 635 FRHGDLRDQDQILQIISLMDKILRKENDLKLTPKYVATATKQGFQFIOISVPAEVL 694
QY 861 QCKGGLKALQFNSHTLHQLKDKXKGLEYDAALDLFTRSAGVCVATPILIGDHNNS 920
DB 695 DRBGSIQNFRRKAYB-----ENGPNGISAEVMDTVYKSCAGCYVITIIIGVGRHLDN 748
QY 921 INWKQDQQLPHIDFGHFLDHKKKFGYKREKRVFVLTODELIVISKAQECTKTRFEFR 980
DB 749 LVLTGKGLPHIDFGYILGRDPKPL-----PPMKLNKE--WVEGNG--TQSEQYQGF 798

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RESULT 12
US-09-771-161A-192
; Sequence 192, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

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QY 981 QEMCYKAYLAIROHANLFINLFSMMLGSGMPELOSPDD--IAVIRKTLALDKTEOEALAY 1038
Db 799 RKOCYTAFLHLRKXSNLILNLFSLMWDPNIPDIALBPDKTVKVKQDFRLDLSDEAVHY 858
QY 1039 FMKQMDAHHGWTTKXMDIETHIKOH 1065
Db 859 MGSILDESVALFAVAVEOI-HKFAQY 884

RESULT 13
US-09-771-161A-193
; Sequence 193, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 193
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-193

Query Match 12.0%; Score 685; DB 10; Length 887;
Best Local Similarity 23.4%; Pred. No. 6,8e-53;
Matches 203; Conservative 158; Mismatches 312; Indels 194; Gaps 23;

QY 354 IYVRTGIHGEPLCDNVNTRVPCSNP-RNMENLNYDIYIPDLPRARLCISCVKGR 412
Db 57 LVYTCQVAEGPSALPRTSTYKAFSTRMNNMELKLVKTPDLPNNQVALTIMDYGP 116
QY 413 KGAKEHEPLAMGNINLFDYDTTLVSGKVALNLWD-VPHGLEDLNPIGVTSNPKETP 471
Db 117 GK-----VPGGTTYSLFGKYGMSQGMNDLKVWNVNVEADGSEPTNTGRTSTLSEDM 172
QY 472 CL-----ELEFDWESSVVKFPDMSIYEENHAMSVSREAGFSI----- 508
Db 173 SRLALTKAHROGHVVKVMDLRLT-FREIEMINE---SVRRSSNFMYLMGCFRCVKCD 227
QY 509 -----SHAGLSNRL--ARDNEIR 524
Db 228 DKEGIYVYEKDGDESSPILTSFELVKKVPDPQMSLENLVESKHNLPRLBAGPSDHDHX 287
QY 525 --ENDKEQJRAICTRDPLSEITEOEKDFLMSHRHYCVTIPILPKLLSVKNSDEVAQ 582
Db 288 PYPSPRDOUKNTVSVPSKRPTEYEBDDLVMEFRYYLTNDKALTKILTSLVIMDLPGAKQ 347
QY 583 MYCLVKNWPPIKPEQAMELLDCNYPDPVYRGFAVRCLEKYLITDDKLSQYLIGLVOLVLYE 642
Db 348 ALALAGKNMPVDEDELISSHYTNPTVRYAVARL-ROADDEDILMYLSQVLQALVLYE 406
QY 643 QY----- 644
Db 407 NFDIDIKNGLEPTKKDSQSSVSGVNSGINSABEDISSQITSELPVSSPPRAKTKEP 466
QY 645 -----LDNLVRFLLKALNTNORIGHPFPHLAKSEMNKTVSQRFGLLESYCRACGMYLK 700
Db 467 DGENLEQDICTFLISAPSKNSTLANLYLVYVIECEDDOTQORDPTHEMYLVNMMRFQ 526
QY 701 HL-----NROYEAM-----EKLINTLIKQEKDETQK-VQMKFLVEQMKRRPDEM 745
Db 527 ALLKGDKSVYVNSLLAAQOTFVDRLVHLMAKAVQRESGNKRKKNERIQALLDGNENKNS 586

QY 746 DALQGFSLPIANRHOGLNRLBECRIMSSAKRPLMLNMENPDIMSELLFONNE-----II 800
Db 587 D-VELLPLLEPOVKRGITIPETATILFYSALMP-----AQLFKETDGGKVPYI 634
QY 801 FKNGDDLRODMTLQIIRIMENIWONQJDLBMLPYGLSICDQVGLIEVNSHTIMQI 860
Db 635 FKNGDDLRODQILLQIISLMDKLRKENLDLKTPTKVLATSTKGFQFQISVPAEVL 694
QY 861 QCKGKGLALQNSHTLHOMLKDKXKGSIYDAIDLFTSCGCGYCATFIIGIDRHNSN 920
Db 695 DTGSIQNFERRKAPB-----ENGPNGISAEMDTYVASCAGYCVITYIILGVGDHLD 748
QY 921 IMWKDQGLFHDIDEGHFLDHKKKKFGYKBERVPVLTQDPLVYISKGAOECTKREFERP 980
Db 749 LVLTGKGKLFHIDEGYTLGRDPKPL-----PPMKLNKE--WVEGNGG---TQSEYQOE 798
QY 981 QEMCYKAYLAIROHANLFINLFSMMLGSGMPELOSPDD--IAVIRKTLALDKTEOEALAY 1038
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RESULT 14
US-09-921-232-2
; Sequence 2, Application US/09921232
; Patent No. US20020102681A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: 0706D4
; CURRENT APPLICATION NUMBER: US/09/921.232
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 09/677,064
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(803)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-921-232-2

Query Match 11.8%; Score 675.5; DB 10; Length 803;
Best Local Similarity 26.3%; Pred. No. 4,3e-52;
Matches 215; Conservative 155; Mismatches 298; Indels 149; Gaps 30;

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QY 519 -----RDNELRENDKEQLRAICTRDPLSEITQEOKDFLMSHRHVCV 559
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Db 748 DI-SADESGGLKQEKFRLLDDEBAIHFPQDLINDS 783

RESULT 15
; Sequence 2, Application US/09921330
; Patent No. US20020102682A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: 0706D3
; CURRENT APPLICATION NUMBER: US/09/921,330
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 08/677,064
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(803)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-921-330-2

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Query Match 11.8%; Score 675.5; DB 10; Length 803;
Best Local Similarity 26.3%; Pred. No. 4.3e-52;
Matches 215; Conservative 155; Mismatches 298; Indels 149; Gaps 30;

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QY 778 PLVMNMENPDMISLLELQNNBILFKNGDDLRQDMLTQIIRINENIMQNGDLRLMLPYG 837
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QY 838 CLSIGDCVGLIEVVRNSHTIMOJCKGKLGALQFNH--TLHOMLKQXKGE-----IYD 891
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QY 892 AAILDFTRSCAGYVATFIIIGIDRHNNSINWVDQGLFHIIDFGHFLDHKKKFGYKRR 951
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QY 952 VPFVLTQDFLIVSKAQOECTKTRFEFERFQEMCYKALAIQHIANLFINFSMNLGSGMP 1011
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Wed Nov 12 14:55:48 2003

us-09-325-095-37.rapb

Page 12

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:41:45 ; Search time 32 Seconds
(Without alignments)
2055.923 Million cell updates/sec

Title: US-09-325-095-37
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 328717

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	5657	99.1	1080	2	US-08-162-081B-36
5	5657	99.1	1080	2	US-08-780-872-36
6	5657	99.1	1080	3	US-09-085-957-36
7	5645	98.9	1068	3	US-08-390-874C-11
8	5645	98.9	1068	4	US-09-265-772-11
9	1978.5	34.7	1044	2	US-08-777-805A-2
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12	1978.5	34.7	1044	4	US-09-841-341-2
13	1976.5	34.6	1044	4	US-09-194-640A-1
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27	1048.5	18.4	1726	2	US-08-609-049A-30

28	1048.5	18.4	1726	3	US-09-170-996-30	Sequence 30, App1
29	1014.5	17.8	1686	4	US-09-355-160D-2	Sequence 2, App1
30	887.5	15.5	171	2	US-08-609-049A-21	Sequence 21, App1
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32	859	15.0	1876	2	US-08-609-049A-12	Sequence 12, App1
33	859	15.0	1876	3	US-09-170-996-12	Sequence 12, App1
34	852	14.9	1876	2	US-08-609-049A-28	Sequence 28, App1
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36	675.5	11.8	803	3	US-09-118-442-2	Sequence 2, App1
37	675.5	11.8	803	3	US-09-677-064-2	Sequence 2, App1
38	648.5	11.4	868	2	US-08-162-081B-33	Sequence 3, App1
39	648.5	11.4	868	2	US-08-780-872-33	Sequence 3, App1
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41	537.5	9.4	171	2	US-08-609-049A-22	Sequence 22, App1
42	537.5	9.4	171	3	US-09-170-996-22	Sequence 22, App1
43	482.5	8.5	171	2	US-08-609-049A-23	Sequence 23, App1
44	482.5	8.5	171	3	US-09-170-996-23	Sequence 23, App1
45	456	8.0	85	2	US-08-162-081B-46	Sequence 46, App1

ALIGNMENTS

RESULT 1
US-08-162-081B-37
Sequence 37, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Watfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Maayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gou, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION: LUD 5256
TELEPHONE: (212) 838-3884
TELEFAX: (212) 838-9200
INFORMATION FOR SEQ. ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1069 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-37
Query Match 100.0%; Score 5708; DB 2; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 37, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volintia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paesqualini, Patricia A.
; REFERENCE/DOCKET NUMBER: 34,894
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1069 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-872-37

Query Match 100.0%; Score 5708; DB 2; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARCLSTISYVGRKGAKEHC 420
Qy 421 PLAMGNINLFDTYDTLVSGKMLNLMVPVPHGEDLNPICVGTGSPNPKETPCLELEDFWF 480
Db 421 PLAMGNINLFDTYDTLVSGKMLNLMVPVPHGEDLNPICVGTGSPNPKETPCLELEDFWF 480
Qy 481 SSVVKEPDMSVIEBHANNVSREAGFSYSHAGLSNRLADNRENDKEQLRAICTRDPL 540
Db 481 SSVVKEPDMSVIEBHANNVSREAGFSYSHAGLSNRLADNRENDKEQLRAICTRDPL 540
Qy 541 SEITTEOKDFLWSHRHYCVTIPEILPKLLSVKNSRDEVAOMYCLVKDMPRIKPEQAME 600
Db 541 SEITTEOKDFLWSHRHYCVTIPEILPKLLSVKNSRDEVAOMYCLVKDMPRIKPEQAME 600
Qy 601 LLDGCVNPDPMVWRCFAVRCLEKYLTDKLSQYLLQVVLKYEQYLDNLVPLKRALTN 660
Db 601 LLDGCVNPDPMVWRCFAVRCLEKYLTDKLSQYLLQVVLKYEQYLDNLVPLKRALTN 660
Qy 661 QRTGHEFFPMLKSEDMNKTVSQRFGLLSEYCAACGYLKLALRQYEAKEKILNTDILK 720
Db 661 QRTGHEFFPMLKSEDMNKTVSQRFGLLSEYCAACGYLKLALRQYEAKEKILNTDILK 720
Qy 721 QEKKDETOKVQMFLEVQONRPPMDALOGFLSPINPAHOLGNRLBEEGINSARPLW 780
Db 721 QEKKDETOKVQMFLEVQONRPPMDALOGFLSPINPAHOLGNRLBEEGINSARPLW 780
Qy 781 LNMENDDIMSELLFONNEIIFKXGDDLRODMTLQIIRIMENIWOQGDLDRLPYCCLS 840
Db 781 LNMENDDIMSELLFONNEIIFKXGDDLRODMTLQIIRIMENIWOQGDLDRLPYCCLS 840
Qy 841 IGDGCVGLIEVNRSHITMOQCKGGLKALQFNSHTLHQWLKONKEIYDAAILDFTRS 900
Db 841 IGDGCVGLIEVNRSHITMOQCKGGLKALQFNSHTLHQWLKONKEIYDAAILDFTRS 900
Qy 901 CAGYCVATFLIGDGRHNSINWKGDDGOLFHDGPHLDHKKKPGKREPVFLTODF 960
Db 901 CAGYCVATFLIGDGRHNSINWKGDDGOLFHDGPHLDHKKKPGKREPVFLTODF 960
Qy 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANLFINLFSMUGSGWPELOSPDDIA 1020
Db 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANLFINLFSMUGSGWPELOSPDDIA 1020
Qy 1021 YIRKTIALDKTBOALEYFKQKONDAHGGWTTKMDWIFHTIKOHALN 1068
Db 1021 YIRKTIALDKTBOALEYFKQKONDAHGGWTTKMDWIFHTIKOHALN 1068

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RESULT 3

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US-09-085-957-37
; Sequence 37, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

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; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085, 957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780, 872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162, 081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ. ID NO.: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1069 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-085-957-37

```

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Query Match 100.0%; Score 5708; DB 3; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPPRSSGELMGHLMPPRIIVLVECLLPNGNITVLECLREATLITTHGLPKARKYPLHQ 60
Db 1 MPPRSSGELMGHLMPPRIIVLVECLLPNGNITVLECLREATLITTHGLPKARKYPLHQ 60
Qy 61 LLODESSYFVSVTOABEEPEDETRRLCDRLPOPKVLEPVGNREKILNREIGFA 120
Db 61 LLODESSYFVSVTOABEEPEDETRRLCDRLPOPKVLEPVGNREKILNREIGFA 120
Qy 121 IGMVCEFDWVMDPEVQDFRRNLIANCKEAVDLRDLNSPSRAMVYYPNVSSPELPRK 180
Db 121 IGMVCEFDWVMDPEVQDFRRNLIANCKEAVDLRDLNSPSRAMVYYPNVSSPELPRK 180
Qy 181 IYKLDKGOITIVITVSPNNDKQYTLKINHDCVBOVIAEALIKKTRSMILSSBOLK 240
Db 181 IYKLDKGOITIVITVSPNNDKQYTLKINHDCVBOVIAEALIKKTRSMILSSBOLK 240
Qy 241 LCYLEYQGYIILKVGCDEYFLEKYPISOYKIRSCIMGRPNMLMAKESISQLPMD 300
Db 241 LCYLEYQGYIILKVGCDEYFLEKYPISOYKIRSCIMGRPNMLMAKESISQLPMD 300
Qy 301 CFTMPSYRRISTATPYNNGETSTKSLWVNSALRIKILCATYVNNIRIDIKIYRTGI 360
Db 301 CFTMPSYRRISTATPYNNGETSTKSLWVNSALRIKILCATYVNNIRIDIKIYRTGI 360
Qy 361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARCLSTISYVGRKGAKEHC 420
Db 361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARCLSTISYVGRKGAKEHC 420
Qy 421 PLAMGNINLFDTYDTLVSGKMLNLMVPVPHGEDLNPICVGTGSPNPKETPCLELEDFWF 480
Db 421 PLAMGNINLFDTYDTLVSGKMLNLMVPVPHGEDLNPICVGTGSPNPKETPCLELEDFWF 480
Qy 481 SSVVKEPDMSVIEBHANNVSREAGFSYSHAGLSNRLADNRENDKEQLRAICTRDPL 540
Db 481 SSVVKEPDMSVIEBHANNVSREAGFSYSHAGLSNRLADNRENDKEQLRAICTRDPL 540
Qy 541 SEITTEOKDFLWSHRHYCVTIPEILPKLLSVKNSRDEVAOMYCLVKDMPRIKPEQAME 600
Db 541 SEITTEOKDFLWSHRHYCVTIPEILPKLLSVKNSRDEVAOMYCLVKDMPRIKPEQAME 600

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QY 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKYEQYLDNLVRFLLKKALTN 660
DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKYEQYLDNLVRFLLKKALTN 660
QY 661 QRIQGFHFMHLKSEMHNTVSQRFGLLLESYCRACGMYLKLNRQVEAMEKILNLTDLK 720
DB 661 QRIQGFHFMHLKSEMHNTVSQRFGLLLESYCRACGMYLKLNRQVEAMEKILNLTDLK 720
QY 721 QEKDETKQVMKFLVEQMRPDMALQGLSPINPAHQNLRECRINSAXKPLW 780
DB 721 QEKDETKQVMKFLVEQMRPDMALQGLSPINPAHQNLRECRINSAXKPLW 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTQIIRIMENIWONQGLDRLMLPYGCLS 840
DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTQIIRIMENIWONQGLDRLMLPYGCLS 840
QY 841 IGDGCVGLEEVNRSHITMOIQCKGGLKALQFNSHTLHQLKDKNGKEIYDAADLFTRS 900
DB 841 IGDGCVGLEEVNRSHITMOIQCKGGLKALQFNSHTLHQLKDKNGKEIYDAADLFTRS 900
QY 901 CAGCVATFIIGIDRHSNIMVWDGQLPHIDFGHFLDHKKKFGYKREVPVLTQDF 960
DB 901 CAGCVATFIIGIDRHSNIMVWDGQLPHIDFGHFLDHKKKFGYKREVPVLTQDF 960
QY 961 LIVISKAQECTKTREREFQEMCYKAYLAIRQHANLFINLPSMLCSGMBELSPDIA 1020
DB 961 LIVISKAQECTKTREREFQEMCYKAYLAIRQHANLFINLPSMLCSGMBELSPDIA 1020
QY 1021 YIRKTLALDKTEOBALFEMKQNDAAHGGWTTQMDMFTIKQHALN 1068
DB 1021 YIRKTLALDKTEOBALFEMKQNDAAHGGWTTQMDMFTIKQHALN 1068

RESULT 4
US-08-162-081B-36
Sequence 36, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hillel, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bales, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarabovich
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasquallini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 1080 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-081B-36
Query Match 99.1%; Score 5657; DB 2; Length 1080;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPRPSSGELMGHIMPPRIIVLVECLIPNGMIYTLBELRPAITLITTHLELFKARAKYPLHQ 60
DB 1 MPRPSSGELMGHIMPPRIIVLVECLIPNGMIYTLBELRPAITLITTHLELFKARAKYPLHQ 60
QY 61 LLDDESSYIFVSTQAESEEPEDFTRICDLRFPQFLKVEPVGNREKILNREIGFA 120
DB 61 LLDDESSYIFVSTQAESEEPEDFTRICDLRFPQFLKVEPVGNREKILNREIGFA 120
QY 121 IGMVCEFDNVKQPEVQDPRRNILANCKEAVDLRLDINSPHSRAMVYYPVVESSPELPHK 180
DB 121 IGMVCEFDNVKQPEVQDPRRNILANCKEAVDLRLDINSPHSRAMVYYPVVESSPELPHK 180
QY 181 IYKKDRGQIIVIVWIVSEPNNDKOKYTLKINHDCVPEQYLAIRKTRSMILSSQOK 240
DB 181 IYKKDRGQIIVIVWIVSEPNNDKOKYTLKINHDCVPEQYLAIRKTRSMILSSQOK 240
QY 241 LCYLEVQKTIILAVCCDEVELEKYPISOYKYTRSCIMGRMNLMMAKESLYSOLPMD 300
DB 241 LCYLEVQKTIILAVCCDEVELEKYPISOYKYTRSCIMGRMNLMMAKESLYSOLPMD 300
QY 301 CFMPSSYRISTATPYMNGESTKSLMIVNSALRIKILCATYVNVNIRIDIKIYRTGI 360
DB 301 CFMPSSYRISTATPYMNGESTKSLMIVNSALRIKILCATYVNVNIRIDIKIYRTGI 360
QY 361 YHGEPLCDNVNTQVPCSNPRNENLNDIYIPDLPRARLCLISCVGRGAKAEHC 420
DB 361 YHGEPLCDNVNTQVPCSNPRNENLNDIYIPDLPRARLCLISCVGRGAKAEHC 420
QY 421 PLANGINLNDYDTTLVSGKALNMPVPGLEDLNPIGVTSNPNKETPCELEBDFW 480
DB 421 PLANGINLNDYDTTLVSGKALNMPVPGLEDLNPIGVTSNPNKETPCELEBDFW 480
QY 481 SSVVKFPMDSVIEEHAWSVSREAGFSYSHAGLSNRLARNDRENDKEOLRAICTRDP 540
DB 481 SSVVKFPMDSVIEEHAWSVSREAGFSYSHAGLSNRLARNDRENDKEOLRAICTRDP 540
QY 541 SEITEOEKFLMSHRAYCVTIPETLPLKLLSVKNSRDEVAQMYCLVKDMPPIRPEQAME 600
DB 541 SEITEOEKFLMSHRAYCVTIPETLPLKLLSVKNSRDEVAQMYCLVKDMPPIRPEQAME 600
QY 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKYEQYLDNLVRFLLKKALTN 660
DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKYEQYLDNLVRFLLKKALTN 660
QY 661 QRIQGFHFMHLKSEMHNTVSQRFGLLLESYCRACGMYLKLNRQVEAMEKILNLTDLK 720
DB 661 QRIQGFHFMHLKSEMHNTVSQRFGLLLESYCRACGMYLKLNRQVEAMEKILNLTDLK 720
QY 721 QEKDETKQVMKFLVEQMRPDMALQGLSPINPAHQNLRECRINSAXKPLW 780
DB 721 QEKDETKQVMKFLVEQMRPDMALQGLSPINPAHQNLRECRINSAXKPLW 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTQIIRIMENIWONQGLDRLMLPYGCLS 840
DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTQIIRIMENIWONQGLDRLMLPYGCLS 840
QY 841 IGDGCVGLEEVNRSHITMOIQCKGGLKALQFNSHTLHQLKDKNGKEIYDAADLFTRS 900
DB 841 IGDGCVGLEEVNRSHITMOIQCKGGLKALQFNSHTLHQLKDKNGKEIYDAADLFTRS 900
QY 901 CAGCVATFIIGIDRHSNIMVWDGQLPHIDFGHFLDHKKKFGYKREVPVLTQDF 960
DB 901 CAGCVATFIIGIDRHSNIMVWDGQLPHIDFGHFLDHKKKFGYKREVPVLTQDF 960

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QY 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANI.FINLFSMILGSGMPELOSFDDIA 1020
DB 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANI.FINLFSMILGSGMPELOSFDDIA 1020
QY 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTIKOHAN 1068
DB 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTIKOHAN 1068

RESULT 5
US-08-780-872-36
; Sequence 36, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780, 872
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-36

Query Match 99.1%; Score 5657; DB 2; Length 1080;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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QY 181 IYNKLDKGOIIVYIWIIVSPNDKOKYTLKINHDVCEQYIAAIRKTRSMILSSFOLK 240
DB 181 IYNKLDKGOIIVYIWIIVSPNDKOKYTLKINHDVCEQYIAAIRKTRSMILSSFOLK 240
QY 241 LCVLEYGOKYILKVCDCDEYFLEKYPLOYKYIRSCIMGRMNMLMAKESLYSQLPMD 300
DB 241 LCVLEYGOKYILKVCDCDEYFLEKYPLOYKYIRSCIMGRMNMLMAKESLYSQLPMD 300
QY 301 CFTMPSYRRIISATPYMNGESTKSLAWINSAARI.KIICATVYNNIRPIDIYRTGI 360
DB 301 CFTMPSYRRIISATPYMNGESTKSLAWINSAARI.KIICATVYNNIRPIDIYRTGI 360
QY 361 YHGBEPLCDNVNTQRPVCSNPRNEMLNNDIYIPDLPRARLCLASICYKRGKAEHC 420
DB 361 YHGBEPLCDNVNTQRPVCSNPRNEMLNNDIYIPDLPRARLCLASICYKRGKAEHC 420
QY 421 PLAMGNINLPDYTDITVSGMALNLPVPHGEDLLNPIGVTSNPNKETPCLLEDFWF 480
DB 421 PLAMGNINLPDYTDITVSGMALNLPVPHGEDLLNPIGVTSNPNKETPCLLEDFWF 480
QY 481 SSVVKFEDMSVLEEHANWSVSRAGFSYSHAGISNRLARDNELRENDKQDLRAICTRDP 540
DB 481 SSVVKFEDMSVLEEHANWSVSRAGFSYSHAGISNRLARDNELRENDKQDLRAICTRDP 540
QY 541 SEITBOEKDFLMSHRYCVTIPEILPKLLSVKMSRDEVAQWYCLVKDMPPIKPCQAME 600
DB 541 SEITBOEKDFLMSHRYCVTIPEILPKLLSVKMSRDEVAQWYCLVKDMPPIKPCQAME 600
QY 601 LLDGNYPDMVNGFAVRCLEKYLTDKLSQYLIQLVQVLYKEQYLDNLVFLFKKALTN 660
DB 601 LLDGNYPDMVNGFAVRCLEKYLTDKLSQYLIQLVQVLYKEQYLDNLVFLFKKALTN 660
QY 661 QRIQHFFFWHLSEMNKTVSQRFGLLBSYCACGMYIKHNRQVEAMEKILNLTDLK 720
DB 661 QRIQHFFFWHLSEMNKTVSQRFGLLBSYCACGMYIKHNRQVEAMEKILNLTDLK 720
QY 721 QEKDETKQVOMFLVEQNRPPDMDALQFSLPPLPAHQNLRLREGRINSSAKRPLM 780
DB 721 QEKDETKQVOMFLVEQNRPPDMDALQFSLPPLPAHQNLRLREGRINSSAKRPLM 780
QY 781 LKMWENDINSELI.FONNEIIFKNGDDLRODMLTLQIIRIMENTIMONQGLDRLM.PYGCLS 840
DB 781 LKMWENDINSELI.FONNEIIFKNGDDLRODMLTLQIIRIMENTIMONQGLDRLM.PYGCLS 840
QY 841 IGDGVLIEVNRSHITMOIQCKGKGLKALQFNSHTLHQLKDXNGEITYDAIDLFTRS 900
DB 841 IGDGVLIEVNRSHITMOIQCKGKGLKALQFNSHTLHQLKDXNGEITYDAIDLFTRS 900
QY 901 CAGYCVATFILIIGDRHNSINWYKDDGOLFHDGFHLDHKKKFGYKXERVPFVLTQDF 960
DB 901 CAGYCVATFILIIGDRHNSINWYKDDGOLFHDGFHLDHKKKFGYKXERVPFVLTQDF 960
QY 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANI.FINLFSMILGSGMPELOSFDDIA 1020
DB 961 LIVISGAOECTRTREFEFOEMCYKAYLAIROHANI.FINLFSMILGSGMPELOSFDDIA 1020
QY 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTIKOHAN 1068
DB 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTIKOHAN 1068

RESULT 6
US-09-085-957-36
; Sequence 36, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE

```

NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felt & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/085,957
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/780,872
 FILING DATE: 09-JAN-1997
 APPLICATION NUMBER: 08/162,081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1080 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-085-957-36

Query Match 99.1%; Score 5657; DB 3; Length 1080;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPRSSGELGIMHMPRIIVECLPNGMIITTECLREALTITIKHBLFKBARKYPLHQ 60
 DB 1 MPPRSSSELGIMHMPRIIVECLPNGMIITTECLREALTITIKHBLFKBARKYPLHQ 60
 QY 61 LLODESSYIFVSVTQEAEREFEFDETRRLCDIRLFOPFLKYTEPVGNREBKILNREIGFA 120
 DB 61 LLODESSYIFVSVTQEAEREFEFDETRRLCDIRLFOPFLKYTEPVGNREBKILNREIGFA 120
 QY 121 IGMPCVEFDWYKDEVPDPRRIILNVCKEAVDLRLNSPHSAMVYPPNVSESPLELPH 180
 DB 121 IGMPCVEFDWYKDEVPDPRRIILNVCKEAVDLRLNSPHSAMVYPPNVSESPLELPH 180
 QY 121 IGMPCVEFDWYKDEVPDPRRIILNVCKEAVDLRLNSPHSAMVYPPNVSESPLELPH 180
 DB 121 IGMPCVEFDWYKDEVPDPRRIILNVCKEAVDLRLNSPHSAMVYPPNVSESPLELPH 180
 QY 181 IYNNLDKGGIIVIVIVISPNNDKOKYTLKINHDCVPEQVIAEAIKRTKTRSMLSSEQIK 240
 DB 181 IYNNLDKGGIIVIVIVISPNNDKOKYTLKINHDCVPEQVIAEAIKRTKTRSMLSSEQIK 240
 QY 241 LCVLEYOGKYLIVKVGCGDEYFLKXPPLSQYKIRSCIMGRPNMLMAKESLYSOLPMD 300
 DB 241 LCVLEYOGKYLIVKVGCGDEYFLKXPPLSQYKIRSCIMGRPNMLMAKESLYSOLPMD 300
 QY 301 CFTMPSYSRISTATPPYMMGETSTSLWYNALRIKILCATYVNNINRIDIKIYRTGI 360
 DB 301 CFTMPSYSRISTATPPYMMGETSTSLWYNALRIKILCATYVNNINRIDIKIYRTGI 360
 QY 361 YHGGEPICNNVATQRPVCSNPRNENLNDIYIPDLPRARLCLISICSVKRGKANEHC 420
 DB 361 YHGGEPICNNVATQRPVCSNPRNENLNDIYIPDLPRARLCLISICSVKRGKANEHC 420
 QY 421 PLAMGNINFDYTDITLVSGRMALNIMPVPHGLEDLNPIGVGTSNNPKETPCLELEFDF 480

DB 421 PLAMGNINFDYTDITLVSGRMALNIMPVPHGLEDLNPIGVGTSNNPKETPCLELEFDF 480
 QY 481 SSVKRPDMSVTEEHANMSVSREAGSYSHAGLSNRLADNELRENDKQLAICTRDL 540
 DB 481 SSVKRPDMSVTEEHANMSVSREAGSYSHAGLSNRLADNELRENDKQLAICTRDL 540
 QY 541 SETTEOKDFLMSHRHYCTIPEILPKLLSVKMSRDEVAQMYCLVKDMPPIKPEQAME 600
 DB 541 SETTEOKDFLMSHRHYCTIPEILPKLLSVKMSRDEVAQMYCLVKDMPPIKPEQAME 600
 QY 601 LLDONYPDPMVGRFAVRCLEKTYTDDKLSQYLIQIVQVTKYEQYLDNLVRLFKALTN 660
 DB 601 LLDONYPDPMVGRFAVRCLEKTYTDDKLSQYLIQIVQVTKYEQYLDNLVRLFKALTN 660
 QY 661 QRTGHPFPMHLKEMNKTVSOFEGLLSYCRACGMV/KHLNROYANEKILNLTDLK 720
 DB 661 QRTGHPFPMHLKEMNKTVSOFEGLLSYCRACGMV/KHLNROYANEKILNLTDLK 720
 QY 721 QEKKDETOKVQMKFVLEQMRPPDMALOGFLSPINPAHQNLRLSECRIMSSAKRPLW 780
 DB 721 QEKKDETOKVQMKFVLEQMRPPDMALOGFLSPINPAHQNLRLSECRIMSSAKRPLW 780
 QY 781 LNMENPDIMSELLFONNEIIFKNGDDLRODMTLLOIIRIMENIMORGLDLRLPYGLS 840
 DB 781 LNMENPDIMSELLFONNEIIFKNGDDLRODMTLLOIIRIMENIMORGLDLRLPYGLS 840
 QY 841 IGDVGLIEVVRNSHTIMOQCKGGLKGAIOENSHTLHOWLKDKNKEIYDAADLFTFS 900
 DB 841 IGDVGLIEVVRNSHTIMOQCKGGLKGAIOENSHTLHOWLKDKNKEIYDAADLFTFS 900
 QY 901 CAGYCATFTILIGIDRHSNINMYKDCQFLHIDFGHLDHKKRFGYKRERVPVLTQDF 960
 DB 901 CAGYCATFTILIGIDRHSNINMYKDCQFLHIDFGHLDHKKRFGYKRERVPVLTQDF 960
 QY 961 LIVISKGAOECTKTREFEFOECYKAYLAIRQHANFIVLFSMGLSGMPELOSFPDIA 1020
 DB 961 LIVISKGAOECTKTREFEFOECYKAYLAIRQHANFIVLFSMGLSGMPELOSFPDIA 1020
 QY 1021 YIRKTLALDKTEQALIEYFMKQMNDAHGGMTTKMDIIFHTIKOHALN 1068
 DB 1021 YIRKTLALDKTEQALIEYFMKQMNDAHGGMTTKMDIIFHTIKOHALN 1068

RESULT 7
 US-08-390-874C-11
 Sequence 11, Application US/08390874C
 Patent No. 6043062
 GENERAL INFORMATION:
 APPLICANT: Klippel, Anke
 APPLICANT: Williams, Lewis T.
 TITLE OF INVENTION: A Constitutively Active
 TITLE OF INVENTION: Phosphatidylinositol 3-kinase and Uses Thereof
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,874C
 FILING DATE: 17-FEB-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 02307K-057000US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1068 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-390-874C-11

Query Match 98.9%; Score 5645; DB 3; Length 1068;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MPPRPSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIKHELFEAKRYPLHQ 60
DB 1 MPPRPSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIKHELFEAKRYPLHQ 60
QY 61 LLODESSYIFVSTQGAEREFEDETRRLCDLRFQFLKVIIEPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSTQGAEREFEDETRRLCDLRFQFLKVIIEPVGNREKILNREIGFA 120
QY 121 IGMPVCEFDWYKDEVDFFRRNLTNVCKEAVLDLNSPFSRAMYVYPPVNESSPELPKH 180
DB 121 IGMPVCEFDWYKDEVDFFRRNLTNVCKEAVLDLNSPFSRAMYVYPPVNESSPELPKH 180
QY 181 IYKRLDKGOIIVYIYVWVSPNNOKOYTLKINHCVGEQVIAERIKKTSMLISSPOLK 240
DB 181 IYKRLDKGOIIVYIYVWVSPNNOKOYTLKINHCVGEQVIAERIKKTSMLISSPOLK 240
QY 241 LCVLEYQKXITLVCGDEYFLEKYPISQYKXIRSCIMLRPMYIMAKESLYSOLPMD 300
DB 241 LCVLEYQKXITLVCGDEYFLEKYPISQYKXIRSCIMLRPMYIMAKESLYSOLPMD 300
QY 301 CFMPYSRISITATPYMNGESTYKSLWVINSALRIKILCATYVNVNIRIDKIYVGTGI 360
DB 301 CFMPYSRISITATPYMNGESTYKSLWVINSALRIKILCATYVNVNIRIDKIYVGTGI 360
QY 361 YHGGEPLCDNVNORVPCSNPRNEMLTNDIYIPDLPRARLCISVSNGRGAKEHC 420
DB 361 YHGGEPLCDNVNORVPCSNPRNEMLTNDIYIPDLPRARLCISVSNGRGAKEHC 420
QY 421 PLAMGNINLFDYITDLVSGKALNLMFVPHGLEDLNPIGVTGSPNKETPCLELEDFMF 480
DB 421 PLAMGNINLFDYITDLVSGKALNLMFVPHGLEDLNPIGVTGSPNKETPCLELEDFMF 480
QY 481 SSVYKFPDMSVIEBHANVSYSREAGFSYSHAGLSNRLARDNELENDKEQLRAICTRDPL 540
DB 481 SSVYKFPDMSVIEBHANVSYSREAGFSYSHAGLSNRLARDNELENDKEQLRAICTRDPL 540
QY 541 SETTEBKDFLNHSHRHCVTIPILPLRLLSVKNNSDEVAQYCLVYKMPPIKPEQAME 600
DB 541 SETTEBKDFLNHSHRHCVTIPILPLRLLSVKNNSDEVAQYCLVYKMPPIKPEQAME 600
QY 601 LLDONYPDPVWRFGEAVRCELEKYLTDPLSQYLLQLVQVLYKEQYLDNLVRFLLKXALTN 660
DB 601 LLDONYPDPVWRFGEAVRCELEKYLTDPLSQYLLQLVQVLYKEQYLDNLVRFLLKXALTN 660
QY 661 QRIQHEFFMHLKSEMNKTVSQRFGLLLESYCRACGMYLXHLNRQYVAMEKLTINTDILK 720
DB 661 QRIQHEFFMHLKSEMNKTVSQRFGLLLESYCRACGMYLXHLNRQYVAMEKLTINTDILK 720
QY 721 QEKKDETKQYKMFVLEQMRPDPFMDALQGLSPLNANHLGSLNLEECYINSAKRPLW 780
DB 721 QEKKDETKQYKMFVLEQMRPDPFMDALQGLSPLNANHLGSLNLEECYINSAKRPLW 780
QY 781 LNNENPDINSELFOUNNEIIFKXGDDLRQDMLTQIIRIMENIMONOGILRLMPYCCLS 840
DB 781 LNNENPDINSELFOUNNEIIFKXGDDLRQDMLTQIIRIMENIMONOGILRLMPYCCLS 840
QY 841 IGDVGLIEVVRNSHTIMOICKGGLKGLALQFNSHTLHQLKDKNGEIVDAAIDLFTRS 900

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DB 841 IGDVGLIEVVRNSHTIMOICKGGLKGLALQFNSHTLHQLKDKNGEIVDAAIDLFTRS 900
QY 901 CAGYCVATFLLIGIDRNSNINWMDGQLPHIDFGHFLDHKKKKFGYKREVPVLQDF 960
DB 901 CAGYCVATFLLIGIDRNSNINWMDGQLPHIDFGHFLDHKKKKFGYKREVPVLQDF 960
QY 961 LIVISKAQECTKTRERFERQEMCYKAYLAIRQANLFINLPSNMLGSGMPELQSPDIA 1020
DB 961 LIVISKAQECTKTRERFERQEMCYKAYLAIRQANLFINLPSNMLGSGMPELQSPDIA 1020
QY 1021 YIRKTLALDKTEQDALEYFMKQWMDAHGCGTTKMDIIFHTIQHALN 1068
DB 1021 YIRKTLALDKTEQDALEYFMKQWMDAHGCGTTKMDIIFHTIQHALN 1068

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RESULT 8

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US-09-265-772-11
Sequence 11, Application US/09265772
Patent No. 6300111
GENERAL INFORMATION:
APPLICANT: Klippel, Anke
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: A Constitutively Active
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/1265, 772
FILING DATE: 10-MAR-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390, 874
FILING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-265-772-11

```

Query Match 98.9%; Score 5645; DB 4; Length 1068;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 MPPRPSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIKHELFEAKRYPLHQ 60
DB 1 MPPRPSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIKHELFEAKRYPLHQ 60
QY 61 LLODESSYIFVSTQGAEREFEDETRRLCDLRFQFLKVIIEPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSTQGAEREFEDETRRLCDLRFQFLKVIIEPVGNREKILNREIGFA 120

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QY 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPELPHK 180
DB 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPELPHK 180
QY 181 IYKLDKGOIIVYIWIIVSPNDKOKYTLKINHDCVBEQVIAEAIKRTSRMLSSQOLK 240
DB 181 IYKLDKGOIIVYIWIIVSPNDKOKYTLKINHDCVBEQVIAEAIKRTSRMLSSQOLK 240
QY 241 LCYLEYQKTIILKCCGDEFELEKPIISOYKYITSCIMLGRMPLMLMAKESLYSOLPMD 300
DB 241 LCYLEYQKTIILKCCGDEFELEKPIISOYKYITSCIMLGRMPLMLMAKESLYSOLPMD 300
QY 301 CFMPSPSRISTATPYMNGESTSKSLMWINSALRIKILCATYVNAVIRIDIKIYVETGI 360
DB 301 SFYVPSISRIISTATPYMNGESTSKSLMWINSALRIKILCATYVNAVIRIDIKIYVETGI 360
QY 361 YHGEPLCDNVNTOVPCSNPRNEMLYDIYIDLPRAARLCLSTCSVKGKAKEBHC 420
DB 361 YHGEPLCDNVNTOVPCSNPRNEMLYDIYIDLPRAARLCLSTCSVKGKAKEBHC 420
QY 421 PLWAGNINLFDYDTTLVSGKALMLVPYHGLBDLNPIDYTGSPNKETPCLELEPWF 480
DB 421 PLWAGNINLFDYDTTLVSGKALMLVPYHGLBDLNPIDYTGSPNKETPCLELEPWF 480
QY 481 SSVVKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDELRENDKEQLRAICTRDEL 540
DB 481 SSVVKPDMSVIEBHAMSVSREAGFSYSHAGLSNRLARDELRENDKEQLRAICTRDEL 540
QY 541 SEITEOEKDFLMSHRHYCVTILPELPLKLLSVKMSRDEVAQMTCLVDEWPIRKEQAME 600
DB 541 SEITEOEKDFLMSHRHYCVTILPELPLKLLSVKMSRDEVAQMTCLVDEWPIRKEQAME 600
QY 601 LLDGNYDPDMRGAVRCLERYLTDGKLSQYLIOLVQVLYKTEQYLDNLVFLKKAALTN 660
DB 601 LLDGNYDPDMRGAVRCLERYLTDGKLSQYLIOLVQVLYKTEQYLDNLVFLKKAALTN 660
QY 661 ORIGHFFPMHLKSMHNKTVSQRFGLLBSYCRACGMVLYKHLNOVEAMEKILNLTDLK 720
DB 661 ORIGHFFPMHLKSMHNKTVSQRFGLLBSYCRACGMVLYKHLNOVEAMEKILNLTDLK 720
QY 721 OEKDETOKVOMKFLVEQMRAPDFMDALQGFSLPLNPAHQLGNLRLBECRIMSSAKRPLW 780
DB 721 OEKDETOKVOMKFLVEQMRAPDFMDALQGFSLPLNPAHQLGNLRLBECRIMSSAKRPLW 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDLEFQDMTLQIIRIMENIMONOGELDRMLPYGCLIS 840
DB 781 LNMENPDIMSELLFQNNELIFKNGDLEFQDMTLQIIRIMENIMONOGELDRMLPYGCLIS 840
QY 841 IGDVGJLEVVNRSHITMOIOCKGSLKALQFNSHTLQWLKDKXKGEITYDAIDLFTRS 900
DB 841 IGDVGJLEVVNRSHITMOIOCKGSLKALQFNSHTLQWLKDKXKGEITYDAIDLFTRS 900
QY 901 CAGYCVATPILIGDRHNSINIMVXDQGLFIHDFSHPLDHKKKFGYKREVRPVLITDGF 960
DB 901 CAGYCVATPILIGDRHNSINIMVXDQGLFIHDFSHPLDHKKKFGYKREVRPVLITDGF 960
QY 961 LIVISKAQOECTKTRERFERFQDMCYKAYLAIRQHANLFINLFSMMLGSGMELQSFDDIA 1020
DB 961 LIVISKAQOECTKTRERFERFQDMCYKAYLAIRQHANLFINLFSMMLGSGMELQSFDDIA 1020
QY 1021 YIRKTLADKTEQEALEYFMKOMDAAHHGWTCKDWIFHTIKOHALN 1068
DB 1021 YIRKTLADKTEQEALEYFMKOMDAAHHGWTCKDWIFHTIKOHALN 1068

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RESULT 9
US-08-777-405A-2
Sequence 2, Application US/08777405A
Patent No. 5858753

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoeckstra, Merl F.
APPLICANT: Holtzman, Douglas A

```

TITLE OF INVENTION: No. 5858753e1 Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall O'Toole Gerstein Murray & Botun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1044 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-777-405A-2

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Query Match 34.7%; Score 1978.5; DB 2; Length 1044;
Best Local Similarity 39.9%; Pred. No. 3.1e-195;
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

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QY 16 MPP-----RLVBECLPNGMIVTLECRBATLTITIKHELFKEARKYPLHQ 60
DB 1 MPPGVDCPMEFWTKEENOSVVDVFLPTGYLNPVSRNANLSTIKOLLNHRQYELFH 60
QY 61 LLDSESYIEFVSTOEAERESEFPDETRLCDLRFQPLKYIEBQVNGREEKILNREIGFA 120
DB 61 MLSGPEAVVFTCINQTEHQDEGRRLCDVQFPLVLRVAREGDRVKKLINSQSLTL 120
QY 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPE---- 176
DB 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPE---- 176
QY 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPE---- 176
DB 121 IGMVCEFDWVDPDEVDPRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESSPE---- 176
QY 177 -----LPHYIYKLDKGOIIVYIWIIVSPNDKOKYTLKINHDCVBEQVIAEAIKRTSRM 232
DB 177 -----LPHYIYKLDKGOIIVYIWIIVSPNDKOKYTLKINHDCVBEQVIAEAIKRTSRM 232
QY 181 GTLRLEPR-----ALVNVAKEGSEBSFTQVSTKDVPLMLMCAALKK----- 224
DB 181 GTLRLEPR-----ALVNVAKEGSEBSFTQVSTKDVPLMLMCAALKK----- 224
QY 223 LLSSEQLKLVLEYQKYILVCCGDEFELEKPIISOYKYITSCIMLGRMPLMLMAKES 292
DB 223 LLSSEQLKLVLEYQKYILVCCGDEFELEKPIISOYKYITSCIMLGRMPLMLMAKES 292
QY 225 ---ATVFRQPLVBEQDEYTLQVNGRHHLYLGNVPLCQFOYICSLHSGLTPLTMVHSS 281
DB 225 ---ATVFRQPLVBEQDEYTLQVNGRHHLYLGNVPLCQFOYICSLHSGLTPLTMVHSS 281
QY 293 LYSQPLMDCFTMPSYRISTATPYMNGESTSKSLMWINSALRIKILCATYVNAVIRIDID 352
DB 293 LYSQPLMDCFTMPSYRISTATPYMNGESTSKSLMWINSALRIKILCATYVNAVIRIDID 352
QY 282 ILAARDEQSNPAPOVQPRAKRPEIPAKKSSVLSMSELPFRITELQGSKYNADER--M 339
DB 282 ILAARDEQSNPAPOVQPRAKRPEIPAKKSSVLSMSELPFRITELQGSKYNADER--M 339
QY 353 KIIVRTGIYHGEPLCDNVNTOVPCSNPRNEMLYDIYIDLPRAARLCLSTCSV-- 409
DB 353 KIIVRTGIYHGEPLCDNVNTOVPCSNPRNEMLYDIYIDLPRAARLCLSTCSV-- 409
QY 340 KLIVQAGLPHGENMICKTVSSSEVSVCSEPVAKORLEPDINICDLPRAARLCLSTCSV 399
DB 340 KLIVQAGLPHGENMICKTVSSSEVSVCSEPVAKORLEPDINICDLPRAARLCLSTCSV 399
QY 410 -----KGRKAKEBHCPLWAGNINLFDYDTTLVSGKALMLVPYHGLBDLNPIDYTG 462
DB 410 -----KGRKAKEBHCPLWAGNINLFDYDTTLVSGKALMLVPYHGLBDLNPIDYTG 462
QY 400 KAKARSTKSKSKADCPDIAMANLMLFDYKQKLTGEGECLYMMSVDEKELLNPTGTV 459
DB 400 KAKARSTKSKSKADCPDIAMANLMLFDYKQKLTGEGECLYMMSVDEKELLNPTGTV 459
QY 463 GSNPKETP-----CLELEFDWFSVVKFPMMSVIEBHAMSVSREAGFSYSHAGLSNRL 517
DB 463 GSNPKETP-----CLELEFDWFSVVKFPMMSVIEBHAMSVSREAGFSYSHAGLSNRL 517
QY 460 RSNPRTDSAAALLTCLP---SVAPHPVYVYVPALEKILB-----L 494
DB 460 RSNPRTDSAAALLTCLP---SVAPHPVYVYVPALEKILB-----L 494

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QY 518 ARDNE---LRENDKEQJRAICTRDPLESLTEOEKDFIMSHRYCVT-IPETLPKLLSVK 573
D 495 GRHSECVHYTEBEOQLREILERRSGSELYEHKDLVWKLREHVEHFPEALRLLVTK 554
QY 574 WNSRDEVAQMYCLVMDWPKIKPEQAMELDCNYPDPMYGFAVRCLEKYLTDKLSOYL 633
D 555 WNKHEBVAQMLYLLCSMPLEPVLSALBLDPSPFCVGSFALKSLRK-LTDELPFYLL 613
QY 634 QLVQVLYKESYLDNLVRFLLKALTNQRIHFFFMHLSKSMHNTVRSORFGLLESYCR 693
D 614 QLVQVLYKESYLDNLVRFLLKALTNQRIHFFFMHLSKSMHNTVRSALRFGILLEYCR 673
QY 694 ACGMYLKLHNRQVDEMEKILNLTDLIKOEKKDETQVQKFLVEQ-MRRDPMDALQGL 752
D 674 GSTHMKVLMKQGBALSKLALNDFVLLSSQ-KTRPKQTKELMHLCKRQVAYLEASHIQ 732
QY 753 SPLNPAHQNLRLRECRIMSSAKRPLMLMNPDMINSSELLFQNNELIFKNGDDLRODML 812
D 733 SPLDSTLLAEVCEQCTFMDSKMKPLMIMYSNEAGSG---GSVGIIFKNGDDLRODML 789
QY 813 TLQIIRIMENIMONOGDLRLPLPGCLSGDVCGLIEVRNHSHTIMQIC-KGGLKGLQ 871
D 790 TLQMIQMDVLMKQGBALNMTPTGCLPTGDRGLIEVLRSDTIANTIQKSNMAATAA 849
QY 872 FNSHTLHQLKDKNKGELIDDAIDLFTRSCAGYCVATFLLIGDRHNSNIMVXDQGLFH 931
D 850 FNDKALNMLKSNKPGELDRALIEEFTLSCAGYCVATYVIGDRHNSNIMIESQGLFH 909
QY 932 IDGHLFDHKKKFGYKREVPFLTODFLIVISKAOECTKRIHFRPOECYKAYLAI 991
D 910 IDGHLFNGKFTFGINREVPFLTYDFVHVIQOG---KTNSKIKFERFRGCEBRAYTIL 967
QY 992 ROHANIIFINFSMWLGSMPLEQSPDIAIRKTLADKTEQELAEFMQNDANHGCM 1051
D 968 RRGGLFLHFLMRAAGLPELSCKDIOYLKOSLALGKTEBEELKHFVKEALRESW 1027
QY 1052 TTYMDWIFHTIKQ 1064
D 1028 KTKVNLMAHVSK 1040

RESULT 10
US-08-977-871A-2
; Sequence 2, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borum
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977, 871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.

```

```

; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TEXT: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1044 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-977-871A-2

Query Match 34.7%; Score 1978.5; DB 2; Length 1044;
Best Local Similarity 39.9%; Pred. No. 3.1e-195;
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MPD-----RILVECLDPLNGMIVTLECLREATLITIKHELFKEARKYPLHQ 60
D 1 MPDGVDCPMEFWTKENQSVVVDFFLPTGYINLFVSRNANLSTIKQLMHRQVLEFLH 60
QY 61 LLODESSYIFVSTQAEERBEFFDETRRLCDRLFPQFLKVBPGVNRREKILNREIGFA 120
D 61 MLSGRAVYFTCINQTAEOQLEDEQRRLCDVQFPLVRLVARBGDRVKKLINSQISLL 120
QY 121 IGMVCEPMMVMDREVDRRNLTANVCXAVDLRLDINSFHRAMYYPVNVSSPE---- 176
D 121 IKGGLHEPFLCDPEVNDPRACKQCFCEBAARQQLGMEALQVSPFQLEPSAQWGP 180
QY 177 ----LPRKATYNKLDKQIIVIVIVISPNNDKQYTLKINHDCVPQVIAEAIRKTRSM 232
D 181 GLRLRPNR-----ALLVNVKFEGBESSTFTQYSTKDVPLALMAALARK- 224
QY 233 LLSSEDLKLCVLEYGQKYLKVCDCDEYFLKYLVSQYVIRSCINLGMNIMLMAKES 292
D 225 ---ATVFRQPLVEQPEDYTLQVNGRHEYLQGNVPLCQFYICSLHSGTLPHLTVHSSS 281
QY 293 LVSQLPMDCTFMPYSRRIRSTATPYMNGSTSTKSLMIVINSALRIKILCATYVNVNRID 352
D 282 ILAMRDEQSNPAPOVKPRAPKEPPIPAKRPSSVSLSLSDPFFILDIQSKVAVDER--M 339
QY 353 KIYVRTGIYHGEPLLDNVNTOVRP-CSNPRNWEMLNVDIYIPDLPRARLCLISGSV-- 409
D 340 KLVVQAKGLHNGEMLCKTVSSSEVSVCSPPWKQRIEFINICDLPKMARLCPALYAVLE 399
QY 410 -----KGRKAKAEHCPLAMGNINLFDYTDLTVSGKMLNLMP-VPHGLIEDLNPIGVT 462
D 400 KAKKARSTKRSKKKADCFIAMNMLFDYKDLKTGERCLTMVPSVPDEKGEILNPTGV 459
QY 463 GSNPNKETP-----CLELFPDMFPSSVYKRPDMSVLEEHANMSVSRAGFSYHAGLSNRL 517
D 460 RSNPNTDSAAALLICLP---EVAHPHVYVPALEKILE-----L 494
QY 518 ARDNE---LRENDKEQJRAICTRDPLESLTEOEKDFIMSHRYCVT-IPETLPKLLSVK 573
D 495 GRHSECVHYTEBEOQLREILERRSGSELYEHKDLVWKLREHVEHFPEALRLLVTK 554
QY 574 WNSRDEVAQMYCLVMDWPKIKPEQAMELDCNYPDPMYGFAVRCLEKYLTDKLSOYL 633
D 555 WNKHEBVAQMLYLLCSMPLEPVLSALBLDPSPFCVGSFALKSLRK-LTDELPFYLL 613
QY 634 QLVQVLYKESYLDNLVRFLLKALTNQRIHFFFMHLSKSMHNTVRSORFGLLESYCR 693
D 614 QLVQVLYKESYLDNLVRFLLKALTNQRIHFFFMHLSKSMHNTVRSALRFGILLEYCR 673
QY 694 ACGMYLKLHNRQVDEMEKILNLTDLIKOEKKDETQVQKFLVEQ-MRRDPMDALQGL 752
D 674 GSTHMKVLMKQGBALSKLALNDFVLLSSQ-KTRPKQTKELMHLCKRQVAYLEASHIQ 732
QY 753 SPLNPAHQNLRLRECRIMSSAKRPLMLMNPDMINSSELLFQNNELIFKNGDDLRODML 812
D 733 SPLDSTLLAEVCEQCTFMDSKMKPLMIMYSNEAGSG---GSVGIIFKNGDDLRODML 789

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QY 813 TLQIIRIMENIWONOGDLRLMLPYGCLSIGDCVGLIEVVRNSHTIMOQC-KGGLKALQ 871
 DB 790 TLQMIQMDVLMKQEBGLDRLMTYGLCPGDRGLIEVLRSDTIANIQLNKSNAATAA 849
 QY 872 FNSHTLHOMLKDKXKEIYDAIDLFTSCAGYCVATFIIIGDRHNSNTMVKDDQLFH 931
 DB 850 FNDKALNLMKSKNPGBALDRAIEEFTLSCAGYCVATYVIGIDRHSNDIMIRESQLFH 909
 QY 932 IDFGHLDHKKKKFKYKREVPVLTODFLIVISKGAQECTKTREPERQEMCYKAYLAI 991
 DB 910 IDFGHFLGNFKTKFGINREVPFLITYDFVHVIOQG--KTNNSEKFERFRGYCERAYTIL 967
 QY 992 ROHANI.FIN.FSMWLGSGMPELOSFDDIAYIRKTLALDKTEOALBYFMKQMDAHNGW 1051
 DB 968 RRHGLFLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEBALKHFRVKNFNEALRESW 1027
 QY 1052 TTKMDWITHTIKQ 1064
 DB 1028 KTKVNLAMHNSK 1040

RESULT 11
 US-09-225-951-2
 ; Sequence 2, Application US/09225951
 ; Patent No. 5985589
 ; GENERAL INFORMATION:
 ; APPLICANT: Chanley, David
 ; APPLICANT: Hoeckstra, Merl F.
 ; APPLICANT: Holtzman, Douglas A
 ; TITLE OF INVENTION: No. 5985589e1 Lipid Kinase
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
 ; STREET: 6300 Sears Tower/233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30
 ; APPLICATION NUMBER: US/09/225,951
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5985589and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/33441
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1044 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-225-951-2

Query Match 34.7%; Score 1978.5; DB 2; Length 1044;
 Best Local Similarity 39.9%; Pred. No. 3.1e-195;
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;
 QY 16 MPP-----RLIVECLLPNGMIVLLECLREATTITIGHELPEKRYKPLHQ 60
 DB 1 MPPGVDCPMEFWTKENOSVVDVFLPTGVYLNFPVSRNNLSTIQQLMHRAQYEPFLH 60
 QY 61 LQDESSYIFVSTQEAEREPEFDETRRLCDRLFLQFPLKVLEPVGNREBKILNREIGFA 120

DB 61 MLSGEBAVYFTCTINQTAQOELEDEQRRLCDVQPLFLVLRVABRGRVKKILNQISLDL 120
 QY 121 TQMPYCFEDMVKDPEVDFRRNINLVCKEAVLDRLNSHSAAMYVPENVSSEPE---- 176
 DB 121 TKGHLIEFDLSLCPDEVNDFRAKQCFCEBAARROQLGMEAWLYQSFPLQLEPSAQTCGP 180
 QY 177 ---LPRKILYNLDDKQIIVVIMVIVSPNNDOKTLKINHCPVEOVAEAIKRTKRSM 232
 DB 181 GTLRLEPNR-----ALLVNVKFGSESEFTFOYSTQDVPLALMAQLRK----- 224
 QY 233 LLSSEQLKLCVLEYQSKYLKVGCDPEYLEKYPISQYKIRSCIMLGMPULMAKS 292
 DB 225 ---ATVFRQPLVQEPDYLQVNGRHELYGVNPLCOFYICSLHSGLTLPHLTWHSSS 281
 QY 293 LYSQLEMDCTFMPYSRRISTATPYMNGSTSKSLMNVINSALRIKILCTVYVNVIRID 352
 DB 282 ILMRDEQSNPAFQVQKPRAPKPPPIPAKPRSSVSLSLQOPRIELIQSKVNADE--M 339
 QY 353 KIYVRTGIYHGGEPFLCDNNTQRPV--CSNPRNEMVNYDIYIPDLPRARLCLTICSV-- 409
 DB 340 KLVVQAGLFPFGNMLCKTVSSSEVSVCEBPWKQRLPEINDICDLPRMARLCPALAVIE 399
 QY 410 -----KGRKAKEBHCPLAMGNINLPDYDTLVSGMALNMP-VPHGLEDLINPIGYT 462
 DB 400 KAKKASTKTKSKKADCPIMANMLPDKYDQDKTGRCILYVMPSPVDEKGBLNPFTGV 459
 QY 463 GSNPNKETP-----CLELEFDWFSVYKPPDMKVIIEHANMSVSRDAGPSYAGLSNRL 517
 DB 460 RSNPNTDSAAALILCP---EVAPHPYYPALKEIE-----L 494
 QY 518 ARDNE---LRNKEQOLRAICTDPSLETRQKDFMASHRYCVT-IPILPKLLSVK 573
 DB 495 GRHSECVHVEEQLOQREILERRGSELYEHKEDLVKLRHVOEHFPAALRLLLVTK 554
 QY 574 WNSRDEVAQWYCLVQDPPPIKPEQAMELDCNYPDPVWRCFAVRCLEKYLTDDKLSOYL 633
 DB 555 WNKHEDYQWLYLCSWPELPVLSALELDFSPFDCHVGSFAIKSLRK-LTDDLELFGYLL 613
 QY 634 QLVQVLKYEQYLDNLVFLIKKALTNQRIQHFFPMLKSEMNKTYSQRFGLLESYCR 693
 DB 614 QLVQVLKYESYLDDELTKFLDRALNARKIGHFLRSEMHVPVALRFFGLLEAYCR 673
 QY 694 ACGMYLKLNRQVAMKTLNLTDLKQKKDEQYQYKMFVLRQ-WRRDPMDALQGL 752
 DB 674 GSTHMKVLMKQGBALSKLALNDFVLSGO-KTRKQTKELMHLCKRQEAYLEALSHQ 732
 QY 753 SPLPAHQGLNLRLEGRIMSSAKRPLMLNWNEDIMSSELLFONNEIIFKXGDDLRODML 812
 DB 733 SPLDPSTILAEVCEQCTFMDSKKPLMIMVSNEDAGS--GSVGIIIFKXGDDLRODML 789
 QY 813 TLQIIRIMENIWONOGDLRLMLPYGCLSIGDCVGLIEVVRNSHTIMOQC-KGGLKALQ 871
 DB 790 TLQMIQMDVLMKQEBGLDRLMTYGLCPGDRGLIEVLRSDTIANIQLNKSNAATAA 849
 QY 872 FNSHTLHOMLKDKXKEIYDAIDLFTSCAGYCVATFIIIGDRHNSNTMVKDDQLFH 931
 DB 850 FNDKALNLMKSKNPGBALDRAIEEFTLSCAGYCVATYVIGIDRHSNDIMIRESQLFH 909
 QY 932 IDFGHLDHKKKKFKYKREVPVLTODFLIVISKGAQECTKTREPERQEMCYKAYLAI 991
 DB 910 IDFGHFLGNFKTKFGINREVPFLITYDFVHVIOQG--KTNNSEKFERFRGYCERAYTIL 967
 QY 992 ROHANI.FIN.FSMWLGSGMPELOSFDDIAYIRKTLALDKTEOALBYFMKQMDAHNGW 1051
 DB 968 RRHGLFLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEBALKHFRVKNFNEALRESW 1027
 QY 1052 TTKMDWITHTIKQ 1064
 DB 1028 KTKVNLAMHNSK 1040

RESULT 12


```

Db 225 ---ATVFRQPIVBPQDYTLQVNGRHEYLKGSYPLQCYICSLHSGLTPLHVMHSSS 281
Qy 293 LVSQLEPMDCTFMSYSRRISTATPYNNGETSTKSLWVINSALIKLCAVYVNVIRID 352
Db 282 ILAMDEQSNAPQOVQFPAKPPPIPAKSSSVLSLEQPFRIELQSKVADER--M 339
Qy 353 KIYVRGIYHGBEPICDNVATQVP--CSNPRMNMVNDIYIPDLPRAAALCLSTGCV-- 409
Db 340 KLVVQAGLEFGNMLCTVSSSEVSVSEVWVQORLEFDINICDLPRMALCPALAVIE 399
Qy 410 -----KGRKAEHECPILAMGNINLPDYDTLVSGMALNMP-VPHGEDLNPICVT 462
Db 400 KAKKASTKKSKKADCPRIAMNLMFDYKQKTKGERCLYMPSPVDEKGEILNPGTV 459
Qy 463 GSNPNKETP-----CLELEFDMSSSVKFPDMSTIEEHAMWSVREAGFSYHAGLSNRL 517
Db 460 RSNPNTDSAAALLICLP---EVAHPVYYPALKEILB-----L 494
Qy 518 ARONE--LAENDKEQJRAICTRDPLEBITEOEKDFLMSHHYCVT-1PEILPCLLSVK 573
Db 495 GRHSECVATVEEBOJQREILERRSGSBLTBEKOLVWKLHVEQHPPELALALLVTX 554
Qy 574 WNSRDEVAQWYCYKDMPPIKPEQAMELLDCNVPDPVVRGFAVCLERYLTDDKLSYLI 633
Db 555 WNKHEDVQOMLYLCSWPELRYLSALBELDPSFPDCHVGFALIKSLRK-LTDDLEFOYLL 613
Qy 634 QLVOLKYEBOYLDNLVRFELKALVNRIGHFHFFHKLKSMHKKYTSQREGLLESQR 693
Db 614 QLVOLKYESYDELTFELDLRALANKIGHFLFWHLRSEMHVSVALARFGLLEACR 673
Qy 694 ACGMYLKLHNOVAMEKILNLTILKQEKDETOKVOMKFLVRO-MRRPDMALQOGL 752
Db 674 GRTHMKVLMKQEGELSKALNDFVLSQ-KTPKPTKELMLCHQGEAVLELSHQ 732
Qy 753 SPLPAHQJLNLREECRIMSASAKPLMINNPNIMSELLFONNEIIFKNGDDLRQML 812
Db 733 SPLDSTILAEVCEQCTFMSXKPLIMWISNEAGSG---GSVGIIFKNGDDLROML 789
Qy 813 TLQIIRIMENIQNGGLDIRMLPYGCLSIGCVGLIEVVRNSHTIMOQC-KGGLKGLQ 871
Db 790 TLQWQLMDVLMKQEGDLRLMTPYGLTGTGRTGLEIVLRSDTLANIQLNSNAAATPA 849
Qy 872 FNSHTLQMLDKNGGEIYDAIDLFTSACAGYATFLIGDSHNSINIMYDGOGLFH 931
Db 850 FNKDALNLWLSKINGEALDRAIEFTLSCAGYCAITVLAGIDRHSNIMIRESGQLFH 909
Qy 932 IDFGHFLDHKKKPKGVKREVPFVLTOPFLVYSKGAOECTKTRFEFERQEMCYAYLAI 991
Db 910 IDFGHFLGFKTKRFGINRERVPILTYDFVHVIQGS-KTNSEKFERRGYCERAYTIL 967
Qy 992 ROHANLFINLFSMILSGMPELOSFDIAYIRKTLALDTQEALLEYFKQKNDADHGM 1051
Db 966 RHGGLFLHFLPALMRAAGLPELSCSKDIQYLDXSLALGTEEBALHGFVKEALRESW 1027
Qy 1052 TTKMDMIFHTIKQ 1064
Db 1028 KTKVMNLAHVSK 1040

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RESULT 14
US-08-916-917-14
Sequence 14, Application US/08916917
Patent No. 5856132
GENERAL INFORMATION:
APPLICANT: Stephens, Ien
APPLICANT: Haskins, Phillip Thomas
APPLICANT: Braedelmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP

```

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fastseq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5856132e
US-08-916-917-14
Query Match 25.7%; Score 1467; DB 2; Length 1101;
Best Local Similarity 35.3%; Pred. No. 3,7e-142;
Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;
Qy 107 NREKILNREIGFALGMPVCEFDVVKPPEVODPPRRNLNCKEAVDRLDLSPHRAMYV 166
Db 143 SEESQAFQRLTALIGVDVDSNVHDELEFTRGLVTPRMAVASRD-----PKLYA 196
Qy 167 YRPVRESPELPHKHNKLDKGOIIVYIWIIVSPNNDKQYTKLINHDCVPEQVIAAIR 226
Db 197 MHPWTSRP-LPEYLMKXIANNCIFVI-----HRTSGTIVASPDPTGALLOGFFT 249
Qy 227 K-KTRSMILSSSEQLKLVLEYQGYLIKVCDEYLEKYPVLSQYKITSCLMKRKN 284
Db 250 KMAKKKSLMDIPES-----QSEQDFVLRCGRDEYLVGETPIKRFQVWRHCLNNGEIRH 303
Qy 285 LML-----MAKESLYSQLPM--DCTWPSYSRRISTATPYMNGE---TSTKSLMVINS 332
Db 304 VVLDTPPPALDEVAKKEEMPLVDDCTGVTGVHEQUL-----IHGDHESVFTVLSMDCR 358
Qy 333 ALRILKILATYVNVNIRID-----KIYVRTG:YHGBEPICDNVATQVPSCNPR 382
Db 359 KFRVK-----IRGIDIPVLPBRNTDLVVEANIOHQOQVLCQRTSPKPTBEVL 408
Qy 383 WNEMLNNDIYIPDLPRAPRLCLSTGCVK-----GKRGAEHECPILAMGNINLPDYDTLV- 437
Db 409 WNVWLEFSIKIDLPKGLNLNQIYGKAPALSSVASSPSSBSKGRVRLIYYVNLILI 468
Qy 438 -----SGKALNLMVPHGLIED--LNPICVT-GSNPNKE-TPCLELEFDMSSSVK 486
Db 469 DHRFLRLRGEVYLHMQISGKEGDSFADLTSLATPDKSNSSISITLNDYCHPLAL 528
Qy 487 PMSVSTIEEHAMWSVREAGFSYHAGLSNRLARNDLEARENDKEQJRAICTRDPLESTIEO 546
Db 529 PKHQPTPDPEGDRV-----RAEMPNQLR---KQLEALITATPPLNPLTAE 569
Qy 547 EXDPLMSHHYCVTPEILPCLLSVKNMSRDEVQWYCL-----VKDMPPIKPEQAMEL 601
Db 570 DKELMHRFYESLKHKPAIKPLFSSVYKMGQCEIVAKTYQLARREVWDQSALDVGITMQL 629

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Wed Nov 12 14:55:48 2003

us-09-325-095-37.rail

Page 14

[illegible]

Search completed: November 6, 2003, 14:45:26
Job time : 26 secs

FT Peptide /note="Peptide L"
 FT 1031..1040
 FT /note="Peptide M"
 FT 1055..1063
 FT /note="Peptide N"
 PN W09403609-A1.
 PD 17-FEB-1994.
 PD 05-AUG-1993; 93WO-GB01651.
 PF 05-AUG-1992; 92GB-0016654.
 PR (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA Goode NT, Nurse PM, Parker PJJ, Waterfield MD;
 PI WPI, 1994-065697/08.
 PS N-PSDB, AA057012.
 XX Bkaryotic cells transformed with mammalian phospholipid or
 PT protein kinase DNA - useful in assays for compounds involved in
 PT cell growth regulation and for treating cancers
 XX Disclosure; Fig 1; 71pp; English.
 XX This sequence represents the 110 kD catalytic subunit of the
 CC phosphatidyl inositol (PtdIns) 3-kinase. The cDNA encoding this
 CC sequence was transformed into Schistosaccharomyces pombe cells under
 CC the regulatory control of the nmt promoter in an embodiment of the
 CC invention. In the presence of thiamine the promoter is inactive and
 CC the cells carrying the Ptdins catalytic subunit plasmid grow as the
 CC parental strain. In the absence of thiamine the nmt promoter functions
 CC and the Ptdins 3-kinase catalytic subunit is induced. Ptdins activity
 CC is substantially increased under these conditions. Cells containing
 CC constructs such as this, are useful in assays for detecting compounds
 CC involved in cell growth regulation. It is also used as the basis for
 CC detecting compounds for treating cancers and the formation of blood
 CC vessel plaques.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 1068 AA;
 Query Match 99.8%; Score 5696; DB 15; Length 1068;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 361 YHGSEPLCDNVNTQVRVPCSNPRNEMWLNVDIYIPDLPRARLCLISCSYKGRGAKEEHC 420
 QY PLAMGINLFDYDTLVSGKMLNLMPVHGLEDLNP:GVGSSNNKSTPCLEFPDW 480
 QY PLAMGINLFDYDTLVSGKMLNLMPVHGLEDLNP:GVGSSNNKSTPCLEFPDW 480
 QY 481 SSVVKFPMDSVIEEHNAMSVSREAGFSYSHAGLSNRNLADNELRENDKQLRAICTRDP 540
 DB 481 SSVVKFPMDSVIEEHNAMSVSREAGFSYSHAGLSNRNLADNELRENDKQLRAICTRDP 540
 QY 541 SEITTEQKDFLWSHRHYCVTIPETLPLLLSVKMSRDEVAQMYCLVKWMPPIKPEQAME 600
 DB 541 SEITTEQKDFLWSHRHYCVTIPETLPLLLSVKMSRDEVAQMYCLVKWMPPIKPEQAME 600
 QY 601 LDDCNYPDMVNGFAFRCLEKYLTDKLSOYLQVLQVLYKRYQYLDNLVRLFKKALTN 660
 DB 601 LDDCNYPDMVNGFAFRCLEKYLTDKLSOYLQVLQVLYKRYQYLDNLVRLFKKALTN 660
 QY 661 ORIGHFFFWHLKSEMANKTVSOFGLLESYCRACGMYLKHNROYEAMEKILNTDILK 720
 DB 661 ORIGHFFFWHLKSEMANKTVSOFGLLESYCRACGMYLKHNROYEAMEKILNTDILK 720
 QY 721 QEKDETOQVQMKFLVEQMRPDMDALOGFLSPINPAHQNLRLSECRIMSSAKRPLM 780
 DB 721 QEKDETOQVQMKFLVEQMRPDMDALOGFLSPINPAHQNLRLSECRIMSSAKRPLM 780
 QY 781 LWMENDINSEILFQNNELIFPKGGDLRQDMITLQIRIMENINQNGJDLRLPVGCS 840
 DB 781 LWMENDINSEILFQNNELIFPKGGDLRQDMITLQIRIMENINQNGJDLRLPVGCS 840
 QY 841 IDBCVGLIEVNRNSTHIMOIOCKGKALQFNSHTLHOMLQKNGEITYDAIDPFTS 900
 DB 841 IDBCVGLIEVNRNSTHIMOIOCKGKALQFNSHTLHOMLQKNGEITYDAIDPFTS 900
 QY 901 CAGYCVATFILDIGRHNNSNIWYKDGQLEHIDFGHLDHKKKKGXKREVPVLTQDF 960
 DB 901 CAGYCVATFILDIGRHNNSNIWYKDGQLEHIDFGHLDHKKKKGXKREVPVLTQDF 960
 QY 961 LIVISKGAQECTKTRFEFERFQMCYKAYLAIQHANLFINLSMMLGSGMPLOSFDDIA 1020
 DB 961 LIVISKGAQECTKTRFEFERFQMCYKAYLAIQHANLFINLSMMLGSGMPLOSFDDIA 1020
 QY 1021 YIRKTLALDKTEQEALEVFMRQNDAHHGWTTKMDWIFHTIKOHALN 1068
 DB 1021 YIRKTLALDKTEQEALEVFMRQNDAHHGWTTKMDWIFHTIKOHALN 1068

RESULT 3
 AAR43342
 ID AAR43342 standard; Protein; 1068 AA.
 AC AAR43342;
 AC
 DT 15-MAR-2003 (updated)
 DT 12-APR-1994 (first entry)
 DE Human p110.
 DE
 XX Phosphoinositide kinase; PI, p85 subunit; screening; agonist;
 KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;
 KW platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
 OS Homo sapiens.
 OS
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT Domain 19..100
 FT /note="binds with p85 subunit"
 PN W09321328-A1.
 XX
 XX
 PD 28-OCT-1993.
 XX

PF 13-APR-1993; 93W0-GB00761.
 XX 13-APR-1992; 92GB-0008135.
 PR (LUDM-) LUDMIG INST CANCER RES.
 PA Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
 PI Panyotou G, Volinia S, Gout I;
 XX WPI; 1993-351738/44.
 DR N-PSDB; AA051156.
 XX
 PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
 activity, useful for controlling cell proliferation
 XX
 PS Claim 24; Fig 16; 146pp; English.
 CC Southern blot analysis was performed using a bovine cDNA probe contg.
 CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated
 CC from a cDNA library constructed from mRNA isolated from the human
 CC cell line K562. Positive clones were sequenced to give the human
 CC p13 kinase p10 sequence. This sequence has 95 percent homology
 CC with the bovine sequence. The domain contg. residues 19-100 of human
 CC p10 is sufficient to associate with the p85 kinase subunit. The
 CC protein with p13 kinase activity is useful for screening for
 CC (ant)agonists or inhibition of cell proliferation and hence
 CC stimulation or inhibition of cell proliferation activity or blood
 CC prophylaxis or therapy. Platelet or neutrophil activity or blood
 CC glucose levels can be controlled using the kinase.
 CC See also AAR3341 and AAR46552-3.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 CC
 SQ Sequence 1068 AA:
 Query Match 99.1%; Score 5657; DB 14; Length 1068;
 Best local similarity 98.9%; Pred. No. 0;
 Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

DB 481 SSVKFPDMSVIEEHANWSVSRGAGFSYSHAGLSNRLARDNLENDKXQLAISTRDPL 540
 QY 541 SEITOEKDFLNSAHNYCTTIPETPKLLSVKNMSRDEVAOMYGLVDMPPKPEQAME 600
 DB 541 SEITOEKDFLNSAHNYCTTIPETPKLLSVKNMSRDEVAOMYGLVDMPPKPEQAME 600
 QY 601 LLDGNYPDPMVAGFAVRCLEKYLTDKLSOYLIDQVQVLYKTEQYLDNLVFLKKAALTN 660
 DB 601 LLDGNYPDPMVAGFAVRCLEKYLTDKLSOYLIDQVQVLYKTEQYLDNLVFLKKAALTN 660
 QY 661 QRIHFFFWHLKSEMNKTVSQRFGLLLESYCRACGNTLKLNRQVEAMEKILNTDILK 720
 DB 661 QRIHFFFWHLKSEMNKTVSQRFGLLLESYCRACGNTLKLNRQVEAMEKILNTDILK 720
 QY 721 QEKDQTVQNMKFLVEQNRPRDPMALOGFLSPNPAHQGNLRLEBCRIMSASAKRPLM 780
 DB 721 QEKDQTVQNMKFLVEQNRPRDPMALOGFLSPNPAHQGNLRLEBCRIMSASAKRPLM 780
 QY 781 LMMENPDIMSELFONNELIFKNGDILRODMTLQIIRIMENIMONOGIDLRLMPYGLCS 840
 DB 781 LMMENPDIMSELFONNELIFKNGDILRODMTLQIIRIMENIMONOGIDLRLMPYGLCS 840
 QY 841 IGDVGLIEVANSHTIWIQCKGKLGALQFNSTHQLKDKNGEITYDAIDLFTS 900
 DB 841 IGDVGLIEVANSHTIWIQCKGKLGALQFNSTHQLKDKNGEITYDAIDLFTS 900
 QY 901 CAGYCATPILGIGDHNNSINWKDGOPLHIDEGHLDHKKKFKGKXERVPVLTDF 960
 DB 901 CAGYCATPILGIGDHNNSINWKDGOPLHIDEGHLDHKKKFKGKXERVPVLTDF 960
 QY 961 LIYISGAOECTRTREPERFOECYKAYLAIRQANLFTNPSMVLGSGMPELOSFDIA 1020
 DB 961 LIYISGAOECTRTREPERFOECYKAYLAIRQANLFTNPSMVLGSGMPELOSFDIA 1020
 QY 1021 YIRKTLADTQBOALEYFMKQNDAHGSGTTKQMTHTTIQAHALN 1068
 DB 1021 YIRKTLADTQBOALEYFMKQNDAHGSGTTKQMTHTTIQAHALN 1068

RESULT 4

AAU09687 standard; Protein; 1068 AA.

AAU09687;

12-MAR-2002 (first entry)

Human p110alpha isoform of p13-kinase.

Human; phosphatidylinositol 3-kinase; p13K; p110alpha isoform;
 LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
 autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
 Type I diabetes mellitus; cytostatic; immunosuppressive.

Homo sapiens.

W0200185986-A2.

15-NOV-2001.

10-MAY-2001; 2001WO-US15065.

10-MAY-2000; 2000US-203346P.

(ICOS-) ICOS CORP.

Sadhu C;

WPI; 2002-075252/10.

N-PSDB; AAS14365.

Identifying a modulator of p110delta polypeptide binding to SH3
 domain-containing polypeptides e.g. LASP-1, comprising allowing the

PT binding partners to interact in the presence and absence of a test compound

Example 1; Page 60-63; 85pp; English.

CC The present invention relates to identifying a modulator of the
CC phosphatidylinositol 3-kinase (PI3K; p10delta) enzyme that binds to
CC the catalytic subunit via a SH3 domain-containing polypeptide such as
CC IASP-1. Also described are methods of assaying the specific binding
CC affinity of the PI3-kinase binding partner. Such modulators are useful
CC for the treatment of diseases characterised by the undesirable or
CC excessive activity of PI3delta. For example the modulators can be used
CC for inhibiting the growth or proliferation of cancer cells
CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC dermatoses (e.g. contact dermatitis; central or peripheral neuritis),
CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC and type I diabetes mellitus. The present sequence represents human
CC p10alpha isoform of PI3K.

XX Sequence 1068 AA;

Query Match 99.1%; Score 5657; DB 23; Length 1068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPRPSSGELMGHLMPPRLIVLECLPNGMTVTIECLRENTLTITKHELFKEARKYPLHQ 60
DB 1 MPRPSSGELMGHLMPPRLIVLECLPNGMTVTIECLRENTLTITKHELFKEARKYPLHQ 60
QY 61 LLODESSYIVSYTQEAREREPFETRRLCDLRFQFLVITEBVGREKTIINREIGFA 120
DB 61 LLODESSYIVSYTQEAREREPFETRRLCDLRFQFLVITEBVGREKTIINREIGFA 120
QY 121 IGMVCEFDWVKDEVDFFRRNITLVCKEAVDLRLDLSPPSRAMYVPPVNESSPELPKH 180
DB 121 IGMVCEFDWVKDEVDFFRRNITLVCKEAVDLRLDLSPPSRAMYVPPVNESSPELPKH 180
QY 121 IGMVCEFDWVKDEVDFFRRNITLVCKEAVDLRLDLSPPSRAMYVPPVNESSPELPKH 180
DB 121 IGMVCEFDWVKDEVDFFRRNITLVCKEAVDLRLDLSPPSRAMYVPPVNESSPELPKH 180
QY 181 IYKLLDKGQIIIVYIVWVSPNDKQKTYLKHNDCEVQVIAEIRKRTSMILSSBQLK 240
DB 181 IYKLLDKGQIIIVYIVWVSPNDKQKTYLKHNDCEVQVIAEIRKRTSMILSSBQLK 240
QY 181 IYKLLDKGQIIIVYIVWVSPNDKQKTYLKHNDCEVQVIAEIRKRTSMILSSBQLK 240
DB 181 IYKLLDKGQIIIVYIVWVSPNDKQKTYLKHNDCEVQVIAEIRKRTSMILSSBQLK 240
QY 241 LCVLEVOGKYLKVCQCGDEYFLEKYPISOYKTRSCITLGRMPMLKMAKESLYSQPLMD 300
DB 241 LCVLEVOGKYLKVCQCGDEYFLEKYPISOYKTRSCITLGRMPMLKMAKESLYSQPLMD 300
QY 241 LCVLEVOGKYLKVCQCGDEYFLEKYPISOYKTRSCITLGRMPMLKMAKESLYSQPLMD 300
DB 241 LCVLEVOGKYLKVCQCGDEYFLEKYPISOYKTRSCITLGRMPMLKMAKESLYSQPLMD 300
QY 301 CFTMPYSRRISTATPYMNGESTSKSLMVINSALRIKILCATYVNVNIRIDIKIYVETGI 360
DB 301 CFTMPYSRRISTATPYMNGESTSKSLMVINSALRIKILCATYVNVNIRIDIKIYVETGI 360
QY 301 CFTMPYSRRISTATPYMNGESTSKSLMVINSALRIKILCATYVNVNIRIDIKIYVETGI 360
DB 301 CFTMPYSRRISTATPYMNGESTSKSLMVINSALRIKILCATYVNVNIRIDIKIYVETGI 360
QY 361 YHGGEPICDQVNTQRYVPCSNPRNEMLYNDIYIPDLPRARLCLISGVKRGKAKEHC 420
DB 361 YHGGEPICDQVNTQRYVPCSNPRNEMLYNDIYIPDLPRARLCLISGVKRGKAKEHC 420
QY 361 YHGGEPICDQVNTQRYVPCSNPRNEMLYNDIYIPDLPRARLCLISGVKRGKAKEHC 420
DB 361 YHGGEPICDQVNTQRYVPCSNPRNEMLYNDIYIPDLPRARLCLISGVKRGKAKEHC 420
QY 421 PLAMGNINLEFDYDTLVSGKALNLMVPBGLDNLNPIGVTSNPKKFTPCLEBEDWF 480
DB 421 PLAMGNINLEFDYDTLVSGKALNLMVPBGLDNLNPIGVTSNPKKFTPCLEBEDWF 480
QY 421 PLAMGNINLEFDYDTLVSGKALNLMVPBGLDNLNPIGVTSNPKKFTPCLEBEDWF 480
DB 421 PLAMGNINLEFDYDTLVSGKALNLMVPBGLDNLNPIGVTSNPKKFTPCLEBEDWF 480
QY 481 SSVYKPEPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDELRENDKEOLKALSTRDPL 540
DB 481 SSVYKPEPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDELRENDKEOLKALSTRDPL 540
QY 541 SEITEDEKDFLMGSHRHCVTTIPETLPULLISVKNMSDEVAQWYCLVKDWPPIKPEQAMZ 600
DB 541 SEITEDEKDFLMGSHRHCVTTIPETLPULLISVKNMSDEVAQWYCLVKDWPPIKPEQAMZ 600
QY 601 LLECNYPDPMPVARGAVACLEKYLTDKLSOYLQOLVQVLYEYOYLDNLVRFLLKALTN 660
DB 601 LLECNYPDPMPVARGAVACLEKYLTDKLSOYLQOLVQVLYEYOYLDNLVRFLLKALTN 660

QY 661 QRIQHFFFWHLKSEMHNTVYSQRFGLLESYCRACGWYLGHLNRQVEMAKLINTLIDLK 720
DB 661 QRIQHFFFWHLKSEMHNTVYSQRFGLLESYCRACGWYLGHLNRQVEMAKLINTLIDLK 720
QY 721 QEKKDEYQKQMFVLEQMRPDMALQGLFSLPAPADLGULRLEECINSSAKPLW 780
DB 721 QEKKDEYQKQMFVLEQMRPDMALQGLFSLPAPADLGULRLEECINSSAKPLW 780
QY 781 LMNENPIMSELLFONNEIIFKNGDDLROMPLTQIIRIMENTWONGELRLMPLYGLS 840
DB 781 LMNENPIMSELLFONNEIIFKNGDDLROMPLTQIIRIMENTWONGELRLMPLYGLS 840
QY 841 IGDGVLIEVVRNSHTIMQIQCKGKLGALQFNSHTLHQWLKDNKGEIYDAAIDLEPTRS 900
DB 841 IGDGVLIEVVRNSHTIMQIQCKGKLGALQFNSHTLHQWLKDNKGEIYDAAIDLEPTRS 900
QY 901 CAGYCAVATPLIGIDRHSNIMWKDQQLPHIDFGHFLDHKKKFGYKRRVFPVLTODF 960
DB 901 CAGYCAVATPLIGIDRHSNIMWKDQQLPHIDFGHFLDHKKKFGYKRRVFPVLTODF 960
QY 961 LIVISGAOECTRTREPERFQEMCYAYALIRQHANLFINLFSMMLGSGMPELOSPDIA 1020
DB 961 LIVISGAOECTRTREPERFQEMCYAYALIRQHANLFINLFSMMLGSGMPELOSPDIA 1020
QY 1021 YIRKTLALDKTEQALEYFMKQNDANHGSGWTTKMDMIFPTIKOHALN 1068
DB 1021 YIRKTLALDKTEQALEYFMKQNDANHGSGWTTKMDMIFPTIKOHALN 1068

RESULT 5
AAM58570
ID AAM58570 standard; Protein; 1044 AA.

AC AAM58570;

DT 12-OCT-1998 (first entry)

XX Human phosphatidylinositol 3-kinase p110 catalytic delta subunit.

DE Phosphatidylinositol 3-kinase; p110 delta; human; immune system;

KW carcinogenesis; diagnosis.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Domain 723..1044 /note="catalytic domain"

FT Binding-site 141..310 /note="proposed Ras binding site"

PN W09823760-A1.

PD 04-JUN-1998.

PF 25-NOV-1997; 97MO-US21655.

PR 25-NOV-1996; 96US-0777405.

PA (ICOS-) ICOS CORP.

PI Chantry DH, Hoekstra MF, Holtzman DA;

XX WPI: 1998-322736/28.

DR N-PDB; AAV31340.

XX *New phosphatidylinositol 3-kinase catalytic subunit - used to

PT develop products for modulating kinase activity in immune system

CC signaling and in carcinogenesis

PS Claim 11; Page 33-37; 53pp; English.

XX This is the deduced amino acid sequence of the catalytic p110

CC delta subunit of human phosphatidylinositol 3-kinase (PI 3-kinase).

CC The sequence was deduced from a composite cDNA clone (see AAV58570)
 CC derived from peripheral blood mononuclear cell and macrophage
 CC cDNA. The following are claimed: (1) a purified and isolated
 CC polynucleotide (PN) encoding p110 delta; (2) a vector comprising a
 CC DNA as in (1); (3) a host cell stably transformed or transfected
 CC with a DNA as in (1); (4) PN encoding a lipid kinase, and
 CC hybridising to PN having the 5220 bp sequence; (5) a purified and
 CC isolated p110 delta polypeptide as in (4); (6) an antibody
 CC specifically immunoreactive with p110 delta; (7) a hybridoma cell
 CC line (especially 208F (HB 12200) producing a monoclonal antibody as
 CC in (6); and (8) a humanised antibody as in (6). p110 delta has
 CC kinase activity and may play a role in p13-kinase mediated
 CC signalling in the immune system and in carcinogenesis. The
 CC products can be used to develop agents that modulating p110 delta
 CC kinase activity and to develop diagnostic reagents (claimed). They
 CC may also be used for detection and diagnosis of p110 delta in a
 CC biological sample.

SO Sequence 1044 AA;

Query Match 34.7%; Score 1978.5; DB 19; Length 1044;

Best Local Similarity 39.9%; Pred. No. 3e-179;

Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MPP-----RIIVECLPVGMIVTLECLREATLTIKHELFKARKYPLHQ 60
 DB 1 MPGVDCMEFWTKENQSVVVDLPLTGVYLNFPVSNANLSTIKQLMRAQIEPLFH 60
 QY 61 LLODESSYIFVSTQGEAREEFDETRRLCDLRLFOPLKYIEPVNGREKILNREIGFA 120
 DB 61 MLSCGEAVFTICINQTAQGLEDEQRRLCDVQPLPLRLVARGDVKKLINSQIL 120
 QY 121 IGMVCEFDVWKDEPVDFRRNINLVCKEAVDLRLDLSPHSRAMVYVPPVNESPE---- 176
 DB 121 ICKGLHEFDLCEPVDNDFRAKMCQFCBEAARQQLGMEAMLOYSFPLQLEPSKOTWGP 180
 QY 177 ----LPRKIYKLDKGOIIVIVIVVSPNNDKOKTKLINDCVEQYIAEIRKTRSM 232
 DB 181 GTLRIPNR-----ALVNVKREGSEBESTFVSTKDVPLAMACLRLKK---- 224
 QY 233 LLSSEQLCLVLEYGKYLKVCDEYFLEKYRPSQYKYSRCSIMLRMNLIMAKES 292
 DB 225 ---ATVPQPLVEQPEDTTLQVNGRHELYGNYPLCOFOYICSCLSHSLTHLIMVHSS 281
 QY 293 LYSQLPMDCTWPSYSRRISTATPYMNGESTKSLWINSALRIILCATYVNVNIRID 352
 DB 282 ILAMDDEQSNPAPQVQKPRAKPPPIPAKKPSVSLMSLEQPRIELIOGSKVADER--M 339
 QY 353 KIIVATGIYHGEPRICDNVNTQRP--GSPNRNEMLANDIYIPDLPRARCLSTICSV-- 409
 DB 340 KLVVQAGLPHGEMLCKTVSSSEVSCBPVKQRLPEPDINICDLPKMARLCLFALAYATE 399
 QY 410 -----KSRGAKSEHCPLAMGNINLFDYDTLVGSKALNIMP--VPRGLDGLNPISVT 462
 DB 400 KAKKARSTKKSQKADCPAMANLMLFDYKOLKTGERCLYMPVPPEKGLNPTGV 459
 QY 463 GSNPKETP-----CLELEFDWFSVVVFPDMSVIEEHANMSVSRDAGESYSHAGLSNRL 517
 DB 460 RSNPTDSAAALLICLP---EVAHPHYVYPALKEILE-----L 494
 QY 518 ARDNE---LRNDKQOLAICTRDPLSETTEQEKPLMHRHYCVT--IPELPKLLLSYK 573
 DB 495 GHSHSECVAHTEBEOQLREILERRSGGELYEHKDLWMLRHEVQEHPEALARLLLVTK 554
 QY 574 WNSRDEVQWYCLVVDMPKIKPEQAMELLDCNYDPDMVAGFARCLIEKLTDLKSOYLI 633
 DB 555 WKHEDEVAMLYLTLCSNPPLPVLSALELDPSFPDCHVSSFAIKSRK--LTDELDFQYLL 613
 QY 634 QLVQVLKYEQYLDNLVRLFKKALTNORIGHFFFWHLKSEMNKTKVSQRFGLLESYCR 693
 DB 614 QLVQVLKYSYLDCELTKFLDLBALANRIGHFLFHLASEMHWPSVALRFGILAEAYCR 673
 QY 694 ACGMYLKLINROVEANMEKLINTLLIKQEKDETQVQVQKFLVBO--MRPDMALQGL 752

DB 674 GSTHHKVLMMKQGEALSKLALNDFVKLSQ--KTPKQTKELMHLGMRQEAYLEALSHLQ 732
 QY 753 SPINPAHQNLRLIECRIMSSAKRPLUNWENPDIMSELLPQNNELIFKNGDPLQDML 812
 DB 733 SPIDPSFLAEVVEECTFMDSKKRLPMYMSNEAGSG--GSVGIIFKNGDPLQDML 789
 QY 813 TLQIRIMENIMONOGJDLMLPYGLSIGDCVGLIEVANSHTIMOQC--KGLKALQ 871
 DB 790 TLQMGMDVLMQOEGDLRMTYGLCPDRLGLEVLIRSTIANIQMSNMATYA 849
 QY 872 FNSHTLHQLKDKKKEIYDAIDLTFRSCAGYCATFTILGIDRHSNIMVQDQLFH 931
 DB 850 FNVQALLNMLKSKNPGALDRAIEEFTLSCAGYCATYVLGIDRHSNDIMIRESQLFH 909
 QY 932 IDFGHFLDKKKKFGYKREVPVLQDPLIVISKGAOECTKTREPERQEMCYKALAI 991
 DB 910 IDFGHFLGNFKTKFGIRERVPILTYDFVHIQQG--KTNNSKEKREFRGTCERATTL 967
 QY 992 ROHANLFINFSMWLGSGMPELOSFDIAYIRKTLALDKTEOBALIEVFMKONDAHNGW 1051
 DB 968 RRHGLPLHLPALMRAAGLPFLSCSKDIQYLKDSIALGKTEEBALKHFRVFNDALESW 1027
 QY 1052 TTKXDWIIFHTIKQ 1064
 DB 1028 KTKVWMLAHNVSK 1040

RESULT 6
 AAW97390
 ID AAW97390 standard; Protein; 1044 AA.
 AC AAW97390;
 DT 14-MAY-1999 (first entry)
 DE p110-delta amino acid sequence.
 KM Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;
 KM PI3-Kinase mediated signalling; immune system; phosphatidylinositol;
 KM PI; kinase activity.
 OS Homo sapiens.
 PN US5882910-A.
 PD 16-MAR-1999.
 PF 25-NOV-1997; 97US-0977871.
 PR 25-NOV-1997; 97US-0977871.
 PR 25-NOV-1996; 96US-0777405.
 PA (ICOS-) ICOS CORP.
 PI Chantry DH, Hoeckstra MF, Holtzman DA;
 DR WPI: 1999-214067/18.
 DR N-PSDB; AAX15932.
 PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase
 PT enzymes - useful as antigens and for identifying agents which
 PT modulate the enzymes kinase activity or binding to substrates and
 PT co-factors
 PS Claim 1; Columns 23-30; 22pp; English.
 CC The present sequence represents a catalytic subunit (p110-delta),
 CC derived from a phosphatidylinositol 3-kinase enzyme which is
 CC involved in p13-kinase mediated signalling in the immune system.
 CC p110-delta phosphorylates phosphatidylinositol (PI), and
 CC derivatives of it at the 3'-hydroxyl of the inositol ring).
 CC p110-delta may be used as an antigen in the production of

CC antibodies (using standard techniques) which may be used, for
 CC example, to modulate (ie blocking, inhibiting or stimulating) the
 CC binding between p110-delta and its binding partner. p110-delta may
 CC also be used in assays to identify modulators which inhibit or
 CC activate its kinase activity.

XX Sequence 1044 AA;

Query Match 34.7%; Score 1978.5; DB 20; Length 1044;
 Best Local Similarity 39.9%; Pred. No. 3e-179;
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MRP-----RILVECLPNEGIVTLECEALITITIKELFEKARRYPLHQ 60
 DB 1 MPPGVDCPMFMTKEKNOVYVDLPLPGVYLVNPNVSRNANLSTIKQLMHRAYQEYELFH 60
 QY 61 LQDESSYIFVSTQREEREFDETRRLGDLRFQFLVIEVGNREKILNREGFA 120
 DB 61 MLSGPEAYVFTCTINQREOELEDEORRLCDVQPLFVLRLVAREGGRVKKLINSQISL 120
 QY 121 IGMPCVEFDVVKDPEVODFRNILLNWCKEAVDLRLDLSNPSHRAMVYVPPVNESSPE--- 176
 DB 121 IKGGLHEFDLSCPENVDFRAKACQPCREAAARQOLGEMALQYFPLQLEFSAQYMG 180
 QY 177 ----LPRHIYNKLDKGOIIVIVIVIVISPNNDKQYTLKINHDCVPEQVLAELAKKTRSM 232
 DB 181 GTLRLEPNR-----ALIVNVFEGSESESFTRQVSTKQVPLALMACARKK---- 224
 QY 223 LLSSEQLKLVLEQYQKYLKVGCCDEYFLEKYPLOSQYKTRICIMLGKRNIMLMAKES 222
 DB 225 --ATVFRQPLVQRPEDYTLQVNGRHEYLGNVPLQCFQYICGLSHGLPRLTMWSSS 281
 QY 293 LVSQLEPMDCFTWESYGRISTATPYMNGETSTKSLWVINGALIKXILCATVYVNIIRDID 352
 DB 282 ILAMREQSNPRAQOVQPRAPKPPPIPAKKSSVSLSLSEPPRIEALIQSKVNADEB--M 339
 QY 353 KIYVRTGIYHGSGPLCDNVNTQRP--CSNPRNEMWNIYDIYIDLPRAALCLISCV-- 409
 DB 340 KLVVQAGLFRHGNMLCKTVSSSEVSCSEPVWKORLEFDINICDLPRLMALCFALAVIE 399
 QY 410 -----KGRKGAEHEHCPLANGINLFDYTLTVSGKMLNLP--VPHGLEDLNPICVT 462
 DB 400 KAKKARSTYKKSKKACPIAMAMLMFYKDLKTERCJLYMWPSPVDEKGLNLPNTGTJV 459
 QY 463 GSNPNKETP-----CLELEFDWSSVVKFPDMSVIEEHANWWSRAGFSYSHAGLSNRL 517
 DB 460 RSNPNQDSAAALLITCLP---EVAHPVYTPALEKILE-----L 494
 QY 518 ARDNE---LRENDKEQYRAICTRDPLEITEQEKDFLMSHRHYCVT--IPEILPKLLSVK 573
 DB 495 GRHSECVHTBEEQQLRBEILBERGSGELYEHENKDLVMKLRHVCHEHFEALALLVTK 554
 QY 574 WNSRDVVAQMYCLVKWMPRIKREQAMELLDCNYPDMVFGFAVRCLKXYLTDDKLSQYLI 633
 DB 555 WNKHEBVAAQMYLCLCWMPRIKREQAMELLDFSPDCHVGSFAIKSIRK--LTDDELQYLL 613
 QY 634 QVVOVLYKXQYQYLDNLVRFLLKALTNORIGHFEFNLKSEMKNKTVSQRFGLLESYOR 693
 DB 614 QVVOVLYKXQYQYLDNLVRFLLKALTNORIGHFEFNLKSEMKNKTVSQRFGLLESYOR 673
 QY 694 ACGMYLXKHLNROVEAMEKLINTLDLKQEKDETQYQWKFIVEJ--MRSPDEFDALQGL 752
 DB 674 GSTHMKVLMKQGEALSKLKALNDPVKLSQ--KTPRQTKELMHLKMRQEAIVIALSHQ 732
 QY 753 STLNPAHQGNRLERECRIMSSAKRPLMTNENPMISLLEFONNEIIFKNGDDIRQDM 812
 DB 733 SPLDSTLLAEVCYECCTFMDSKMKPLMTYSNEBAGSG---GSVGIIFKNGDDIRQDM 789
 QY 813 TLQIIRIMENONOGDLRLPYGCLTSGDCVGLLEVVRNSTIMQIQ--KGLKGLAQ 871
 DB 790 TLQMIQLMVLWKQEBDLRMTPIYGCPLGRDRTGLLEVLRSPSTLANIQLSNMAATTA 849
 QY 872 FNSHTLHQLKDKNKGEIYDAAIDLFTRSCAGYCVATFIIGDRHNSNIMVXDQDLPH 931

DB 850 FNDQALNMLKSKNPGBALDRAIEBFTLSCAGYCVATYVLGIGDRSDNIMRESGLFH 909
 QY 932 IDFGFLDHKKKKKFGYKREVPVVLVODPLIVYSKAGQECTKREBERPQEMKYKAYLA 991
 DB 910 IDFGFLDHKKKKKFGYKREVPVVLVODPLIVYSKAGQECTKREBERPQEMKYKAYLA 967
 QY 992 ROHANEFINLFSMWSGMPLEOSFDDIAYIRKTLALDKTEOBALFPMKQNDALHNGW 1051
 DB 968 RRGGLFELHFLAMRAAGBELSCSDIOTLKDSLGLTEEBALKHFRVKEALRESH 1027
 QY 1052 TYQMDWIFHTIKQ 1064
 DB 1028 KTKVNLVAHVSK 1040

RESULT 7
 AAY50179
 ID AAY50179 standard; Protein; 1044 AA.
 XX
 AC AAY50179;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Human PI 3-kinase-related catalytic subunit p110-delta.
 XX
 KW Lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;
 KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;
 KW phosphatidylinositol (3, 4, 5) triphosphate; PI3; activation; G protein;
 KW cellular response; growth; differentiation; apoptosis;
 KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;
 KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;
 KW antagonist; agonist; treatment; disorder; cell growth;
 KW cell differentiation; immune activation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 141..310
 FT Domain /note="Ras regulatory region"
 FT /note="723..1044
 FT /note="Catalytic domain"
 PN US5985589-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 06-JAN-1999; 99US-0225951.
 XX
 PR 25-NOV-1997; 97US-0977871.
 PR 25-NOV-1996; 96US-0777405.
 XX
 PA (ICOS-) ICOS CORP.
 PI Holtzman DA, Hoekstra MF, Chantry DH;
 DR MPI, 2000-012785/01.
 DR N-FSDB; AA32882.
 PT Identifying modulators of lipid kinase subunit p110delta activity -
 PS Claim 1; Columns 232-28; 22pp; English.
 XX
 CC This sequence represents a novel lipid kinase catalytic subunit,
 CC p110-delta, related to phosphatidylinositol 3-kinase (PI
 CC 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-
 CC localizing p85 subunit and a catalytic p110 subunit. These subunits both
 CC have isoforms; p85 has two isoforms (alpha and beta) which are
 CC differentially expressed, and p110 has to date three isoforms
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at
 CC the 3' hydroxyl of the inositol ring with the primary product of PI
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)

CC broad phosphoinositide specificity and specific tissue localisation,
 CC possibly involved in regulation of melanoma metastases (it is not
 CC expressed in normal melanocytes). DNA fragments encoding the present
 CC sequence are used to detect tissue-specific expression, and a
 CC similar analysis can be done at the protein level using antibodies in
 CC standard immunoassays. These assays are particularly used for diagnosing
 CC and predicting motility/invasiveness of metastatic cancer cells. The
 CC protein can be used in human or veterinary medicine for controlling
 CC motility of cells, where the protein increases motility while antisense
 CC sequences are used to reduce it.
 CC note: this record is revised to include second DR line which gives the
 CC nucleotide sequence.
 CC
 XX
 SQ Sequence 1044 AA;

Query Match 34.6%; Score 1976.5; DB 19; Length 1044;
 Best Local Similarity 39.9%; Pred. No. 46e-179; Mismatches 183; Indels 97; Gaps 19;
 Matches 436; Conservative 163;

16 MPP-----RILVECLLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
 1 MPPGVDCPMEFMTKEENQSVVDLPLPTGVYLNFPVSRNANLSTIKQLWHRAYQELPLH 60
 61 LLDDESSYIFVSYTOEAREEFDETRRLCDLLPQFLAVIYVGVNREKILNREIGFA 120
 61 MLSGPRAYVFTCTNQTAEOQLEDEORRLCDVQPLFLVRLVARSGDRVKKLINSQISLT 120
 121 IGMVCEFDVWVKDPEVODFRNRIILNCKEAVDLRLDINSPHSRAMVYVPVNESSPS--- 176
 121 IKGGLHFFBLSCPREVDPFPAKACQCFEEAARQOLGMAWLOYSFPLDLESACQWCP 180
 177 ---LPHKHYLNKLDKQIIVIVIVISPNNDKQYTLKINHDCVPEQVIAEIRKTRSM 232
 181 GTLRLLPNR-----ALIVNVKFEGBSESFTFQVSTKOVPLALMACALRRK---- 224
 233 LLSSEDLKCLVLEQGYKILKYCCGBYLEKTPLSQYKTRSCINLGMENIMLMAKES 232
 225 ---ATVFRQPLVQRPEDYTLQVNGRHEYLGSYPLCOFYICSCILHSGILPLTMVHSSS 281
 293 LVSQLEMDCFMTMSYSRRISTATPYMNGESTKSLWVINSALRIKILCATVYVNVTRDID 352
 282 ILAMREQSNPAPQOVQPRAPKPPPIPAKKPSSVLSLSEDFRPIELIQSKVADER--M 339
 353 KIYVRTGIYHGGRPLCDNVNTQRP--CSNPRNEMNIYDIYIDLPRAARLCLGISV-- 409
 340 KLVVQAGLFRHGNMLCKTVSSSEVSCSEPVWKORLEFDINICDLPRMALCALVAIE 399
 410 -----KGRKGAKEHCPLAMGINLFDYTDTLVSGRMALNMP--VPHGLELLNPIGVT 462
 400 KAKKARSTKSKSKKACCPILAMNMLFDYDOLKTGERCLYMWPVYDEKGEILLNPTGV 459
 463 GSNPNKETP-----CLELEFDWSSVYKPRDMSVIEEHANWSVSRAGPSYHAGISNL 517
 460 RSNPNNTSAAALLICLP--EVAHPVYYPALKEKLE-----L 494
 518 ARDNE---LRENDKEOLRAICTRDPLEITECEKDFLMSHRHYCVL--IPEILFKLLSYK 573
 495 GHHSCECVHTBEQQLRLEILERRSGGELYEHKDLVMKLRHNVGHFEPALARLLLVK 554
 574 WNSRDVVAQNYCLVQKMPPIKPEQAMELLDCNYPDMVNGFAVRCLEKYLITDKLSQYLI 633
 555 WNKHBEVVAQMLYLCSMPLELPVLSALELLDFSEPDCHGVSPALSKDRK--LTDELELQYLI 613
 634 QLVQVYLKAYOYLDNLVRFLLKKALINORIGHFFHNLSEMNKTVQSORFGILLSEYOR 693
 614 QLVQVYLKAYSDCELTJTKFLDLBALNRKIGHLPHNLSSEHVPVVALRFLITRAYOR 673
 694 ACGMYLKHNLNRQVEAMEKLINTLILKOKKDETQYVQMKFLVEQ--MRBPDFDALQGL 752
 674 GRTHHKVLMKQGEALSKLALNDPVYKLSQ--KTRPQIKELMHLKMRQEAIVYEAASHIQ 732
 753 SPLNPHQIGNRLERECRIWSSAKRPLMLWENPDIMSELIFONNEIIFKNGDILRODM 812

DB 733 SPLDPTLLAEVCEQCTFMSDKKPLMIWYNSEAGSG---GSVGIIFKNGDILRODM 789
 QY 813 TLQIIRIMENIWNQGLDRLMLPYGCLSIDCVGLIEVVRNSHTIMQIQ--KGLKALQ 871
 DB 790 TLQIMQIMDLVMQBSIDRLMTYGLCPGDRGLIEVLRSTTIANIQLNKSNMAATA 849
 QY 872 FNSHTLHQLDKDNKKEIYDAIDLFTSCAGYCVATFIIIGIDRHSNINWDDQLFH 931
 DB 850 FNKDALNMLKSNKPGDALDRAIEEFTLLSCAGYCVATYVLIGIDRHSNINMIESGLFH 909
 QY 932 IDFGHFLDKKKKFGYKREVPFVLTQDFLIYVSKAGQECTKTRFERPQEMCYKAYLAI 991
 DB 910 IDFGHFLGNFKTKFGINRERVPFILTYPFVHIQQG--KTNNSKEKEFRFGYCERAYTIL 967
 QY 992 ROHANLFINLFSMWLGSMPLELSPDDIAYIRKTLALDKTEQALFEMKQMDAHNGW 1051
 DB 968 RHHGLLFLHLFALMRAGLPELSCSDIOYLKQSLALGKTEBALHFRYKVEALRESW 1027
 QY 1052 TTKMDWIFPTIKQ 1064
 DB 1028 KTKVNMVLAINVSK 1040

RESULT 9
 AAY88372
 ID AAY88372 standard; Protein; 1044 AA.
 AC AAY88372;
 DT 17-JUL-2000 (first entry)
 DE Phosphatidy] inositol 3 kinase (PI3K) p110 subunit amino acid sequence.
 XX
 KW Phosphatidy] inositol 3 kinase, PI3K; antisense oligonucleotide; p110;
 KW catalytic subunit; treatment; rheumatoid arthritis; asthma; research;
 KW diagnostic; infection; inflammation; tumour formation; inhibitor.
 OS Homo sapiens.
 XX
 PN US6046049-A.
 PD 04-APR-2000.
 XX
 PF 19-JUL-1999; 99US-0357070.
 XX
 PR 19-JUL-1999; 99US-0357070.
 XX
 PA (ISIS-) ISIS PHARM INC.
 PI Monia BP, Cowseert LM;
 XX
 DR WPI, 2000-282691/24.
 DR N-PSDB; AAA13154.
 XX
 PT New antisense compounds targeting nucleic acids encoding human PI3
 PT kinase p110 delta useful for treating a disease or condition associated
 PT with PI3 kinase p110 delta expression, e.g. Rheumatoid arthritis,
 PT asthma
 XX
 PS Disclosure; Column 45-52; 35pp; English.
 XX
 CC This sequence represents the amino acid sequence of the delta catalytic
 CC subunit of human phosphatidy] inositol 3 kinase. Phosphatidy] inositol 3
 CC kinases (PI3K) act as downstream effectors of hormone and growth factor
 CC receptors, and have been implicated in growth factor mediated cell
 CC transformation, mitogenesis, protein trafficking, cell survival and
 CC proliferation, and many other cellular activities. PI3K is a heterodimer,
 CC consisting of a 110kD catalytic subunit (p110), and an 85kD regulatory
 CC subunit (p85). The invention relates to antisense oligonucleotides which
 CC target the p110 delta mRNA of PI3K. The antisense oligonucleotides
 CC specifically hybridise with various regions of the PI3K mRNA sequence,
 CC and inhibit the expression of PI3K. The antisense oligonucleotides may be
 CC used to treat an animal, particularly human, suspected of having or being

CC prone to a disease or condition associated with the expression of PI3K,
CC e.g. rheumatoid arthritis or asthma. The treatment works through the
CC modulation (preferably inhibition) of the expression of PI3K. The
CC antisense oligonucleotides may also be used for research and diagnostics,
CC in pharmaceutical compositions and formulations, in the preparation of
CC kits for detecting the level of PI3K in a sample, and as prophylaxis,
CC e.g. to prevent or delay infection, inflammation or tumour formation.
CC Antisense oligonucleotides, which are able to inhibit gene expression
CC specifically, are used to elucidate the function of particular genes, and
CC to distinguish between functions of various members of a biological
CC pathway.

SQ Sequence 1044 AA;

Query Match	34.6%	Score	1976.5	DB 21	length	1044			
Best Local Similarity	39.9%	Pred. No.	4.6e-179						
Matches	436	Conservative	183	Mismatches	377	Indels	97	Gaps	19

```

0Y 16 MP-----RILVECLLPMGMVLTLESCAEALTLITKHLEFKAARYPLHQ 60
Db 1 MPBGDCMEFWTKEENOSVVDFLLPLGVALNPFVSNANLSTIKOLLIMRAOYERLPH 60
0Y 61 LLODESSYIPVSVTOEAREEPEFDETRLCULRFOPLKATIEPVGNEEKLINREIGFA 120
Db 61 MLSGBEAVFTTCINOTABOQELDEBORLSDVOPLPLVLRABRGDVKKLINSOISLL 120
0Y 121 IGMPCYCFDMVKDBEVODFRNINLVCKEAYDLRLNBSHSMVVPYNBESPE----- 176
Db 121 IKGHHEFDLSDPEVNDFRAMTCOFCEBAARROOLGMEALQSPLODEPSQOTWGP 180
0Y 177 ----LPKHLYNLDYGOIIVVIMVYVSPNNDOXTLKNHOCVEQVLAERIKTRSM 232
Db 181 GTLRPNR-----ALVNVKRGESSESTFOVSTDVYDLAMACLRKK----- 224
0Y 223 LLSSEQLKLVLEYOGKYLKAVCGDEYELKPYLSOYKYIRSCIMLGEMNYLMMAKES 292
Db 225 ---ATVFRPLVBEQREDYTLQVNGRHELYGYSYPLCOFYICSLHSIGTLPHLTWSSS 281
0Y 293 LYSOLMDCFTMPSRRISTATPYMNGSTSKLSMIVINSALRIKLTATYNNVNRID 352
Db 282 IIMADEQSNPAVOVKPRAKPEPLIPAKPPSSVLSLSQPRRELIOSSKYNADER--M 339
0Y 353 KIYVFRGIYHGGEPLCDNVNTOVR--CSNPRNEMVNLNDIYIPDLPRARLCLISCV-- 409
Db 340 KLVVOGLPHNGNMLCKTVSSSEVSCSEYVMKORLEPINI CDLPRMARLGFALYAIE 399
0Y 410 -----KGRKAKEHCPLAMGINLPDYTDITVSGKMLNLMR-VPHGEDLINIGT 462
Db 400 KAKKARSTYKKSXKACCPAMAMLMFDYDOUKTEGRCLYMPSPVDEKGETLINTGV 459
0Y 463 GSNPNKETP-----CLBEFDMFSSVYKPRDMSVIEBHAWSVSRBAGFSYHAGLSNBL 517
Db 460 RSNPNNTDSAAALLICRP--EVAPHEVUYALKELE-----L 494
0Y 518 ARONE---LRENDKEQLRAICTRDPRLSEITOEKDFLMSRHYCVT-IPERLKLILSVK 573
Db 495 GRHSECHVHEEBOLOREILBERSGELEYEHEDOLWMLKRHEOEHFPEALRLLVTK 554
0Y 574 WNSRDEVAOMYCLVOMPRIPKREOAMLLDNCNPRDPMVRGPAVRCLEKUTLTDKLSOYL 633
Db 555 WNKREDAVOMIYLLCSMPBELPVLSALRLDPSFPDCHVGSPALSKLK-LTDELLFOYLL 613
0Y 634 OLVOULKXEOYLDNMLVRLPLKVALTGORIGHFPEFMHLSKSEMHNKTVSOBFGLLESYCR 693
Db 614 OLVOULKXESTLDELTFFLLDRLLARXKIGHFEMHRSBMHNPVSAALRFGILTEAYCR 673
0Y 694 ACGMYLKLHNRQVEAMERILNLTDLKOEKDETOXOVKFLVQ-MRRPDMALOGFL 755
Db 674 GRTHNMKVLMOGEALSKLKALNDFVXLSQ-KTRPKQOTEIMHICMRQEVUYEALSHLO 722
0Y 753 SPLPRAHOLGNRLBECKIMSAGRPMLNENENDINSELLFONNEIIFKRGDRLORDML 812
Db 733 SPLRPSLTLLAVCEQCTFNDSKKKRPMTIMSNBAGS---GSVGIIIFKRGDRLORDML 785

```

[illegible]

RESULT 10

AAU09685 standard; Protein; 1044 AA

AC AAU09685;

DT 12-MAR-2002 (first entry

DE Human p110delta isoform of PI3-kinase

AA Human; phosphatidylinositol 3-kinase; PI3K; p110delta isoform;
 KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
 KW Type 1 diabetes mellitus; cytostatic; immunosuppressive.

OS Homo sapiens.

PN WO200185986-A2

PD 15-NOV-2001

PF 10-MAY-2001; 2001WO-US15065

10-MAY-2000; 2000US-203346P
PR

PA (ICOS-) ICOS CORP

PI Sadhu C

DR WPI; 2002-075252/10.

DR N-PSDB; AAS14363.

AA Identifying a modulator of p10delta polypeptide binding to SH3
PT domain-containing polypeptides e.g. IASP-1, comprising allowing the
PT binding partners to interact in the presence and absence of a test
PT compound -

PS Example 1; Page 48-51; 85pp; English

The present invention relates to identifying modulators of the phosphatidylinositol 3-kinase (PI3K, p110delta) enzyme that binds to the catalytic subunit via a SH domain-containing polypeptide such as LAMP-1. Also described are methods of assaying the specific binding affinity of the PI3-kinase binding partner. Such modulators are useful for the treatment of diseases characterised by the undesirable or excessive activity of PI3Kdelta. For example the modulators can be used for inhibiting the growth or proliferation of cancer cells (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues, e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues, e.g. Hodgkin's lymphoma, leukemias), inflammatory diseases (e.g. rheumatoid arthritis), opthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory

CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
 CC dermatoses (e.g. contact dermatitis), central or peripheral nervous
 CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
 CC and Type 1 diabetes mellitus. The present sequence represents human
 CC p10delta isoform of p13k.
 XX
 SQ Sequence 1044 AA;
 Query Match 34.6%; Score 1976.5; DB 23; Length 1044;
 Best Local Similarity 39.9%; Pred. No. 4.6e-179;
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;
 16 MPP-----RIVVECLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
 Db 1 MPPGVDCPMFMTKEENQSVVDFLLPTGYLNPVSRNNALSTIKOLMHRAGYSLFH 60
 61 LLDGESSYIVSVQAEEREFDETRLCDLRFQFPIKIEVGVGRREKILNREIGFA 120
 Db 61 MLSGFEAYVFTCTNQTAEQDEBQRRLCDVQFPLRLVAREGDKVKLLINSQISL 120
 121 IGMVCEFDVWKDEVDQFRRLINLVCKEAVDLRLNSPBRAMVYVPPNVESSE--- 176
 Db 121 IKGHHEFDLCEVDVDFRAKMGCFCEMAARQULGEMANLQYSPFLQLEBQAQWGP 180
 177 ----LPHIYNKLDKQIIVIVIVISPNNDKQRYTLKINHDCVPEQVIAEIRKTRSM 232
 Db 181 GTLRLPNR-----ALVNVKFESESEFTQVSTKDVPLALMCALARK--- 224
 223 LLSSEQLCVLEVOGKIILKVCQCDVPLEKPYLSQYKIRSCIMGRPNMLMAKES 292
 Db 225 ---ATVRQPLVEQPEDYTLQVNGRHELYGSGYPLCOFOYICSLHGLPPLHLMVHSS 281
 293 LYSQLPMDCTFMPYSRISATATPYMNGETSKLWVINSALRIKICATVNVNINRDI 352
 Db 282 ILMRDQSPAPQOVQPRAPKRPPIPAKSSSVLSLSEQFRIELIGQSVNADER--M 339
 353 KIYVRTGIYHGEELCDNVATQVVP--CSNPRMELNYDIYIPDLPRARLCLSCSV-- 409
 Db 340 KLVVQAGLPHGNEMLCVTSSEVSCSEPVWQRQLRPFIDINCOLPRMARLCPALYVITE 399
 410 -----KGRKGAEEHNPFLWAGNINLPDYITDLVSGMALNLP--VPHGLEDLINP 462
 Db 400 KAKKARSTKSKKADCPRIAMLMFLDYQDLTGRCCLYMPVSVDEKCELLNPQTG 459
 463 GSNPNKETP-----CLELEDFMFGSVYKPPDMSVTEEHAMSVSREAGFSGHAGSLNRL 517
 Db 460 RSNPNDSAAALLICLP--EVAPHYVYPALEKILF-----L 494
 518 ARDNE--LRENDKEQDLRAICTRDLSEITEOEKDFLMSHRHYCVT--IPEILPCLLSV 573
 Db 495 GRHSECVHTEEBQDLQREILERRGSGELYEHEDLVWKLRIHQEHPRFELARLLVTK 554
 574 WNSRDEVAQNYCVKMPPIKPEQAMLLDQNYRDPNVGRFVAVCLEKYLTDKLSYLI 633
 Db 555 WNGHEDVAQWLYLLCSMPBELPVLSALRLDPSFEDCHGVFAIKSLRK--LTDDELFG 613
 634 QLVQVLKYEQYLNILVFLKALTNQRIQHPRFMHLKSEMNKTKYQSRGILLSEYCR 693
 Db 614 QLVQVLKTESYLDCELFKFLDLRLANKRGHFLFMHLRESEHNPVALPFGILLEVYCR 673
 694 ACGMYLNLNROYEAMEKILNLTDLKQEKDETQKQVMFLVEQ--NRAPDFMDALQGL 752
 Db 674 GRTHMKVLMKQEBALSKLKALNDFVLSQ--KTPKQTEHMLKCRQANVLEALSHQ 732
 753 SPUNPAHQNLRLSECRINSSAKRPLMLWENDIMSEILPONNEIIFPNQDDLRODML 812
 Db 733 SPIDPSTLAEVCEQCTFMDSKKPLMIMVSEASG--GSVGIIIFKNGDRLRODML 769
 813 TLGIIRMENIMONQGLRLMLPYGCLSIDGCVGLIVVNSHTIMQIC--KQGLKALQ 871
 Db 790 TLQWQGLMDVLMQOBGLDKTRTPGCLPTGDRGLLEIVLRSDTIANIQLNKSNMAATYA 849
 872 FNSHTLHQLKDXKGEIYDAIDLFTSCAGYCVATFIIGDRHNSNIMVXDQGLFH 931

Db 850 FNXKALLNWLKSKNPGBALDRAIEEFTLSCAGYCVATYVIGIDRHSNIMIRSGQLFH 909
 Qy 932 IDEGHFDHKKKRGYREVPFVLTODPLIVISKQOECKTRFERFQEMCKAYLAI 991
 Db 910 IDEGHFDKNTKFGINREVPFLTYDPVHVIOQG--KTNNSEKFERFQYCERAYTIL 967
 Qy 992 ROHANLFINFMMWLSGMPDELQSFDDIAYIRKTLADKTEQALBYFMQMDAHNGW 1051
 Db 968 RHGHLFLHLPLMRAAGLPELSCSKDIQYLIKSLALGKTEBEALKIFRYKFNALRESW 1027
 Qy 1052 TTKQDWTFHTIKQ 1064
 Db 1028 KTKVMNLAHNVSK 1040
 RESULT 11
 AAB11124
 ID AAB11124 standard; Protein; 1070 AA.
 XX
 AC AAB11124;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Human P13 kinase p10delta protein.
 XX
 KW Human; p13 kinase p10 beta; antisense inhibition; primer; cyostatic;
 KW antinflammatory; antinfective.
 XX
 OS Homo sapiens.
 XX
 FN US6131032-A.
 XX
 PD 17-OCT-2000.
 XX
 PF 09-SEP-1999; 99US-0392350.
 XX
 PR 09-SEP-1999; 99US-0392350.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowesert LM;
 XX
 DR WPI: 2000-686014/67.
 XX
 DR N-PSDB; AAC65690.
 XX
 PT Antisense compound 8-30 nucleobases in length targeted to a start codon
 PT of the coding region of human p13 kinase p10delta, useful for
 PT inhibiting the expression of the human polynucleotide -
 XX
 PS Example 1; Column 43-50; 34pp; English.
 XX
 CC This invention describes a novel antisense compound (I) 8-30 nucleobases
 CC in length targeted to a start codon or nucleobases 4-3174 of the coding
 CC region of human p13 kinase p10delta (II), in which (I) specifically
 CC hybridizes with and inhibits the expression of (II). The products of the
 CC invention have cyostatic, antinflammatory and antinfective activity.
 CC (I) is useful for inhibiting the expression of (II) in human cells or
 CC tissues. The antisense compound can be utilized for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits. The
 CC antisense compounds may also be useful prophylactically, e.g. to prevent
 CC or delay infection, inflammation or tumor formation. The antisense
 CC compounds are useful for research and diagnostics, because these
 CC compounds hybridize to nucleic acids encoding (II).
 XX
 SQ Sequence 1070 AA;
 Query Match 34.4%; Score 1966; DB 21; Length 1070;
 Best Local Similarity 40.1%; Pred. No. 4.9e-178;
 Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;
 Qy 1 MPPRPS--GELWGIH--LMPRIIVECLPNGMIVTLECLREATLTITIKHELFKEARKY 56

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Db      7 MPAMADLIDIAVDSQIASDGSIPVDLPTGIYIOLEVPREATTIYIKOMLMKVHNY 66
QY      57 PLHQLIDESSYIFVSVTQEAEREPEFDETRRLCDLRLFOFLKVIIEPVGNREKILNRE 116
Db      67 PMRPLMDISYMACNQRAVYELEDETRRLCDVAPFLPVKLTVRSQDPSGK-LDSK 125
QY      117 IGFAIGMPVCEFDNVKDEVDQFERRLINCKEAV-DLRDLNSPHSRAMYYPPNVSSP 175
Db      126 IGVLIIGLHEFDLSKDPEVNEFRRKRRKFESEKILSLVGL-SWMDMLKQTPP--BHEP 182
QY      176 ELPRHINIKDKGQIYIVIVIVIVISPPNDKQYTKIKINHDCQPEQYIAEAIKKRRSMLS 235
Db      183 SIPENLDEKLYGKLIYAVHF---ENCQDFSFQVSNMNPPIVNEALAIQR----- 231
QY      236 SEQKLCVLEYQK-----YILKVGCDSEYEFLEKPELQYXYSICIMAGMPNMLT 287
Db      232 -----LTHGEDEVSFYDYLOVQSGRVEYFGDHPILQFOYIRNCVNRALPHIL 283
QY      288 MAKESLYSQLPMDCFMPSYSRRISTATPYNNGETSTK--SLWVINSALRIKILCATYV 344
Db      284 VECCKIKMYEQEMIAIEAIIINRSSNLPRLPLPKTRIISHVWENNPPQIVLVKGN-- 341
QY      345 NVNIRIDIKTYVRGTYHGERPLCDNVTORVPCSNPR-VNEMINVDYIPDLPPAARLC 403
Db      342 KLNTEETVKVVRAGLPHGTBLCTIVSSEVSGKNDHIWEPLEFDINICDLPRMARLC 401
QY      404 LSTCS---VKGRKAK-----EEHCPLAMGNINLFEDYDTLVSGMALNL 445
Db      402 PAVYAVLDKVTKKSTKTIINSKYOTIKAKGNHVPVAMVNTMVFDFGQRLGTGILHS 461
QY      446 W-PVPHGEDLLNPIGVTGSMNPKETPCLELEFDFSSVVKFPDM-----SYIE 493
Db      462 WSPFDELEEMLNPMGTIVQTPYENAT-----ALHVKPEKKOPYYVPPDKIIE 513
QY      494 EHAMSVSRBAGFSYSHAGLSNRRLARDNELRNDKQRLAICTRPLSEITEQEDPMS 553
Db      514 KAAELTASDSANVS-SRGG-----KKPLPVLEKIIDRPLSLCENEDLIWT 560
QY      554 HRHYCVTI-PELTPKLLISVKNNSRDEVAQMYCLVMDPPIKPEQAMELLDCNYPDPNVR 612
Db      621 EYAVGCL-RQMSDELSQYLIQVQVLYKYEPLDCALSRFLERALLGNRRIOQFLFMR 679
QY      673 SEMENKTVSQRGLLIESYCRACGMVTKRLNQVEMETLINLTILKQEKXDETOQVQM 732
Db      680 SEVHLPASVQDGVILEAVCRGSVGMKVLKQVEALNKLKTLNLSLITKLNAVKLNRKX 739
QY      733 KFLVQMRPRPDMALOGFLSPINPAHQGNLRECRIMSSAKRPLMWNENPDIIMSEL 792
Db      740 EMNHTCLKQSAVREALSDQSPINPVCVILSELYVECKXMDSKMLMVLVNN-KYFGE- 797
QY      793 LFQNNELIPKNGDDRLQDMLTQIRIMENIQONQGLDIRMLPYGCLSGDCYGLIEVVR 852
Db      798 --DSGVGIFKNGDRLRQDMLTQMLRLMDLWKREALDIRMLPYGCLATGDSGLLEVS 855
QY      853 NSHTIWOJC-KGGLKGAIQNSHTLHQLKDKNGKEIYDAALDETRSCAGCVATFLL 911
Db      856 TSETIADIDNSSVAAAAFNKDALINMLKEVNSGDDLRALIEFTLSCAGCVASYVL 915
QY      912 GIGDRNSINIMVDDQQLFHIDGFHLDHKKKFGKRRERVPVLTODFLIVISKAQOC 971
Db      916 GIGDRSDINIMVKKTQQLFHIDGFHLGNKSKFGIKREKREVPILTYDFHVIQOG-KT 973
QY      972 TKTREFEROEMCYKAYLAIQHANLPINLSMILSGNPELOSFPDIAYIRKTLALDKT 1031
Db      974 GNTREKGRPRQCEADAYLIRHGNLFTLFALMTLAGBELTSVDIOYIKDSLALGKS 1033
QY      1032 EGEALEYFMKQNDAAHGGCTTGMDFITIKQ 1064
Db      1034 EEEALKQFKQFDEALRESWTTKVNMAHATVRK 1066

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RESULT 12
ABP65170
ID ABP65170 standard; Protein; 1070 AA.
XX
AC ABP65170;
XX
DT 12-NOV-2002 (first entry)
XX
DE Hypoxia-regulated protein #44.
XX
KW Cytosolic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preclampsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human.
XX
OS Homo sapiens.
XX
PN MO200246465-A2.
XX
PD 13-JUN-2002.
XX
PE 10-DEC-2001; 2001WO-GB05458.
XX
PR 08-DEC-2000; 2000GB-0030076.
PR 08-FEB-2001; 2001GB-0003156.
PR 25-OCT-2001; 2001GB-0025666.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI Rayner WN;
XX
DR MPI. 2002-627238/67.
XX
PT Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene.
XX
PS Claim 35; Page 363; 538pp; English.
XX
CC The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV77873-ABV78116
CC and ABP65061-ABP65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preclampsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss.
XX
SQ Sequence 1070 AA;
XX
Query Match 34.4%; Score 1966; DB 23; Length 1070;
Best Local Similarity 40.1%; Pred. No. 4,9e-178;
Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;
QY 1 MPPRPS-GEIWCIR--IMPRILVECLLPNGMVTLECLAEATLITIKELFKEARX 56
Db 7 MPAMADLIDIAVDSQIASDGSIPVDLPTGIYIOLEVPREATTIYIKOMLMKVHNY 66

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QY 57 PLHQLQDESSYTFVSTQAEAREEFDETRLCDLRLFOPLKVIPEVGNREBKILNRE 116
Db 67 PMFNLLMDIDSYMFACVNOQTAAYVELEDETRLCDOVRPFLPVKLVTYRSCDPGER-LDSK 125
QY 117 IGFAIGMPVCEFDWKDEVDQDFRRNIIINVCKEAV-DLRDLNSHSAAMVYPPNVSSP 175
Db 126 IGVLLIGKGLHFPDLSKDEPNVRRRRKRRKSEEEKISLVGL-SYMDMLKOTYPR--HEP 182
QY 176 ELFRKHIYNKLDKQIIIVIVIVIVISPNNDKQYTLKINHDCVPEQVIAEARIKTRSMILS 235
Db 183 SIEBENEDKLGGKLIIVAHVF---EKCDVFSQVPSPMNPIKVNBLAIQKR----- 231
QY 236 SEBOLKCVLEQOK-----YIKVCGCDEFLFLEKYPISQYKTRSCIMLGMPNML 287
Db 232 -----LTIHCKEDEVSPDYVLQVSGRVEYVFGDHPILQFOYIRNCVMBALPHFIL 283
QY 288 MAKESLYSQPMOCFTMPYSRRISTATPYMNGETSX---SLMVINSARIKILCTYV 344
Db 284 VECCKIKKWEQEMIAIEAIIINSSNVLPLPPKKTRIISHWENNPFQIYLVKGN-- 341
QY 345 MNVIRIDIKIYVGTGYHGEPLCDNVNTOVPCSNR--NMENLVNDIYIPDLPRARLC 403
Db 342 KUNTEETVAVKVAAGLHGFHLLCKTIVSEVSGKNDHINNEPLEPDIINCDLPRARLC 401
QY 404 LSTICS-----VKGRKAK-----EBHCLAMGNINLPDYTTDLVSGKMAI 445
Db 402 FAYYAVLDKVKTKKSTKTIINPSKYOTIRKAGKHYPVAVNVTWVPBKQLATGDIILHS 461
QY 446 M--PVPHGEDLNPICVTGTSNPKETPCLELEFDWSSVYKFPDM-----SVTE 493
Db 462 WSSFPELEBEMLPWGVQNTNYTENAT-----ALAHKFPENKKOPYYPFPKITE 513
QY 494 EHAMSVSBEAGFSYHAGLSNRLARDNELRENDKQLRAICRPDLSEITEQEKPLWS 553
Db 514 KAABIASSSANVS-SRGC-----KFLPVAKIILDRDPLSOUCHEMDLIWT 560
QY 554 HRRYCVTI-PEILPKLLSVKMSRDEVAOMCYLVKDWPEIKEDQAMELLDCNYPDMVR 612
Db 561 LRQDCBEIFPOSJPKLLSIIKMKLEDAVQLQALLOIWPFLPREALELDFNYPOQYV 620
QY 613 GFAVRCLBKYLTDDKLSOYLIOYVQYAKYQOYLDNLLVRLKALTNORIGFFWHLK 672
Db 621 EYAVGCL-KOMSEBESQYLDQVQYAKTEPFLDCAISRLEERAAIGNRITGFLFWHLR 679
QY 673 SEMHNKTSQRFGLLIESYCRACGYLKLINROVABMEKILNLTDLIKOEKKDEQXQVM 732
Db 680 SEVHIRAVSVQGVIIIEAYCRGSGVGMKVLKSKQVEALNKLTINSILKLVAVKLNRAK 739
QY 733 KFLVEQMRPFDALQGLSPLNPAHQNLRLBECRIWSSAKRPLMWNENPDIMSEL 792
Db 740 EAMHTCLKQSAVREASLDIOSPLNPCIILSELYVEKCYWVDSKXKFLMLVYNN-KVFG- 797
QY 793 LRQNNELIKRQNDLQDMTLTLOITIMENINONQGLDMLRPGCLSGDCVGLIEVVR 852
Db 798 --DSVAVIIRKNGDRLQDMTLQMLMLMLMWEKAGIDLRMPYGCILAGDSGLLEVVS 855
QY 853 NSHTIWOIC-KGSLKGALEQNSHTLQWLKQNKGEIYDAIDLTFRSAGAGCAVATFI 911
Db 856 TSETTIDIDLNSNVAAAAAFKDALINMLKEVNSGDDLDRALESTTLSCAGCVASVYL 915
QY 912 GIGDRHNSINMYKDDQDLFIHGFHLDHKKKFGYKRERVPVLTODEFLIVISKAQEC 971
Db 916 GIGDRSDIMYKTKQGLPHIDFGHITLGNFKSGFKGRKRVPIFLYDILHVIQOG--KT 973
QY 972 TITREBERQEMCYKAYLAIROHANLFIULFSMGLSGMPELOSFDIAYIRKTLADLT 1031
Db 974 GNTBKRGRQCCEDAYLLIRRHGNLFTILFALMLTAGLPBLTYSVDIOYLKDSLALGKS 1033
QY 1032 BOEALLEYFMKQMDAHNGMTTKMDVIFHTIKO 1064
Db 1034 EEBALKQFKQKDEALRESWTTKVNMMALTVRK 1066

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RESULT 13
AAU09688
ID AAU09688 standard; Protein; 1070 AA.
XX
AC AAU09688;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human p110beta isoform of PI3-kinase.
XX
KW Human; phosphatidylinositol 3-kinase; PI3K; p110beta isoform;
KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
OS Homo sapiens.
XX
PN WO200185986-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001MO-US15065.
XX
PR 10-MAY-2000; 2000US-203346P.
XX
PA (ICOS-) ICOS CORP.
XX
PI Sadhu C;
XX
DR WPI; 2002-075252/10.
DR N-FSDB; AAS14366.
XX
PT Identifying a modulator of p110delta polypeptide binding to SH3
PT domain-containing polypeptides e.g. LAMP-1, comprising allowing the
PT binding partners to interact in the presence and absence of a test
PT compound.
XX
PS Example 1; Page 68-71; 85pp; English.
XX
CC The present invention relates to identifying a modulator of the
CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC the catalytic subunit via a SH3 domain-containing polypeptide such as
CC LAMP-1. Also described are methods of assaying the specific binding
CC affinity of the PI3-kinase binding partner. Such modulators are useful
CC for the treatment of diseases characterised by the undesirable or
CC excessive activity of PI3Kdelta. For example the modulators can be used
CC for inhibiting the growth or proliferation of cancer cells
CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC and Type I diabetes mellitus. The present sequence represents human
CC p110beta isoform of PI3K.
XX
SQ Sequence 1070 AA;
XX
Query Match 34.4%; Score 1966; DB 23; Length 1070;
Best Local Similarity 40.1%; Pred. No. 4, 9e-176;
Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;

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QY 365 EPLCDNVNTQVPCSNPRNBNML-----NDYIYIPDLPPAARLCLISCV---KRRKG 414
DB 379 KKLCAORSTD---SPNCPFTFELFNDLWDFDIQMRNLPRWTRICIVIEFTYKMSRSKKS 435
QY 415 AKEEHC-----PLAGNINILFDYITLVSGKALNLMWPVPHGLE--DLNIPGVY 462
DB 436 SNNKDIATKQVPVKNKPLAMVNTTTFDHKDLRTGHTLTWTYADDIQSVEVEHPAGTI 495
QY 463 GSNPNKETPCLLEEFDFSS---VVKFPMDSVIEEHANWSVSREAGFSYSHAGLSNRLAR 519
DB 496 EPNPRKE-ECALVDLFTLSSGTGYVRPSEEVLYQVA---ADRDQ-----VNLQR 542
QY 520 DNELRENDKQDLAICTR---DPLSEITQEKDFLMSHRHYCV-TIPELLPKLLSVKM 574
DB 543 QLAGPEKPIELKELMANVYTGDKIYEMVDNRNAVIERENDILRELPEELSLILHCYVM 602
QY 575 NSRDEVANQWYCLVADWPPIKPEQAMELLDCNYPMPWGRGAVNRLKLYLDDKLSQVLIQ 634
DB 603 KERDDVADMYVLYKQWPLISIERSELDYAVPDPVARRPARRICUH-FLKDEDLTYLLQ 661
QY 635 LVQVLKVEQYLDNLVFLFKKALTNRIGHFFFMHLKSEMNKTVSQRFGILLSEYGRA 694
DB 662 LVQALKHESYLESLSLVFELERALNRIGHFFFMHLKSEMNKTVSQRFGILLSEYGRA 721
QY 695 CGNYTLHLNRQVAMEKYLTLTDLKQEKDETOQVQMKFLVQGMRRPDMALQGFLLSP 754
DB 722 CKRHVAPLRKQHLVLEKLGKQSLIAKKGSKKXYKTMLODFLRDQNSAVF---QNTQNP 777
QY 755 LNFPAHQGNRLKECRIMSSAKRPLYMNMENPDMISLLFQNNELIKNGDDLRQDMTL 814
DB 778 LNFSPKSGTTPDRCKVMSKMRPLWVVFENAVUNA---SDVHLLIFKNDLDRQDMTL 833
QY 815 QIIRIMENIWOQGLDLFMLPYGLSIGDCVGLIEVVRNNGHTIMQJCKGGLGALQ-FN 873
DB 834 QMLRVADQMLKRGKGMDFRKNVYICISWESLGMIEVVRNNAETIANIOCKGMSATSPFK 893
QY 874 SHTLHQLKDKNK-GEIYDAIDLFTSCAGYCVATFILLIGDRHNSNINVKDQGLFHI 932
DB 894 KGLSLTMLKEHNRPADKLANKAINEFTLSCAGYCVATVGLVADRHSNINVKNGQLFHI 953
QY 933 DEGHFIDHKKKKKGYRERVPFLTODFLVLSKGAOCEKTKTEPERFQMCYKAYLAIR 992
DB 954 DREHILGHFEKELGVRRERVPFLTDFVYVINKGEND-RESKEFCHFOELCERAFVLR 1012
QY 993 QHANLEFINFSMILGSGMPELQSFDDIAYIRKTLALDKTEQALAEYPMQMDAHHGWT 1052
DB 1013 KHGCLLSLFSMWISITGLPELSEKLDYLRFTLVLDYTEKAREHPRAKFSBALANSWK 1072
QY 1053 TKMDWIFHTIKOH 1065
DB 1073 TSLMWASHNFSKN 1085

RESULT 15
AAW90089 standard; Protein; 1101 AA.
ID AAW90089;
AC AAW90089;
XX
XX
XX 09-MAR-1999 (first entry)
DE Human G-protein regulated PI3K p120 adapter subunit protein.
XX
XX Phosphoinositide 3-hydroxylase; PI3K; trimeric G protein; human;
XX adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
XX detection; diagnosis; activation disorder; haematopoietic system;
XX treatment; immune disorder; inflammation; arthritis; septic shock;
XX adult respiratory distress syndrome; pneumonia; asthma; allergy;
XX reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
OS Homo sapiens.
XX
XX US5856132-A.

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XX 05-JAN-1999.
PD 15-AUG-1997; 97US-0916917.
XX
PE 15-AUG-1997; 97US-0916917.
XX
XX 15-AUG-1997; 97US-0916917.
PR 27-JUN-1996; 96US-0672211.
XX
PA (ONXX-) ONXX PHARM.
XX
XX BrasseLmann S, Hawkins PT, Stephens L;
XX WPI; 1999-105107/09.
DR N-PSDB; AAW74104.
XX
PT Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT in treatment and diagnosis of immune system disorders, e.g.
PT arthritis, cancer and Alzheimer's disease
XX
PS Claim 15; Fig 13; 75pp; English.
XX
XX This sequence represents a novel catalytic subunit, p120, from human
XX phosphoinositide 3-hydroxylase (PI3K) which is regulated by beta-gamma
XX subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
XX their fragments, are used as probes and primers for identifying p101 or
XX p120 gene mutations, allelic variations or regulatory defects,
XX particularly for the diagnosis of activation disorders (or
XX susceptibility) in cells of the haematopoietic system. The related
XX proteins, antibodies, agonists and antagonists can be used similarly. The
XX p101 and p120 proteins, peptides or fusion proteins are used to treat or
XX screen for potential agents for treating immune disorders, particularly
XX inflammation, e.g. arthritis, septic shock, adult respiratory distress
XX syndrome, pneumonia, asthma, allergies, reperfusion injury,
XX atherosclerosis, Alzheimer's disease and cancer.
XX
SQ Sequence 1101 AA.

Query Match 25.7%; Score 1467; DB 20; Length 1101;
Best Local Similarity 35.3%; Pred. No. 2,8e-130;
Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;

QY 107 NREKILNEIGFALIMPCEFDVMDKPEVODRRRIILNVCKEAVLDRLNSHRAMY 166
DB 143 SEESQAFQQLTRLTIDYDVTDSNVHDELEFRRLGVPRRAEVSRD-----PKLYA 196
QY 167 YEPNVESSPELPHGIYNKLDKQIIVIVIVIVSPPNDKOKYTLKINHDCVPEQVIAEAR 226
DB 197 MHPWVTSKP-LPEYLMKTIANNCTFIVL-----HRTTSQITKVSPPDTFGAILQSF 249
QY 227 K-KTRSMILSSQQLKLVLEIQKYLIVYCCGDEYFLKRYPLSQYKTYIRSCIMGRMEN 284
DB 250 KMAKKKSLMDIPES-----QSEODFVLVCGSDVETLGPKNQWVRHCHIKNEEIH 303
QY 285 LML-----MAKESLSQLEPM--DCFTMPSYRRISTARPNYNG-----TSTSLVINS 332
DB 304 VVLDTPPPDALDBVAKKEWPLVDDCTGVTHQLT-----IHGKHESVFTVSLMDCOR 358
QY 333 ALRIKILCATYVNVNIRID-----KIYVRIGIYHSGEPLCDNVNTQVPCSNPR 382
DB 359 KFRVRK-----IRGIDIPVLRPNRDLTVYFVEANIGHQGVLCQRTSPKPFEEVL 408
QY 383 VNEWLNLYDIYIDLPRAAFLCISGVK---GRKAKEHRCPLAWGNINLFDYDTLV- 437
DB 409 MWVWLEFSIKIDLPGLALNIQICGKAPALSSKASAPSSSESGKVRLLYYVLLLI 468
QY 438 -----SGKMLNIMPVPHGED--LNLPIGVY-GSNPNKE-TPELEFPDFSSVVKF 486
DB 469 DHRPLLRGEVLYLHMWISGKEDQSFADKULTATNPDKNSISITLIDNYCHPIL 528
QY 487 PDMSVIEEHANWSVSREAGFSYSHAGLSNRLARNDLENDKEQULRAICTRDPLSEITEQ 546
DB 529 PKHQPTPDEGDRV-----RAEMPNQLR-----KQLEAIATATPILNLTAE 569

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QY 547 EKDFLMSHRHYCTIPEILPKLLSYKNSRDEVAQWCL-----VKDWPPIKPEQAMEL 601
DB 570 DKELLMHFRPESJLKHFKAYPKLSSVKNQGEIVAKTYQLARREYWDOSALDVLGTLMO 629
QY 602 LDCNYPDPWVGFVAVRCLERYLTDDKLSQYLLQVLKYEQYLDNLVRFLLKALTNO 661
DB 630 LDCNFSDEENRAIVAVOKLES-LEDDDVLYLQVLQVAKPEPYHDSALAFLLKRGIRNK 688
QY 662 RIGHFFFWHLKSEM-HNKTVSQRPGLLSEYCRACGYLKH-LNRQVEAMEKILNT-DI 718
DB 689 RIGHFLFWFLRSEIAOSRHYQORFAVILEAYLRGCGTAMLDFTQOVQVLEMLQKVTLDI 748
QY 719 --LKOEKXDETOKY--OMKFLVEQMRPDMFMDALQGFSLSPNPAHQULGNLLECRIMSS 774
DB 749 KSLSAEKYDVSSOVISOLKOKLEMLQNSQLPES---FRVYPDPGLKAGALALEKCKYMAS 805
QY 775 AKRPLMLNWE--NPDIMSELLFONNE--IFKNGDDLRODMLTLQIIRIMENIWONQGL 829
DB 806 KKKPLMEFPKCADPTALS-----NETIGIIFKHGDDLRODMLILQILRIMESIMETESL 859
QY 830 DLRLMPYGLSIGDCVGLIEVVRNSHTIMQI-OCKGGLKCALQPNSHTLQOMLKDN-KG 887
DB 860 DLCLPYGCIISTGDKIMIEIVKDATTIAKIQOSTVANTGA--PKDEVILNHWLKEKSPTE 917
QY 888 EIVYNAIDLFTRGAGYCVATFIIIGDRHNSNIMVKDDGOLFRIIDFGHFLDHKKKKFGY 947
DB 918 EKFOAAVERFYSCAGYCVATFVLIGDRHNDNIMITETGNLFHIDFGHILGNKXFLGI 977
QY 948 KREVRPVLTDQFLIVISKGAQECTKREFRFOEMCYKAYLAIRQANLFINLPSMMLG 1007
DB 978 NKEVRPVLTPDFLFWMGTSKKTSP--HFQKFODICVKAYLALRHHTNLLIILFSWMLM 1035
QY 1008 SCMPLOSFDIAYIRKTLADKTEQEALEYFMKQMDAHGCGWTKKMDIENHTI 1062
DB 1036 TGMPLTSKEDIERYIRDALTVGKNEEDAKKYFLDOIIEVCRDKGWTQVQPMFLHIV 1090

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Job time : 52 secs